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(74) Agents: **BASTIAN, Kevin, L.** et al.; Townsend and Townsend and Crew LLP, Two Embarcadero Center, 8th Floor, San Francisco, CA 94111 (US).

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(54) Title: METHODS OF DIAGNOSIS OF OVARIAN CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF OVARIAN CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in ovarian cancer. Related methods and compositions that can be used for diagnosis and treatment of ovarian cancer are disclosed. Also described herein are methods that can be used to identify modulators of ovarian cancer.



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INTERNATIONAL SEARCH REPORT

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A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C12Q 1/68; C07H 21/04

US CL : 435/6, 91.1; 536/23.1

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6, 91.1; 536/23.1

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Continuation Sheet

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WU, D. et al. Characterization and Molecular Cloning of a Putative Binding Protein for Heparin-binding Growth Factors. The Journal of Biological Chemistry. 05 September 1991, Vol. 266, No. 25, pages 16778-16785, see especially page 16778, col. 1, page 16783, Fig. 7, Fig. 8.	1-5, 9-12
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Y	US 5,700,637 A (SOUTHERN) 23 December 1997 (23.12.1997) see whole document.	6
Y		6

☐ Further documents are listed in the continuation of Box C.

☐ See patent family annex.

Special categories of cited documents:	
* "A" document defining the general state of the art which is not considered to be of particular relevance	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"E" earlier application or patent published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O" document referring to an oral disclosure, use, exhibition or other means	"&" document member of the same patent family
"P" document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

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INTERNATIONAL SEARCH REPORT

International application No.

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Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-12, directed to heparin binding growth factor binding protein

Remark on Protest

☐
☐

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

Groups 1-12000, claim(s) 1-12, drawn to nucleic acids and methods of detecting nucleic acids. It is noted that each group named above corresponds to each of the genes or nucleic acids set forth in tables 1-26. Therefore, if applicant does not choose to pay additional fees for search, Group 1 and claims 1-12 will be searched to the extent that they apply to heparin binding growth factor. If applicant wishes to elect and pay for additional groups for search, applicant is requested to indicate which nucleic acid from tables 1-26 are elected.

Groups 12001-24000, claim(s) 13 and 23, drawn to polypeptides and methods of detecting polypeptides. It is noted that each group named above corresponds to proteins encoded by each of the genes or nucleic acids set forth in tables 1-26. Therefore, if applicant wishes to elect and pay for additional groups for search, applicant is requested to indicate which nucleic acid from tables 1-26 are elected.

Groups 24001-36000, claim(s) 14-22, drawn to antibodies and methods of using antibodies. It is noted that each group named above corresponds to an antibody that binds a protein encoded by each of the genes or nucleic acids set forth in tables 1-26. Therefore, if applicant wishes to elect and pay for additional groups for search, applicant is requested to indicate which nucleic acid from tables 1-26 are elected.

Groups 36001-48000, claim(s) 24, drawn to drug screening assays. It is noted that each groups named above correspond to detection of gene expression of each of the genes or nucleic acids set forth in tables 1-26. If applicant wishes to elect and pay for additional groups for search, applicant is requested to indicate which nucleic acid from tables 1-26 are elected.

The inventions listed as Groups 1-48000 do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: The products claimed in groups 1-12000 (see e.g., claim 1) include genes or nucleic acid sequences which are both structurally and functionally unrelated to any of the other nucleic acids in the tables. As such the products of groups 1-12000 do not represent a contribution over the prior art, the claims lack a special technical feature that is the same as or that corresponds to a special technical feature of the other claimed inventions. Thus there is no special technical feature linking the recited Groups, as would be necessary to fulfill the requirement for unity of invention.

Groups 1-36000 are additionally drawn to multiple distinct products lacking the same or corresponding special technical features. The nucleic acids of Groups 1-12000 are composed of nucleotides and function in, e.g., methods of nucleic acid hybridization or amplification. The polypeptides of groups 12001-24000, which are composed of amino acids are structurally distinct molecules from polynucleotides or antibodies and can function in, e.g. catalysis of reactions. While the inventions of both groups 12001-24000 and groups 24001-36000 are polypeptides, in this instance the polypeptides of groups 12001-24000 are single chain molecules whereas the polypeptides of groups 24001-36000 encompasses antibodies including IgG which comprises 2 heavy and 2 light chains containing constant and variable regions, and including framework regions which act as a scaffold for the 6 complementarity determining regions (CDRs) that function to bind an epitope, and can function, e.g. in eliciting an immune response. Thus the polypeptides of groups 12001-24000 and the antibodies of groups 24001-36000 are structurally distinct molecules. As the products of the different sets of groups differ from each other in structure, function, and effect, they do not belong to a recognized class of chemical compounds, or have both a "common property or activity" and a common structure, as would be required to show that the inventions are "of a similar nature".

Further, the methods of Groups 36001-48000 do not require either the peptides of groups 12001-24000 or the antibodies of groups 24001-36000. Further, the methods of groups 36001-48000 (involve administering a test compound) have different objectives and require different process steps than the methods or nucleic acids of groups 1-12000. Further, the methods of groups 1-12000 do not require the method steps of groups 36001-48000. In addition to differences in objectives, effects, and method steps, it is again noted that the claims of the present groups are not directed to the detection or identification of molecules having the same or common special technical feature, for the reasons discussed above.

INTERNATIONAL SEARCH REPORT

PCT/US02/19297

Continuation of B. FIELDS SEARCHED Item 3:
medline, caplus, NCBI
search terms: heparin binding growth factor binding protein

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| 60/372,246 | 12 April 2002 (12.04.2002) | US |
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(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in ovarian cancer. Related methods and compositions that can be used for diagnosis and treatment of ovarian cancer are disclosed. Also described herein are methods that can be used to identify modulators of ovarian cancer.



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METHODS OF DIAGNOSIS OF OVARIAN CANCER, COMPOSITIONS AND
METHODS OF SCREENING FOR MODULATORS OF OVARIAN CANCER

CROSS-REFERENCES TO RELATED APPLICATIONS.

5 This application is related to USSN 60/299,234, filed June 18, 2001; USSN 60/315,287, filed August 27, 2001; USSN 60/317,544, filed September 5, 2001; USSN 60/350,666, filed November 13, 2001; and USSN 60/372,246, filed April 12, 2002, each of which is incorporated herein by reference for all purposes.

10 FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in ovarian cancer; and to the use of such expression profiles and compositions in the diagnosis, prognosis, and therapy of ovarian cancer. The invention further relates to methods for
15 identifying and using agents and/or targets that inhibit ovarian cancer.

BACKGROUND OF THE INVENTION

Ovarian cancer is the sixth most common cancer in women, accounting for 6% of all female cancers. It ranks fifth as the cause of cancer death in women. The American Cancer
20 Society predicts that there will be about 23,100 new cases of ovarian cancer in this country in the year 2000 and about 14,000 women will die of the disease. Because many ovarian cancers cannot be detected early in their development, they account for a disproportionate number of fatal cancers, being responsible for almost half the deaths from cancer of the female genital tract; more deaths than any other reproductive organ cancer.

25 Most patients with epithelial ovarian cancer, the predominant form, are asymptomatic in early-stage disease and usually present with stage III or IV disease. Their five-year survival is less than 25%, with lower survival among African-American women. The minority of patients discovered with early-stage disease have a five-year survival rate of 80%-90%. See, Parker, et. al., (1997) "Cancer Statistics, 1997" CA Cancer J. Clin. 47:5-27.

30 In the absence of a family history of ovarian cancer, lifetime risk of ovarian cancer is 1/70. Risk factors include familial cancer syndromes (risk of up to 82% by age 70 in women

with hereditary breast/ovarian syndrome); family history (1.4% lifetime risk with no affected relatives, 5% with one affected relative, 7% with two affected relatives; Kerlikowske, et.al. (1992) Obstet. Gynecol. 80:700-707); nulliparity; advancing age; obesity; personal history of breast, endometrial, or colorectal cancer; fewer pregnancies; or older age (>35 years) at first pregnancy. However, 95% of all ovarian cancers occur in women without risk factors. Use of hormonal contraceptives, oophorectomy, and tubal sterilization reduce risk of ovarian cancer (Kerlikowske, et. al. (1992) Obstet. Gynecol. 80:700-707; Grimes (1992) Am J. Obstet. Gynecol. 166:1950-1954; Hankinson, et. al. (1993) JAMA 270:2813-2818); however, even bilateral oophorectomy may not be completely effective in preventing ovarian cancer.

Treatment of ovarian cancer consists largely of surgical oophorectomy, anti-hormone therapy, and/or chemotherapy. Although many ovarian cancer patients are effectively treated, the current therapies can all induce serious side effects which diminish quality of life. Deciding on a particular course of treatment is typically based on a variety of prognostic parameters and markers (Fitzgibbons, et al. (2000) Arch. Pathol. Lab. Med. 124:966-978; Hamilton and Piccart (2000) Ann. Oncol. 11:647-663), including genetic predisposition markers BRCA-1 and BRCA-2 (Robson (2000) J. Clin. Oncol. 18:113sup-118sup).

The identification of novel therapeutic targets and diagnostic markers is essential for improving the current treatment of ovarian cancer patients. Recent advances in molecular medicine have increased the interest in tumor-specific cell surface antigens that could serve as targets for various immunotherapeutic or small molecule strategies. Antigens suitable for immunotherapeutic strategies should be highly expressed in cancer tissues and ideally not expressed in normal adult tissues. Expression in tissues that are dispensable for life, however, may be tolerated. Examples of such antigens include Her2/neu and the B-cell antigen CD20. Humanized monoclonal antibodies directed to Her2/neu

(Herceptin®/trastuzumab) are currently in use for the treatment of metastatic breast cancer. Ross and Fletcher (1998) Stem Cells 16:413-428. Similarly, anti-CD20 monoclonal antibodies (Rituxin®/rituximab) are used to effectively treat non-Hodgkin's lymphoma. Maloney, et al. (1997) Blood 90:2188-2195; Leget and Czuczman (1998) Curr. Opin. Oncol. 10:548-551.

Potential immunotherapeutic targets have been identified for ovarian cancer. One such target is polymorphic epithelial mucin (MUC1). MUC1 is a transmembrane protein, present at the apical surface of glandular epithelial cells. It is often overexpressed in ovarian cancer, and typically exhibits an altered glycosylation pattern, resulting in an antigenically

distinct molecule, and is in early clinical trials as a vaccine target. Gilewski, et al. (2000) Clin. Cancer Res. 6:1693-1701; Scholl, et al. (2000) J. Immunother. 23:570-580. The tumor-expressed protein is often cleaved into the circulation, where it is detectable as the tumor marker, CA 15-3. See, e.g., Bon, et al. (1997) Clin. Chem. 43:585-593. However, many patients have tumors that express neither HER2 nor MUC-1; therefore, it is clear that other targets need to be identified to manage localized and metastatic disease.

Mutations in both BRCA1 and BRCA2 are associated with increased susceptibility to ovarian cancer. Mutations in BRCA1 occur in approximately 5 percent (95 percent confidence interval, 3 to 8 percent) of women in whom ovarian cancer is diagnosed before the age of 70 years. See Stratton, et al. (1997) N.E.J. Med. 336:1125-1130. And, in BRCA1 gene carriers, the risk for developing ovarian cancer is .63. See Easton (1995) Am. J. Hum. Genet. 56:267-xxx; and Elit (2001) Can. Fam. Physician 47:778-84.

Other biochemical markers such as CA125 have been reported to be associated with ovarian cancer, but they are not absolute indicators of disease. Although roughly 85% of women with clinically apparent ovarian cancer have increased levels of CA125, CA125 is also increased during the first trimester of pregnancy, during menstruation, in the presence of non-cancerous illnesses, and in cancers of other sites.

While industry and academia have identified novel gene sequences, there has not been an equal effort exerted to identify the function of these novel sequences. The elucidation of a role for novel proteins and compounds in disease states for identification of therapeutic targets and diagnostic markers is essential for improving the current treatment of ovarian cancer patients. Accordingly, provided herein are molecular targets for therapeutic intervention in ovarian and other cancers. Additionally, provided herein are methods that can be used in diagnosis and prognosis of ovarian cancer. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate ovarian cancer.

SUMMARY OF THE INVENTION

The present invention therefore provides nucleotide sequences of genes that are up- and down-regulated in ovarian cancer cells. Such genes are useful for diagnostic purposes, and also as targets for screening for therapeutic compounds that modulate ovarian cancer, such as hormones or antibodies. The methods of detecting nucleic acids of the invention or their encoded proteins can be used for many purposes, e.g., early detection of ovarian cancers, monitoring and early detection of relapse following treatment, monitoring response to therapy, selecting patients for postoperative chemotherapy or radiation therapy, selecting therapy, determining tumor prognosis, treatment, or response to treatment (of primary or metastatic tumors), and early detection of pre-cancerous lesions. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

In one aspect, the present invention provides a method of detecting an ovarian cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26.

In one embodiment, the present invention provides a method of determining the level of an ovarian cancer associated transcript in a cell from a patient.

In one embodiment, the present invention provides a method of detecting an ovarian cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26.

In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1-26.

In one embodiment, the biological sample is a tissue sample. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label.

In one embodiment, the polynucleotide is immobilized on a solid surface.

In one embodiment, the patient is undergoing a therapeutic regimen to treat ovarian cancer. In another embodiment, the patient is suspected of having metastatic ovarian cancer.

In one embodiment, the patient is a human.

In one embodiment, the ovarian cancer associated transcript is mRNA.

In one embodiment, the method further comprises the step of amplifying nucleic acids

before the step of contacting the biological sample with the polynucleotide.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of ovarian cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of an ovarian cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26, thereby monitoring the efficacy of the therapy. In a further embodiment, the patient has metastatic ovarian cancer. In a further embodiment, the patient has a drug resistant form of ovarian cancer.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the ovarian cancer-associated transcript to a level of the ovarian cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

Additionally, provided herein is a method of evaluating the effect of a candidate ovarian cancer drug comprising administering the drug to a patient and removing a cell sample from the patient. The expression profile of the cell is then determined. This method may further comprise comparing the expression profile to an expression profile of a healthy individual. In a preferred embodiment, said expression profile includes a gene of Tables 1-26.

In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1-26.

In one embodiment, an expression vector or cell comprises the isolated nucleic acid.

In one aspect, the present invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-26.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-26.

In one embodiment, the antibody is conjugated to an effector component, e.g., a fluorescent label, a radioisotope or a cytotoxic chemical.

In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

In one aspect, the present invention provides a method of detecting an ovarian cancer cell in a biological sample from a patient, the method comprising contacting the biological

sample with an antibody as described herein.

In another aspect, the present invention provides a method of detecting antibodies specific to ovarian cancer in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprising a sequence from

5 Tables 1-26.

In another aspect, the present invention provides a method for identifying a compound that modulates an ovarian cancer-associated polypeptide, the method comprising the steps of: (i) contacting the compound with an ovarian cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical
10 to a sequence as shown in Tables 1-26; and (ii) determining the functional effect of the compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect.

In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell
15 membrane. In another embodiment, the polypeptide is recombinant.

In one embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting proliferation of an ovarian cancer-associated cell to treat ovarian cancer in a patient, the method
20 comprising the step of administering to the subject a therapeutically effective amount of a compound identified as described herein.

In one embodiment, the compound is an antibody.

In another aspect, the present invention provides a drug screening assay comprising the steps of: (i) administering a test compound to a mammal having ovarian cancer or to a cell sample
25 isolated from; (ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell sample or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of ovarian cancer.

30 In one embodiment, the control is a mammal with ovarian cancer or a cell sample that has not been treated with the test compound. In another embodiment, the control is a normal cell or mammal, or is non-malignant tissue.

In one embodiment, the test compound is administered in varying amounts or

concentrations. In another embodiment, the test compound is administered for varying time periods. In another embodiment, the comparison can occur after addition or removal of the drug candidate.

5 In one embodiment, the levels of a plurality of polynucleotides that selectively hybridize to a sequence at least 80% identical to a sequence as shown in Tables 1-26 are individually compared to their respective levels in a control cell sample or mammal. In a preferred embodiment the plurality of polynucleotides is from three to ten.

10 In another aspect, the present invention provides a method for treating a mammal having ovarian cancer comprising administering a compound identified by the assay described herein.

In another aspect, the present invention provides a pharmaceutical composition for treating a mammal having ovarian cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

15 In one aspect, the present invention provides a method of screening drug candidates by providing a cell expressing a gene that is up- and down-regulated as in an ovarian cancer. In one embodiment, a gene is selected from Tables 1-26. The method further includes adding a drug candidate to the cell and determining the effect of the drug candidate on the expression of the expression profile gene.

20 In one embodiment, the method of screening drug candidates includes comparing the level of expression in the absence of the drug candidate to the level of expression in the presence of the drug candidate, wherein the concentration of the drug candidate can vary when present, and wherein the comparison can occur after addition or removal of the drug candidate. In a preferred embodiment, the cell expresses at least two expression profile genes. The profile genes may show an increase or decrease.

25 Also provided is a method of evaluating the effect of a candidate ovarian cancer drug comprising administering the drug to a transgenic animal expressing or over-expressing the ovarian cancer modulatory protein, or an animal lacking the ovarian cancer modulatory protein, for example as a result of a gene knockout.

30 Moreover, provided herein is a biochip comprising one or more nucleic acid segments of Tables 1-26, wherein the biochip comprises fewer than 1000 nucleic acid probes. Preferably, at least two nucleic acid segments are included. More preferably, at least three nucleic acid segments are included.

Furthermore, a method of diagnosing a disorder associated with ovarian cancer is

provided. The method comprises determining the expression of a gene of Tables 1-26 in a first tissue type of a first individual, and comparing the distribution to the expression of the gene from a second normal tissue type from the first individual or a second unaffected individual. A difference in the expression indicates that the first individual has a disorder associated with ovarian cancer.

In a further embodiment, the biochip also includes a polynucleotide sequence of a gene that is not up- and down-regulated in ovarian cancer.

In one embodiment a method for screening for a bioactive agent capable of interfering with the binding of an ovarian cancer modulating protein (ovarian cancer modulatory protein) or a fragment thereof and an antibody which binds to said ovarian cancer modulatory protein or fragment thereof. In a preferred embodiment, the method comprises combining an ovarian cancer modulatory protein or fragment thereof, a candidate bioactive agent and an antibody which binds to said ovarian cancer modulatory protein or fragment thereof. The method further includes determining the binding of said ovarian cancer modulatory protein or fragment thereof and said antibody. Wherein there is a change in binding, an agent is identified as an interfering agent. The interfering agent can be an agonist or an antagonist. Preferably, the agent inhibits ovarian cancer.

Also provided herein are methods of eliciting an immune response in an individual. In one embodiment a method provided herein comprises administering to an individual a composition comprising an ovarian cancer modulating protein, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from those of Tables 1-26.

Further provided herein are compositions capable of eliciting an immune response in an individual. In one embodiment, a composition provided herein comprises an ovarian cancer modulating protein, preferably encoded by a nucleic acid of Table 1-26 or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, said composition comprises a nucleic acid comprising a sequence encoding an ovarian cancer modulating protein, preferably selected from the nucleic acids of Tables 1-26, and a pharmaceutically acceptable carrier.

Also provided are methods of neutralizing the effect of an ovarian cancer protein, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization. In another embodiment, the protein is encoded by a nucleic acid selected from those of Tables 1-26.

In another aspect of the invention, a method of treating an individual for ovarian cancer is provided. In one embodiment, the method comprises administering to said individual an inhibitor of an ovarian cancer modulating protein. In another embodiment, the method comprises administering to a patient having ovarian cancer an antibody to an ovarian cancer modulating protein conjugated to a therapeutic moiety. Such a therapeutic moiety can be a cytotoxic agent or a radioisotope.

5

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and prognosis evaluation for ovarian cancer (OC), including metastatic ovarian cancer, as well as methods for screening for compositions which modulate ovarian cancer. Also provided are methods for treating ovarian cancer and related conditions, e.g., ovarian carcinoma (e.g., epithelial (including malignant serous tumors, malignant mucinous tumors, and malignant endometrioid tumors), germ cell (including teratomas, choriocarcinomas, polyembryomas, embryonal carcinoma, endodermal sinus tumor, dysgerminoma, and gonadoblastoma), and stromal carcinomas (e.g., granulosa stromal cell tumors)), fallopian tube carcinoma, and peritoneal carcinoma.

Tables 1-26 provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in ovarian cancer samples. Tables 1-26 also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster.

Definitions

The term "ovarian cancer protein" or "ovarian cancer polynucleotide" or "ovarian cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologues that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a gene of Tables 1-26; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-26, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1-26 and conservatively modified variants thereof; or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-26. A polynucleotide or polypeptide

sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. An "ovarian cancer polypeptide" and an "ovarian cancer polynucleotide," include both naturally occurring or recombinant forms.

5 A "full length" ovarian cancer protein or nucleic acid refers to an ovarian cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains all of the elements normally contained in one or more naturally occurring, wild type ovarian cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translation processing or splicing, including alternative splicing.

10 "Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of an ovarian cancer protein, polynucleotide or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes,
15 blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or a bird; reptile; or fish. Livestock and domestic animals are of
20 particular interest.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the
25 methods of the invention in vivo. Archival tissues, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same
30 (e.g., about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default

parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site <http://www.ncbi.nlm.nih.gov/BLAST/> or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes sequences that have deletions and/or additions, as well as those that have substitutions, as well as naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of one of the number of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482-489, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443-453, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l. Acad. Sci. USA 85:2444-2448, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology Lippincott.

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990)

J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This

5 algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing
10 them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word
15 hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences)
20 uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a word length of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Nat'l Acad. Sci. USA 89:10915-919) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

25 The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) Proc. Nat'l Acad. Sci. USA 90:5873-5887). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid
30 is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be large negative numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions, as described below. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells in vivo, and the like. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells, such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant from the composition to be purified. In this sense, purification does not require that the purified compound be homogenous, e.g., 100% pure.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymers.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ -

5 carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain the same basic
10 chemical structure as a naturally occurring amino acid. Amino acid mimetics refers to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that functions similarly to a naturally occurring amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical
15 Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino
20 acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can
25 be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and
30 TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions, or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds, or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton (1984) Proteins Freeman).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts, et al. (2001) Molecular Biology of the Cell (4th ed.) Garland Pub.; and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules Freeman. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the non-covalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50, or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds,

although in some cases, nucleic acid analogs are included that may have at least one different linkage, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford University Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 of Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ASC Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

A variety of references disclose such nucleic acid analogs, including, e.g., phosphoramidate (Beaucage, et al. (1993) Tetrahedron 49:1925-1963 and references therein; Letsinger (1970) J. Org. Chem. 35:3800-3803; Sprinzl, et al. (1977) Eur. J. Biochem. 81:579-589; Letsinger, et al. (1986) Nucl. Acids Res. 14:3487-499; Sawai, et al. (1984) Chem. Lett. 805; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; and Pauwels, et al. (1986), Chemica Scripta 26:141-149), phosphorothioate (Mag, et al. (1991) Nucl. Acids Res. 19:1437-441; and U.S. Patent No. 5,644,048), phosphorodithioate (Brill, et al. (1989) J. Am. Chem. Soc. 111:2321-2322), O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford Univ. Press), and peptide nucleic acid backbones and linkages (see Egholm (1992) J. Am. Chem. Soc. 114:1895-897; Meier, et al. (1992) Angew. Chem. Int. Ed. Engl. 31:1008-1010; Nielsen (1993) Nature, 365:566-568; Carlsson, et al. (1996) Nature 380:207, each of which is incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:6097-101; non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141 and 4,469,863; Kiedrowski, et al. (1991) Angew. Chem. Intl. Ed. English 30:423-426; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; Jung, et al. (1994) Nucleoside and Nucleotide 13:1597; Chapters 2 and 3, in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ASC Symposium Series 580; Mesmaeker, et al. (1994) Bioorganic and Medicinal Chem. Lett. 4:395-398; Jeffs,

et al. (1994) J. Biomolecular NMR 34:17-xx; Horn, et al. (1996) Tetrahedron Lett. 37:743-xxx) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ASC Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins, et al. (1995) Chem. Soc. Rev. pp 169-176). Several nucleic acid analogs are described in Rawls (p. 35 June 2, 1997) C&E News. Each of these references is hereby expressly incorporated by reference.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched base pairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic,

photochemical, biochemical, immunochemical, chemical, or other physical means. For example, useful labels include ^{32}P , fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to
5 detect antibodies specifically reactive with the peptide. The labels may be incorporated into the ovarian cancer nucleic acids, proteins and antibodies at any position. Any method known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter, et al. (1962) Nature 144:945-xxx; David, et al. (1974) Biochemistry 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth. 40:219-230; and Nygren (1982) J.
10 Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or non-covalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties
15 including radioactive compounds, fluorescent compounds, an enzyme or substrate, tags such as epitope tags, a toxin; activatable moieties, a chemotherapeutic agent; a lipase; an antibiotic; or a radioisotope emitting "hard" e.g., beta radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or non-covalently, through ionic, van der
20 Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of
25 binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (e.g., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not functionally interfere with
30 hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the

stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or
5 subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic
10 acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid, e.g., using
15 polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or
20 organism, it will replicate non-recombinantly, e.g., using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention. Similarly, a "recombinant protein" is a protein made using recombinant techniques, e.g., through the expression of a recombinant nucleic
25 acid as depicted above.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes
30 arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is defined as an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed operably linked to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Hybridization with Nucleic Probes (Laboratory Techniques in Biochemistry and Molecular Biology) (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target

sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., 10 to 50 nucleotides) and at least about 60° C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times background, preferably 10 times background

hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32-48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50° C to about 65° C, depending on the primer length and specificity.

Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90-95° C for 30-120 sec, an annealing phase lasting 30-120 sec, and an extension phase of about 72° C for 1-2 min. Protocols and guidelines for low and high stringency amplification reactions are available, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications Academic Press, N.Y.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is at least twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided, e.g., Ausubel, et al. (ed. 1991 and supplements) Current Protocols in Molecular Biology Lippincott.

The phrase "functional effects" in the context of assays for testing compounds that

modulate activity of an ovarian cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the ovarian cancer protein or nucleic acid, e.g., a functional, physical, physiological, or chemical effect, such as the ability to decrease ovarian cancer. It includes ligand binding activity; cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis, and other characteristics of ovarian cancer cells. "Functional effects" include in vitro, in vivo, and ex vivo activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of an ovarian cancer protein sequence, e.g., functional, enzymatic, physical, physiological, and chemical effects. Such functional effects can be measured by any means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the ovarian cancer protein; measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring cellular proliferation. Determination of the functional effect of a compound on ovarian cancer can also be performed using ovarian cancer assays known to those of skill in the art such as an in vitro assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis, and other characteristics of ovarian cancer cells. The functional effects can be evaluated by means known to those skilled in the art, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for ovarian cancer-associated sequences, measurement of RNA stability, or identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators", and "modulators" of ovarian cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using in vitro and in vivo assays of ovarian cancer polynucleotide and

polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of ovarian cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate ovarian cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of ovarian cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules, and the like. Assays for inhibitors and activators include, e.g., expressing the ovarian cancer protein in vitro, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of ovarian cancer can also be identified by incubating ovarian cancer cells with the test compound and determining increases or decreases in the expression of one or more ovarian cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50, or more ovarian cancer proteins, such as ovarian cancer proteins encoded by the sequences set out in Tables 1-26.

Samples or assays comprising ovarian cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25% or less. Activation of an ovarian cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more preferably 200-500% (e.g., 2-5 fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to a change in cell growth and proliferation characteristics in vitro or in vivo, e.g., cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, change in contact inhibition or density limitation of growth, loss of growth factor or serum requirements, change in cell morphology, gain or loss of immortalization, gain or loss of tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., pp. 231-241 in Freshney (1994) Culture of Animal Cells: A Manual of Basic Technique (3d ed.) Wiley-Liss.

"Tumor cell" refers to pre-cancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is typically associated with phenotypic changes, such as immortalization of cells, aberrant growth control, non-morphological changes, and/or malignancy. See, Freshney (1994) Culture of Animal Cells.

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See, e.g., Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself is a light chain joined to V_H -CH1 by a disulfide bond. The $F(ab)'_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region. See Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven. While various antibody fragments are defined in terms of the digestion of an intact antibody,

one of skill will appreciate that such fragments may be synthesized de novo either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized de novo using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries. See, e.g., McCafferty, et al. (1990) Nature 348:552-554.

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many techniques known in the art can be used (see, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al., pp. 77-96 in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; Coligan (1991) Current Protocols in Immunology Lippincott; Harlow and Lane (1988) Antibodies: A Laboratory Manual CSH Press; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.) Academic Press. Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Transgenic mice, or other organisms, e.g., other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens. See, e.g., McCafferty, et al. (1990) Nature 348:552-554; and Marks, et al. (1992) Biotechnology 10:779-783.

A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a portion thereof, is altered, replaced or exchanged with a variable region having a different or altered antigen specificity.

Identification of ovarian cancer-associated sequences

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is

characteristic of the state of the cell. That is, normal tissue (e.g., normal ovarian or other tissue) may be distinguished from cancerous or metastatic cancerous tissue of the ovarian, or ovarian cancer tissue or metastatic ovarian cancerous tissue can be compared with tissue samples of ovarian and other tissues from surviving cancer patients. By comparing

5 expression profiles of tissue in known different ovarian cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of a cancer.

The identification of sequences that are differentially expressed in ovarian cancer
10 versus non-ovarian cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate ovarian cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, does existing treatment induce expression of a target. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known
15 expression profiles. Metastatic tissue can also be analyzed to determine the stage of ovarian cancer in the tissue or origin of the primary tumor. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the ovarian cancer expression profile. This may be done by making biochips comprising sets of
20 the important ovarian cancer genes, which can then be used in these screens. These methods can also be based on evaluating protein expression; that is, protein expression levels of the ovarian cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the ovarian cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense or RNAi nucleic acids, or the
25 ovarian cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in ovarian cancer relative to normal tissues and/or non-malignant tissues, herein termed "ovarian cancer sequences." As outlined below, ovarian cancer
30 sequences include those that are up-regulated (e.g., expressed at a higher level) in ovarian cancer, as well as those that are down-regulated (e.g., expressed at a lower level). In a preferred embodiment, the ovarian cancer sequences are from humans; however, as will be appreciated by those in the art, ovarian cancer sequences from other organisms may be useful

in animal models of disease and drug evaluation; thus, other ovarian cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (e.g., dogs, cats, etc.). Ovarian cancer sequences, e.g., counterpart genes, from other organisms may be obtained using the techniques outlined below.

Ovarian cancer sequences can include both nucleic acid and amino acid sequences. Ovarian cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids. Screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the ovarian cancer sequences, are also provided.

An ovarian cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the ovarian cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

For identifying ovarian cancer-associated sequences, the ovarian cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing ovarian cancer samples with metastatic cancer samples from other cancers, such as lung, ovarian, gastrointestinal cancers, etc. Samples of different stages of ovarian cancer, e.g., survivor tissue, drug resistant states, and tissue undergoing metastasis, are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated for the preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal ovarian, but also including, and not limited to, lung, heart, brain, liver, ovarian, kidney, muscle, colon, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the ovarian cancer screen that are expressed in any significant amount in other tissues are removed from the profile, although in some embodiments, expression in non-essential tissues may be tolerated. That is, when screening for drugs, it is usually preferable that the target be disease specific, to minimize possible side

effects by interaction with target present in other organs.

In a preferred embodiment, ovarian cancer sequences are those that are up-regulated in ovarian cancer; that is, the expression of these genes is higher in the ovarian cancer tissue as compared to non-cancerous tissue. "Up-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. Other embodiments are directed to sequences up regulated in non-malignant conditions relative to normal.

Unigene cluster identification numbers and accession numbers herein refer to the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, et al. (1998) Nucl. Acids Res. 26:1-7; and <http://www.ncbi.nlm.nih.gov/>. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, e.g., FGENESH. See Salamov and Solovyev (2000) Genome Res. 10:516-522. In other situations, sequences have been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, ovarian cancer sequences are those that are down-regulated in ovarian cancer; that is, the expression of these genes is lower in ovarian cancer tissue as compared to non-cancerous tissue. "Down-regulation" as used herein often means at least about a two-fold change, preferably at least about a three-fold change, with at least about five-fold or higher being preferred.

Informatics

The ability to identify genes that are over or under expressed in ovarian cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. Expression profiles can be used in diagnostic or prognostic evaluation of patients with ovarian cancer. Subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson (June 11-12, 1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA) or in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable

exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes
5 at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database, and can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the
10 World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent to those of skill in the art that similar databases can be assembled for any assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or
15 absolute abundance of a variety of molecular and macromolecular species from a biological sample undergoing ovarian cancer, e.g., the identification of ovarian cancer-associated sequences described herein, provide an abundance of information which can be correlated with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological
20 status, and outcome data, among others. Although data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database
25 system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for
30 obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method

using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures.

Fundamentals of bioinformatics are provided, e.g., in Mount, et al. (2001)

Bioinformatics: Sequence and Genome Analysis CSH Press, NY; Durbin, et al. (eds. 1999)

Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids

Cambridge Univ. Press; Baxeavanis and Oeullette (eds. 1998) Bioinformatics: A Practical

Guide to the Analysis of Genes and Proteins (2d ed.) Wiley-Liss; Rashidi and Buehler (1999)

Bioinformatics: Basic Applications in Biological Science and Medicine CRC Press; Setubal,

et al. (eds 1997) Introduction to Computational Molecular Biology Brooks/Cole; Misener and

Krawetz (eds. 2000) Bioinformatics: Methods and Protocols Humana Press; Higgins and

Taylor (eds. 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical

Approach Oxford Univ. Press; Brown (2001) Bioinformatics: A Biologist's Guide to

Biocomputing and the Internet Eaton Pub.; Han and Kamber (2000) Data Mining: Concepts

and Techniques Kaufmann Pub.; and Waterman (1995) Introduction to Computational

Biology: Maps, Sequences, and Genomes Chap and Hall.

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for ovarian cancer. In another variation, assay records cross-tabulate one or more of the following parameters for a target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or

characteristic separation coordinate (e.g., electrophoretic or genomic position coordinates); (2) sample source; and (3) absolute and/or relative quantity of target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells)

composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal
5 includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of
10 identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

15 The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor
20 can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can
25 be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, e.g., which typically comprises one or more of: (1) a computer; (2) a stored bit pattern encoding a
30 collection of peptide sequence specificity records obtained by methods of the inventions, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

Characteristics of ovarian cancer-associated proteins

Ovarian cancer proteins of the present invention may be categorized as secreted proteins, transmembrane proteins, or intracellular proteins. In one embodiment, the ovarian cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or dysregulated cellular processes. See, e.g., Alberts, et al. (eds. 1994) Molecular Biology of the Cell (3d ed.) Garland. For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity, and the like. Intracellular proteins can also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are often involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden. See, e.g., Bateman, et al. (2000) Nuc. Acids Res. 28:263-266; Sonnhammer, et al. (1997) Proteins 28:405-420; Bateman, et al. (1999) Nuc. Acids Res. 27:260-262; and Sonnhammer, et al. (1998) Nuc. Acids Res. 26:320-

322.

In another preferred embodiment, the ovarian cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain.

However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site <http://psort.nibb.ac.jp/>). Important transmembrane protein receptors include, but are not limited to the insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, interleukin receptors, e.g., IL-1 receptor, IL-2 receptor, etc.

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their

cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules, or may be processed or shed to the blood stream. In this respect, they can mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via
5 a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Ovarian cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for immunotherapeutics, as are
10 described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins in situ. Alternatively, antibodies can also label intracellular proteins, in which case samples are typically permeabilized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual
15 fragment. Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful ovarian markers of disease.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be
20 secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the ovarian cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve
25 to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion into the blood stream), or exocrine (secretion, e.g., through a duct or to an adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts,
30 lacrimal glands, mammary glands, wax producing glands of the ear, etc.). Thus, secreted molecules often find use in modulating or altering numerous aspects of physiology. Ovarian cancer proteins that are secreted proteins are particularly preferred as good diagnostic markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be

antibody or small molecule therapeutic targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms, as protein or DNA vaccines.

Use of ovarian cancer nucleic acids

5 As described above, ovarian cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the ovarian cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on
10 the same molecule.

The ovarian cancer nucleic acid sequences of the invention, e.g., in Table 1-26, can be fragments of larger genes, e.g., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein,
15 extended sequences, in either direction, of the ovarian cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, et al., supra. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, <http://www.ncbi.nlm.nih.gov/UniGene/>).

20 Once the ovarian cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire ovarian cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised as a linear nucleic acid segment, the recombinant ovarian cancer nucleic acid can be further-used as a probe to identify and isolate other ovarian cancer
25 nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant ovarian cancer nucleic acids and proteins.

The ovarian cancer nucleic acids of the present invention are useful in several ways. In a first embodiment, nucleic acid probes to the ovarian cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for
30 administration, e.g., for gene therapy, vaccine, RNAi, and/or antisense applications. Alternatively, the ovarian cancer nucleic acids that include coding regions of ovarian cancer proteins can be put into expression vectors for the expression of ovarian cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to ovarian cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the ovarian cancer nucleic acids, e.g., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a particular target. The probes can be overlapping (e.g., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent

attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds.

- 5 Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

10 In general, the probes are attached to the biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified to contain
15 discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene,
20 polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. See, e.g., WO0055627 Reusable Low Fluorescent Plastic Biochip.

Generally the substrate is planar, although as will be appreciated by those in the art,
25 other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be
30 derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxyl groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using

functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers as are known in the art; e.g., homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases,
5 additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized as is known in the art, and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an
10 internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in
15 the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using well known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment
20 form the basis of the Affymetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of ovarian cancer-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, an ovarian cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or
25 PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of ovarian cancer-associated RNA. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative PCR are available. See, e.g., Innis, et al.(1990) PCR Protocols: A Guide to
30 Methods and Applications Academic Press.

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be

extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of

5 amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR; see Wu and Wallace (1989) Genomics 4:560-569; Landegren, et al. (1988) Science 241:1077-1980; and Barringer, et al. (1990) Gene 89:117-122), transcription amplification (Kwoh, et al. (1989) Proc. Nat'l Acad. Sci. USA 86:1173-1177), self-sustained

10 sequence replication (Guatelli, et al. (1990) Proc. Nat'l Acad. Sci. USA 87:1874-1878), dot PCR, linker adapter PCR, etc.

Expression of ovarian cancer proteins from nucleic acids

In a preferred embodiment, ovarian cancer nucleic acids, e.g., encoding ovarian

15 cancer proteins are used to make a variety of expression vectors to express ovarian cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known and are used to express proteins. See, e.g., Ausubel, supra; and Fernandez and Hoeffler (eds. 1999) Gene Expression Systems Academic Press. The expression vectors may be either self-replicating extrachromosomal vectors or

20 vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the ovarian cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an

25 operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a pre-sequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a pre-protein that participates

30 in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation; and two sequences may be operably linked when they are physically part of the same polymer. Generally,

“operably linked” means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the ovarian cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences typically encode constitutive or inducible promoters. The promoters may be naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, an expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a procaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are available. See, e.g., Fernandez and Hoeffler, *supra*.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The ovarian cancer proteins of the present invention are produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding an ovarian cancer protein, under the appropriate conditions to induce or cause expression of the ovarian cancer protein. Conditions appropriate for ovarian cancer protein expression will vary with

the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculovirus systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

In a preferred embodiment, the ovarian cancer proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral and adenoviral systems. One expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048, both of which are hereby expressly incorporated by reference. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter. See, e.g., Fernandez and Hoeffler, supra. Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, ovarian cancer proteins are expressed in bacterial systems. Bacterial expression systems are well known in the art. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters

are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences.

Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable.

5 The expression vector may also include a signal peptide sequence that provides for secretion of the ovarian cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been
10 transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin, and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and
15 include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others. See Fernandez and Hoeffler, supra. The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, ovarian cancer proteins are produced in insect cells. Expression
20 vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, an ovarian cancer protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*,
25 *Kluyveromyces fragilis* and *K. lactis*, *Pichia guillerimondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The ovarian cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the ovarian cancer protein may be fused to a carrier protein to form an
30 immunogen. Alternatively, the ovarian cancer protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the ovarian cancer protein is an ovarian cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In a preferred embodiment, the ovarian cancer protein is purified or isolated after expression. Ovarian cancer proteins may be isolated or purified in a variety of ways known to those skilled in the art depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the ovarian cancer protein may be purified using a standard anti-ovarian cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes (1982) Protein Purification Springer-Verlag. The degree of purification necessary will vary depending on the use of the ovarian cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the ovarian cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, etc.

Variants of ovarian cancer proteins

In one embodiment, the ovarian cancer proteins are derivative or variant ovarian cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative ovarian cancer peptide will often contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion, or deletion may occur at most any residue within the ovarian cancer peptide.

Also included within one embodiment of ovarian cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the ovarian cancer protein, using cassette or PCR mutagenesis or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant ovarian cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the ovarian cancer protein amino acid sequence. The variants typically exhibit the same

qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is predetermined, the mutation per se need not be predetermined. For example, in order to
5 optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed ovarian cancer variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using
10 assays of ovarian cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be tolerated. Deletions range from about 1 to about 20 residues, although in some cases deletions may be much larger.

15 Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the ovarian cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution
20 relationships provided in the definition section.

The variants typically exhibit the same qualitative biological activity and will elicit the same immune response as the naturally-occurring analog, although variants also are selected to modify the characteristics of the ovarian cancer proteins as needed. Alternatively, the variant may be designed such that the biological activity of the ovarian cancer protein is
25 altered. For example, glycosylation sites may be altered or removed.

Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those described above. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure;
30 the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, e.g., serine or threonine is substituted for (or by) a hydrophobic residue, e.g., leucine, isoleucine, phenylalanine,

valine, or alanine; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g., lysine, arginine, or histidine, is substituted for (or by) an electronegative residue, e.g., glutamic or aspartic acid; (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine; or (e) a proline residue is incorporated or substituted, which changes the degree of rotational freedom of the peptidyl bond.

Covalent modifications of ovarian cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of an ovarian cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C-terminal residues of an ovarian cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking ovarian cancer polypeptides to a water-insoluble support matrix or surface for use in the method for purifying anti-ovarian cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimide.

Other modifications include deamidation of glutamine and asparagine residues to the corresponding glutamic and aspartic acid residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serine, threonine, or tyrosine residues, methylation of the amino groups of the lysine, arginine, and histidine side chains (e.g., pp. 79-86, Creighton (1983) Proteins: Structure and Molecular Properties Freeman), acetylation of the N-terminal amine, and amidation of a C-terminal carboxyl group.

Another type of covalent modification of the ovarian cancer polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence ovarian cancer polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence ovarian cancer polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express ovarian cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to ovarian cancer polypeptides may also be

accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence ovarian cancer polypeptide (for O-linked glycosylation sites). The ovarian cancer amino acid sequence may optionally be altered through changes at the DNA level,

5 particularly by mutating the DNA encoding the ovarian cancer polypeptide at pre-selected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the ovarian cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide.

See, e.g., WO 87/05330, and pp. 259-306 in Aplin and Wriston (1981) CRC Crit. Rev.

10 Biochem. CRC Press.

Removal of carbohydrate moieties present on the ovarian cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are applicable. See, e.g., Sojar and Bahl (1987) Arch. Biochem. Biophys. 259:52-57; and Edge, et al. (1981) Anal. Biochem. 118:131-137. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and

15 exo-glycosidases. See, e.g., Thotakura, et al. (1987) Meth. Enzymol., 138:350-359.

Another type of covalent modification of ovarian cancer comprises linking the ovarian cancer polypeptide to one of a variety of non-proteinaceous polymers, e.g.,

20 polyethylene glycol, polypropylene glycol, or polyoxyalkylene. See, e.g., U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192; or 4,179,337.

Ovarian cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules, e.g., comprising an ovarian cancer polypeptide fused to another heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric

25 molecule comprises a fusion of an ovarian cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the ovarian cancer polypeptide. The presence of such epitope-tagged forms of an ovarian cancer polypeptide can be detected

using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the ovarian cancer polypeptide to be readily purified by affinity purification using an anti-tag

30 antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of an ovarian cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of

the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; His6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7, and 9E10 antibodies thereto (Evan, et al. (1985) Mol. Cell. Biol. 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3:547-553). Other tag polypeptides include, e.g., the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth et al. (1990) Proc. Nat'l Acad. Sci. USA 87:6393-6397).

Also included are other ovarian cancer proteins of the ovarian cancer family, and ovarian cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related ovarian cancer proteins from humans or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include the unique areas of the ovarian cancer nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. The conditions for the PCR reaction are well known in the art (e.g., Innis, PCR Protocols, supra).

Antibodies to ovarian cancer proteins

In a preferred embodiment, when the ovarian cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the ovarian cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller ovarian cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are known to the skilled artisan (e.g., Coligan, supra; and Harlow and Lane, supra). Polyclonal antibodies can be raised in a

mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of the figures or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495-497. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of Tables 1-26 or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (e.g., pp. 59-103 in Goding (1986) Monoclonal Antibodies: Principles and Practice Academic Press). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at

least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid Table 1-26 or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to ovarian cancer protein are capable of reducing or eliminating a biological function of an ovarian cancer protein, as is described below. That is, the addition of anti-ovarian cancer protein antibodies (either polyclonal or preferably monoclonal) to ovarian cancer tissue (or cells containing ovarian cancer) may reduce or eliminate the ovarian cancer. Generally, at least a 25% decrease in activity, growth, size or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the ovarian cancer proteins are humanized antibodies (e.g., Xenerex Biosciences; Medarex, Inc.; Abgenix, Inc.; Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. Humanization can be essentially performed following the method of Winter and co-workers, e.g., by substituting rodent CDRs or CDR sequences for the

corresponding sequences of a human antibody. See, e.g., Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; Presta (1992) Curr. Op. Struct. Biol. 2:593-596; and Verhoeyen, et al. (1988) Science 239:1534-1536). Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein
5 substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries (see, e.g., Hoogenboom and Winter (1991) J. Mol. Biol. 227:381-388; and Marks, et al. (1991) J. Mol. Biol. 222:581-597) or human monoclonal
10 antibodies (see, e.g., p. 77, Cole, et al. in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; and Boerner, et al. (1991) J. Immunol. 147:86-95). Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which
15 closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. See, e.g., U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016; Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Neuberger (1996) Nature Biotechnology 14:826 commenting on Fishwild, et al. (1996)
20 Nature Biotechnology 14:845-51; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

By immunotherapy is meant treatment of ovarian cancer, e.g., with an antibody raised against ovarian cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient
25 (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for
30 expression of the antigen, leading to an immune response.

In a preferred embodiment the ovarian cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby

inactivating the secreted ovarian cancer protein.

In another preferred embodiment, the ovarian cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment, bind the extracellular domain of the ovarian cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane ovarian cancer protein. As will be appreciated by one of ordinary skill in the art, the antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the ovarian cancer protein. The antibody is also an antagonist of the ovarian cancer protein.

Further, the antibody prevents activation of the transmembrane ovarian cancer protein. In one aspect, when the antibody prevents the binding of other molecules to the ovarian cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ , and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, ovarian cancer is treated by administering to a patient antibodies directed against the transmembrane ovarian cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be any number of molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of the ovarian cancer protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the ovarian cancer protein. The therapeutic moiety may inhibit enzymatic activity such as protease or collagenase or protein kinase activity associated with ovarian cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to ovarian cancer tissue or cells, results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with ovarian cancer. Cytotoxic agents are numerous and varied and include, but are not limited to,

cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against ovarian cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane ovarian cancer proteins not only serves to increase the local concentration of therapeutic moiety in the ovarian cancer afflicted area, but also serves to reduce deleterious side effects that may be associated with the untargeted therapeutic moiety.

In another preferred embodiment, the ovarian cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the ovarian cancer protein can be targeted within a cell, e.g., the nucleus, an antibody thereto contains a signal for that target localization, e.g., a nuclear localization signal.

The ovarian cancer antibodies of the invention specifically bind to ovarian cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding is also important.

Detection of ovarian cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the ovarian cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing ovarian cancer) and in ovarian cancer tissue (and in some cases, for varying severities of ovarian cancer that relate to prognosis, as outlined below, or in non-malignant disease are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states,

information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

5 "Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus ovarian cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A
10 qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is modulated, either up-regulated, resulting in an increased amount of
15 transcript, or down-regulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays. See, e.g., Lockhart (1996) Nature Biotechnology 14:1675-1680. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis, and RNase
20 protection. As outlined above, preferably the change in expression (e.g., up-regulation or down-regulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript, or the protein level. The amount of gene
25 expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the ovarian cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to ovarian
30 cancer genes, e.g., those identified as being important in an ovarian cancer or disease phenotype, can be evaluated in an ovarian disease diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed, or on an individual basis.

In this embodiment, the ovarian cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of ovarian cancer sequences in a particular sample. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity.

5 In a preferred embodiment nucleic acids encoding the ovarian cancer protein are detected. Although DNA or RNA encoding the ovarian cancer protein may be detected, of particular interest are methods wherein an mRNA encoding an ovarian cancer protein is detected. Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined
10 herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed in situ. In this method
15 permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding an ovarian cancer protein is detected by binding the digoxigenin with an anti-digoxigenin
20 secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The ovarian cancer proteins, antibodies, nucleic acids, modified proteins and cells
25 containing ovarian cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

30 As described and defined herein, ovarian cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as prognostic or diagnostic markers of ovarian disease. Detection of these proteins in putative ovarian cancer tissue allows for detection, diagnosis, or prognosis of ovarian disease, and for selection of therapeutic strategy. In one

embodiment, antibodies are used to detect ovarian cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the ovarian cancer protein is detected, e.g., by immunoblotting with antibodies raised against the ovarian cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the ovarian cancer protein find use in in situ imaging techniques, e.g., in histology. See, e.g., Asai (ed. 1993) Methods in Cell Biology: Antibodies in Cell Biology (vol. 37) Academic Press. Cells are contacted with from one to many antibodies to the ovarian cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label. In another method the primary antibody to the ovarian cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of ovarian cancer proteins. As will be appreciated by one of ordinary skill in the art, many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing ovarian cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of ovarian cancer proteins. Antibodies can be used to detect an ovarian cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIAcore technology, and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous ovarian cancer protein.

In a preferred embodiment, in situ hybridization of labeled ovarian cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including ovarian cancer tissue and/or normal tissue, are made. In situ hybridization (see, e.g., Ausubel, supra) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It

is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the ovarian cancer proteins, antibodies, nucleic acids, modified proteins and cells containing ovarian cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to ovarian cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of a plurality of genes being preferred. As above, ovarian cancer probes may be attached to biochips for the detection and quantification of ovarian cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

Assays for therapeutic compounds

In a preferred embodiment members of the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The ovarian cancer proteins, antibodies, nucleic acids, modified proteins and cells containing ovarian cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent. See, e.g., Zlokarnik, et al. (1998) Science 279:84-88; and Heid (1996) Genome Res. 6:986-994.

In a preferred embodiment, the ovarian cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified ovarian cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the ovarian cancer phenotype or an identified physiological function of an ovarian cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent. See, e.g., Zlokarnik, supra.

Having identified the differentially expressed genes herein, a variety of assays may be executed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in ovarian cancer, test

compounds can be screened for the ability to modulate gene expression or for binding to the ovarian cancer protein. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing ovarian cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in ovarian cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in ovarian cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the ovarian cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene expression or protein monitoring of a number of entities, e.g., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the ovarian cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of ovarian cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the expression of one or more ovarian cancer-associated sequences, e.g., a polynucleotide sequence set out in Tables 1-26. Generally, in a preferred embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate ovarian cancer, modulate ovarian cancer proteins, bind to an ovarian cancer protein, or interfere with the binding of an ovarian cancer protein and an antibody or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes any molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the ovarian cancer phenotype or the expression of an ovarian cancer sequence,

e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses an ovarian cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induced an ovarian cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, e.g., at zero concentration or below the level of detection.

Drug candidates encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or less than 1500 or less than 1000 or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof. Particularly preferred are peptides.

In one aspect, a modulator will neutralize the effect of an ovarian cancer protein. By "neutralize" is meant that activity of a protein is inhibited or blocked and the consequent effect on the cell.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to an ovarian cancer polypeptide or to modulate activity.

Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that

display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (e.g., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks. See, e.g., Gallop, et al. (1994) J. Med. Chem. 37:1233-1251.

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175; Furka (1991) Pept. Prot. Res. 37:487-493; and Houghton, et al. (1991) Nature 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Nat'l Acad. Sci. USA 90:6909-913), vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568-570), non-peptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et al. (1992) J. Amer. Chem. Soc. 114:9217-218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661-662), oligocarbamates (Cho, et al. (1993) Science 261:1303-305), and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658-xxx). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385-401, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14:309-314; and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522; and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, page 33, Baum (Jan. 18, 1993) C&E News; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available.

See, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY; Symphony, Rainin, Woburn, MA; 433A Applied Biosystems, Foster City, CA; 9050 Plus, Millipore, Bedford, MA.

A number of well known robotic systems have also been developed for solution phase
5 chemistries. These systems include automated workstations like the automated synthesis
apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic
systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, MA; Orca,
Hewlett-Packard, Palo Alto, CA), which mimic the manual synthetic operations performed by
10 a chemist. Any of the above devices are suitable for use with the present invention. The
nature and implementation of modifications to these devices (if any) so that they can operate
as discussed herein will be apparent to persons skilled in the relevant art. In addition,
numerous combinatorial libraries are themselves commercially available (see, e.g.,
ComGenex, Princeton, N.J.; Asinex, Moscow, RU; Tripos, Inc., St. Louis, MO; ChemStar,
Ltd, Moscow, RU; 3D Pharmaceuticals, Exton, PA; Martek Biosciences, Columbia, MD;
15 etc.).

The assays to identify modulators are amenable to high throughput screening.
Preferred assays thus detect enhancement or inhibition of ovarian cancer gene transcription,
inhibition or enhancement of polypeptide expression, and inhibition or enhancement of
polypeptide activity.

20 High throughput assays for the presence, absence, quantification, or other properties
of particular nucleic acids or protein products are well known to those of skill in the art.
Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S.
Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent
No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (e.g., in
25 arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of
screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g.,
Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman
Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems
30 typically automate entire procedures, including all sample and reagent pipetting, liquid
dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate
for the assay. These configurable systems provide high throughput and rapid start up as well
as a high degree of flexibility and customization. The manufacturers of such systems provide

detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or
5 fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly
10 useful test compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring
15 proteins as is outlined above, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate any nucleotide or amino acid at any position. The synthetic process can be
20 designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some
25 positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains,
30 serines, threonines, tyrosines or histidines for phosphorylation sites, etc., or to purines, etc.

Modulators of ovarian cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids.

For example, digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

5 After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example,
10 an in vitro transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FTTC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as,
15 alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin
20 is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

As will be appreciated by those in the art, these assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702; 5,597,909; 5,545,730; 5,594,117;
25 5,591,584; 5,571,670; 5,580,731; 5,571,670; 5,591,584; 5,624,802; 5,635,352; 5,594,118; 5,359,100; 5,124,246; and 5,681,697, each of which is hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

30 A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step

parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the ovarian cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product.

In addition screens can be done for genes that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress an ovarian cancer expression pattern leading to a normal expression pattern, or to modulate a single ovarian cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated ovarian cancer tissue reveals genes that are not expressed in normal tissue

or ovarian cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for ovarian cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated ovarian cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of ovarian cancer cells, that have an associated ovarian cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (e.g., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once the test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., ovarian cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress the ovarian cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on ovarian cancer activity. By defining such a signature for the ovarian cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "ovarian cancer proteins" or a "ovarian cancer modulatory protein". The ovarian cancer modulatory protein may be a fragment, or alternatively, be the full length protein to the fragment encoded by the nucleic acids of the Tables. Preferably, the ovarian cancer modulatory protein is a fragment. In a preferred embodiment, the ovarian cancer amino acid sequence which is used to determine

sequence identity or similarity is encoded by a nucleic acid of the Tables. In another embodiment, the sequences are naturally occurring allelic variants of a protein encoded by a nucleic acid of the Tables. In another embodiment, the sequences are sequence variants as further described herein.

5 Preferably, the ovarian cancer modulatory protein is a fragment of approximately 14 to 24 amino acids long. More preferably the fragment is a soluble fragment. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the fragment has an N-terminal Cys to aid in solubility. In another embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in coupling, e.g., to
10 cysteine. Or, the ovarian cancer proteins are conjugated to an immunogenic agent, e.g., to BSA.

Measurements of ovarian cancer polypeptide activity, or of ovarian cancer or the ovarian cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the ovarian cancer polypeptides can be
15 measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of ovarian cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone
20 release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian ovarian cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed in vitro.
25 For example, an ovarian cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the ovarian cancer polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively binds to the ovarian cancer polypeptide
30 or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or

enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using the ovarian cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment
5 with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of
10 the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "ovarian cancer proteins." The ovarian cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is
15 performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated
20 gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the ovarian cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining an ovarian cancer
25 protein and a candidate compound, and determining the binding of the compound to the ovarian cancer protein. Preferred embodiments utilize the human ovarian cancer protein, although other mammalian proteins, e.g., counterparts, may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein,
30 variant or derivative ovarian cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the ovarian cancer protein or the candidate agent is non-diffusably bound to an insoluble support having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be

made of any composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of any convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, 5 teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition and is non-diffusible. Preferred methods of binding include the use of 10 antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), 15 casein or other innocuous protein or other moiety.

In a preferred embodiment, the ovarian cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the ovarian cancer protein is added. Novel binding agents include specific 20 antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

25 The determination of the binding of the test modulating compound to the ovarian cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the ovarian cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. 30 Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one

component can be labeled with different labels, e.g., ^{125}I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive
5 binding assay. The competitor is a binding moiety known to bind to the target molecule (e.g., an ovarian cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to
10 the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically 4–40° C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically between 0.1 and 1 hr will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is
15 followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by the test compound. Displacement of the competitor is an indication that the test compound is binding to the ovarian cancer protein and thus is capable of binding to, and potentially modulating, the activity of the ovarian cancer protein. In this embodiment, either component can be
20 labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate
25 that the test compound is bound to the ovarian cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the ovarian cancer protein.

In a preferred embodiment, the methods comprise differential screening to identity
30 agents that are capable of modulating the activity of the ovarian cancer proteins. In this embodiment, the methods comprise combining an ovarian cancer protein and a competitor in a first sample. A second sample comprises a test compound, an ovarian cancer protein, and a

competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the ovarian cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the ovarian cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native ovarian cancer protein, but cannot bind to modified ovarian cancer proteins. The structure of the ovarian cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of an ovarian cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of an ovarian cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising ovarian cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes an ovarian cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including

chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate ovarian cancer agents are identified.

- 5 Compounds with pharmacological activity are able to enhance or interfere with the activity of the ovarian cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting ovarian cancer cell division is provided.

- 10 The method comprises administration of an ovarian cancer inhibitor. In another embodiment, a method of inhibiting ovarian cancer is provided. The method comprises administration of an ovarian cancer inhibitor. In a further embodiment, methods of treating cells or individuals with ovarian cancer are provided. The method comprises administration of an ovarian cancer inhibitor.

- 15 In one embodiment, an ovarian cancer inhibitor is an antibody as discussed above. In another embodiment, the ovarian cancer inhibitor is an antisense or RNAi molecule.

A variety of cell viability, growth, proliferation, and metastasis assays are known to those of skill in the art, as described below.

Soft agar growth or colony formation in suspension

- 20 Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and
25 grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of ovarian cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

- 30 Techniques for soft agar growth or colony formation in suspension assays are described in Freshney (1994) Culture of Animal Cells: A Manual of Basic Technique (3d ed.) Wiley-Liss, herein incorporated by reference. See also, the methods section of Garkavtsev, et al. (1996), supra, herein incorporated by reference.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (^3H)-thymidine at saturation density can be used to measure density limitation of growth. See, e.g., Freshney (1994), supra. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (^3H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with an ovarian cancer-associated sequence and are grown for 24 hr at saturation density in non-limiting medium conditions. The percentage of cells labeling with (^3H)-thymidine is determined autoradiographically. See, e.g., Freshney (1994), supra.

Growth factor or serum dependence

Transformed cells typically have a lower serum dependence than their normal counterparts. See, e.g., Temin (1966) J. Nat'l Cancer Inst. 37:167-175; Eagle, et al. (1970) J. Exp. Med. 131:836-879; and Freshney, supra. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g., Gullino, pp. 178-184 "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) Biological Responses in Cancer Plenum. Similarly,

tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) Sem Cancer Biol. 3:89-96.

Various techniques which measure the release of these factors are described in Freshney (1994), *supra*. Also, see, Unkeless, et al. (1974) J. Biol. Chem. 249:4295-4305; Strickland and Beers (1976) J. Biol. Chem. 251:5694-5702; Whur, et al. (1980) Br. J. Cancer 42:305-312; Gullino, pp. 178-184 "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) Biological Responses in Cancer Plenum; and Freshney (1985) Anticancer Res. 5:111-130.

10 Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate ovarian cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Alternatively, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by pre-labeling the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), *supra*.

Tumor growth in vivo

Effects of ovarian cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the ovarian cancer gene is disrupted or in which an ovarian cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous ovarian cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous ovarian cancer gene with a mutated version of the ovarian cancer gene, or by mutating the endogenous ovarian cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. By breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion. See, e.g., Capecchi, et al. (1989) Science 244:1288-1292. Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual CSH Press; and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) J. Nat'l Cancer Inst. 52:921-930), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) Br. J. Cancer 38:263-272; Selby, et al. (1980) Br. J. Cancer 41:52-61) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing an ovarian cancer-associated sequences are injected subcutaneously. After a suitable length of time, preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

Polynucleotide modulators of ovarian cancer

Antisense and RNAi Polynucleotides

In certain embodiments, the activity of an ovarian cancer-associated protein is down-regulated, or entirely inhibited, by the use of antisense polynucleotide, e.g., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., an ovarian cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-

sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the ovarian cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

5 Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized in vitro. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.

Antisense molecules as used herein include antisense or sense oligonucleotides.

10 Sense oligonucleotides can, e.g., be employed to block transcription by binding to the antisense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for ovarian cancer molecules. A preferred antisense molecule is for an ovarian cancer sequences in Tables 1-26, or for a ligand or activator thereof. Antisense or
15 sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. An antisense or a sense oligonucleotide can be developed based upon a cDNA sequence encoding a given protein. See, e.g., Stein and Cohen (1988) Cancer Res. 48:2659-2668; and van der Krol, et al. (1988) BioTechniques 6:958-976.

20 RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) Sciencexpress (21March2002); Sharp (1999) Genes Dev. 13:139-141; and Cathew (2001) Curr. Op. Cell Biol. 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) Nature 411:494-
25 498. The mechanism may be used to down-regulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

Ribozymes

In addition to antisense polynucleotides, ribozymes can be used to target and inhibit
30 transcription of ovarian cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. Pharmacol. 25: 289-

317 for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparing them are well known to those of skill in the art. See, e.g.,
5 WO 94/26877; Ojwang, et al. (1993) Proc. Nat'l Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Hum. Gene Ther. 1:39-45; Leavitt, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:699-703; Leavitt, et al. (1994) Hum. Gene Ther. 5:1151-120; and Yamada, et al. (1994) Virology 205:121-126.

Polynucleotide modulators of ovarian cancer may be introduced into a cell containing
10 the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its
15 corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of ovarian cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be
20 used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating ovarian cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-ovarian cancer antibody that reduces or eliminates the biological activity of an endogenous ovarian cancer protein. Alternatively, the methods comprise administering to a
25 cell or organism a recombinant nucleic acid encoding an ovarian cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the ovarian cancer sequence is down-regulated in ovarian cancer, such state may be reversed by increasing the amount of ovarian cancer gene product in the cell. This can be accomplished, e.g., by over-expressing the endogenous ovarian cancer gene or administering a gene
30 encoding the ovarian cancer sequence, using known gene-therapy techniques, e.g.. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, e.g., when

the ovarian cancer sequence is up-regulated in ovarian cancer, the activity of the endogenous ovarian cancer gene is decreased, e.g., by the administration of an ovarian cancer antisense or RNAi nucleic acid.

In one embodiment, the ovarian cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to ovarian cancer proteins. Similarly, the ovarian cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify ovarian cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to an ovarian cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The ovarian cancer antibodies may be coupled to standard affinity chromatography columns and used to purify ovarian cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the ovarian cancer protein.

15 Methods of identifying variant ovarian cancer-associated sequences

Without being bound by theory, expression of various ovarian cancer sequences is correlated with ovarian cancer. Accordingly, disorders based on mutant or variant ovarian cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant ovarian cancer genes, e.g., determining all or part of the sequence of at least one endogenous ovarian cancer genes in a cell. This may be accomplished using any number of sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the ovarian cancer genotype of an individual, e.g., determining all or part of the sequence of at least one ovarian cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced ovarian cancer gene to a known ovarian cancer gene, e.g., a wild-type gene.

The sequence of all or part of the ovarian cancer gene can then be compared to the sequence of a known ovarian cancer gene to determine if any differences exist. This can be done using any number of known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the ovarian cancer gene of the patient and the known ovarian cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the ovarian cancer genes are used as probes to determine the number of copies of the ovarian cancer gene in the genome.

In another preferred embodiment, the ovarian cancer genes are used as probes to determine the chromosomal localization of the ovarian cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the ovarian cancer gene locus.

Administration of pharmaceutical and vaccine compositions

In one embodiment, a therapeutically effective dose of an ovarian cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques. See, e.g., Ansel, et al. (1999) Pharmaceutical Dosage Forms and Drug Delivery Systems Lippincott; Lieberman (1992) Pharmaceutical Dosage Forms (vols. 1-3) Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding Amer. Pharmaceutical Assn.; and Pickar (1999) Dosage Calculations Thomson. Adjustments for ovarian cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction, and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art. U.S. Patent Application No. 09/687,576, further discloses the use of compositions and methods of diagnosis and treatment in ovarian cancer is hereby expressly incorporated by reference.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the ovarian cancer proteins and modulators thereof of the present invention can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intra-nasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the ovarian cancer

proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise an ovarian cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as

5 pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, 10 propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid, and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, 15 manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, 20 tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

25 The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules, and lozenges. It is recognized that ovarian cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, 30 should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are well known in the art.

The compositions for administration will commonly comprise an ovarian cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be
5 sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary
10 widely, and will be selected primarily based on fluid volumes, viscosities, body weight, and the like in accordance with the particular mode of administration selected and the patient's needs. See, e.g., Remington's Pharmaceutical Science (15th ed., 1980) and Hardman and Limbird (eds. 2001) Goodman and Gillman: The Pharmacological Basis of Therapeutics (10th ed.) McGraw-Hill. Thus, a typical pharmaceutical composition for intravenous
15 administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions are readily available.

20 The compositions containing modulators of ovarian cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and/or its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts
25 effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing
30 the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc. Such prophylactic

treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, e.g., in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

5 It will be appreciated that the present ovarian cancer protein-modulating compounds can be administered alone or in combination with additional ovarian cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in Tables 1-26, such as RNAi, antisense
10 polynucleotides or ribozymes, will be introduced into cells, in vitro or in vivo. The present invention provides methods, reagents, vectors, and cells useful for expression of ovarian cancer-associated polypeptides and nucleic acids using in vitro (cell-free), ex vivo or in vivo (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for
15 expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell. See,
20 e.g., Berger and Kimmel (1987) Guide to Molecular Cloning Techniques from Methods in Enzymology (vol. 152) Academic Press; Ausubel, et al. (eds. 1999 and supplements) Current Protocols Lippincott; and Sambrook, et al. (2001) Molecular Cloning: A Laboratory Manual (3d ed., Vol. 1-3) CSH Press.

In a preferred embodiment, ovarian cancer proteins and modulators are administered
25 as therapeutic agents, and can be formulated as outlined above. Similarly, ovarian cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the ovarian cancer coding regions) can be administered in a gene therapy application. These ovarian cancer genes can include antisense applications, either as gene therapy (e.g., for incorporation into the genome) or as antisense compositions, as will be appreciated by those
30 in the art.

Ovarian cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses.. Such vaccine compositions can include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) J. Clin. Invest. 95:341-

349), peptide compositions encapsulated in poly(D,L-lactide-co-glycolide, "PLG") microspheres (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in immune stimulating complexes (ISCOMS; see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin. Exp. Immunol. 113:235-243), multiple antigen peptide systems (MAPs; see, e.g., Tam (1988) Proc. Nat'l Acad. Sci. USA 85:5409-5413; Tam (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p. 379, in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Chakrabarti, et al. (1986) Nature 320:535-537; Hu, et al. (1986) Nature 320:537-540; Kieny, et al. (1986) AIDS Bio/Technology 4:790-795; Top, et al. (1971) J. Infect. Dis. 124:148-154; Chanda, et al. (1990) Virology 175:535-547), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25-35; Eldridge, et al. (1993) Sem. Hematol. 30:16-24; Falo, et al. (1995) Nature Med. 7:649-653), adjuvants (Warren, et al. (1986) Ann. Rev. Immunol. 4:369-388; Gupta, et al. (1993) Vaccine 11:293-306), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585-1589; Rock (1996) Immunol. Today 17:131-137), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745-1749; Robinson, et al. (1993) Vaccine 11:957-960; Shiver, et al., p. 423, in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Cease and Berzofsky (1994) Ann. Rev. Immunol. 12:923-989; and Eldridge, et al. (1993) Sem. Hematol. 30:16-24). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bortadella pertussis, or Mycobacterium tuberculosis derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be

used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. See, e.g., Wolff et. al. (1990) Science 247:1465-1468; U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; and WO 98/04720. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode ovarian cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors useful for therapeutic administration or immunization e.g., adeno and adeno-associated virus vectors, retroviral vectors, Salmonella typhi vectors, detoxified anthrax toxin vectors, and the like, will be apparent. See, e.g., Shata, et al. (2000) Mol. Med. Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; and Hipp, et al. (2000) In Vivo 14:571-85.

Methods for the use of genes as DNA vaccines are well known, and include placing an ovarian cancer gene or portion of an ovarian cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in an ovarian cancer patient. The ovarian cancer gene used for DNA vaccines can encode full-length ovarian cancer proteins, but more preferably encodes portions of the ovarian cancer proteins including peptides derived from the ovarian cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from an ovarian cancer gene. For example, ovarian cancer-associated genes or sequence encoding subfragments of an ovarian cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the ovarian cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

5 In another preferred embodiment ovarian cancer genes find use in generating animal models of ovarian cancer. When the ovarian cancer gene identified is repressed or diminished in cancer tissue, gene therapy technology, e.g., wherein antisense RNA directed to the ovarian cancer gene will also diminish or repress expression of the gene. Animal models of ovarian cancer find use in screening for modulators of an ovarian cancer-associated sequence or modulators of ovarian cancer. Similarly, transgenic animal
10 technology including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the ovarian cancer protein. When desired, tissue-specific expression or knockout of the ovarian cancer protein may be necessary.

15 It is also possible that the ovarian cancer protein is overexpressed in ovarian cancer. As such, transgenic animals can be generated that overexpress the ovarian cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene.
20 Animals generated by such methods find use as animal models of ovarian cancer and are additionally useful in screening for modulators to treat ovarian cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

For use in diagnostic, research, and therapeutic applications suggested above, kits are
25 also provided by the invention. In the diagnostic and research applications such kits may include any or all of the following: assay reagents, buffers, ovarian cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, siRNA or antisense polynucleotides, ribozymes, dominant negative ovarian cancer polypeptides or polynucleotides, small molecules inhibitors of ovarian cancer-associated sequences etc. A therapeutic product may
30 include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing directions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. Any medium

capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of ovarian cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: an ovarian cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing ovarian cancer-associated activity. Optionally, the kit contains biologically active ovarian cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

EXAMPLES

Example 1: Gene Chip Analysis

Molecular profiles of various normal and cancerous tissues were determined and analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

TABLE 1A lists about 1119 genes up-regulated in ovarian cancer compared to normal adult tissues. These were selected from 59000 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 5.0. The "average" ovarian cancer level was set to the 80th percentile value amongst various ovarian cancers. The "average" normal adult tissue level was set to the 85th percentile amongst various non-malignant tissues.

TABLE 1A: ABOUT 1119 UP-REGULATED OVARIAN CANCER GENES

Pkey: Primkey
Ex. Accn: Exemplar Accession

UG ID: UniGene ID

Title: UniGene title

ratio: ratio tumor vs normal tissues

Pkey	Ex. Accn	UG ID	Title	ratio
423634	AW959908	Hs.1690	heparin-binding growth factor binding protein	65.7
423017	AW178761	Hs.227948	"serine (or cysteine) proteinase inhibitor, clade B(ovalbumin	63.6
432938	T27013	Hs.3132	steroidogenic acute regulatory protein	58.3
445810	AW265700	Hs.155660	ESTs	35.9
431938	AA838471	Hs.115242	developmentally regulated GTP-binding protein 1	32.0
407112	AA070801	Hs.51615	"ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAM	31.3
425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen)	30.0
402075			predicted exon	27.9
400301	X03635	Hs.1657	estrogen receptor 1	26.4

	402639			predicted exon	25.3
	421948	L42583	Hs.111758	keratin 6A	24.7
	414540	BE379050		*gb:601236655F1 NIH_MGC_44 Homo sapiens cDNA clon	24.6
5	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecule 1)	24.5
	401675			predicted exon	23.6
	457024	AA397546	Hs.119151	ESTs	23.2
	440684	AI253123	Hs.127356	*ESTs, Highly similar to NEST_HUMAN NEST1 [H.sapien	23.1
	459006	AW298631	Hs.27721	hypothetical protein FLJ20353	22.8
10	400964			predicted exon	22.5
	402421			predicted exon	20.9
	437329	AA811977	Hs.291761	ESTs	20.8
	414605	BE390440		*gb:601283601F1 NIH_MGC_44 Homo sapiens cDNA clon	20.7
	411004	AW813242		*gb:MR3-ST0191-020200-207-g10 ST0191 Homo sapiens	20.4
	401283			predicted exon	20.3
15	440633	AI140686	Hs.263320	ESTs	19.9
	445603	H08345	Hs.106234	ESTs	19.7
	403786			predicted exon	19.7
	436508	AW604381	Hs.121121	ESTs	19.6
20	459390	BE385725		*gb:601276347F1 NIH_MGC_20 Homo sapiens cDNA clon	19.2
	421823	N40850	Hs.28625	ESTs	19.0
	417366	BE185289	Hs.1076	small proline-rich protein 1B (comifin)	18.9
	422525	AA758797	Hs.192807	ESTs	18.5
	458121	S42416	Hs.74547	Human T-cell receptor active alpha-chain mRNA from JM c	18.3
25	430520	NM_016190	Hs.242057	chromosome 1 open reading frame 10	18.1
	450192	AA263143	Hs.24596	RAD51-interacting protein	18.0
	416839	H94900	Hs.17882	ESTs	17.9
	440788	AI806594	Hs.128577	ESTs	17.9
	451072	AA013451	Hs.117929	ESTs	17.7
30	402203			predicted exon	17.3
	417811	AW993983		*gb:RC1-BN0035-130400-013-e04 BN0035 Homo sapiens	17.3
	438658	AI222068	Hs.123571	ESTs	17.3
	403747			predicted exon	17.2
	444958	AW292843	Hs.167047	ESTs	17.2
35	404097			predicted exon	17.1
	459375	BE251770		*gb:601112470F1 NIH_MGC_16 Homo sapiens cDNA clon	16.9
	443198	AI039813		gb:ox49d06.x1 Soares_tetal_fetus_Nb2HF8_9w Homo sapi	16.9
	441557	AW452647	Hs.270482	ESTs	16.9
	433871	W02410	Hs.205555	ESTs	16.8
40	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo sapiens cD	16.7
	443406	AI056238	Hs.143316	ESTs	16.7
	400613			predicted exon	16.6
	448372	AW445168	Hs.170802	ESTs	16.5
	410929	H47233	Hs.30643	ESTs	16.5
45	445887	AI263105	Hs.145597	ESTs	16.1
	422036	AA302647	Hs.271891	ESTs	16.0
	404767			predicted exon	15.9
	420831	AA280824	Hs.190035	ESTs	15.8
	405196			predicted exon	15.8
50	452947	AW130413		*gb:ox50i04.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clo	15.8
	429538	BE182592	Hs.139322	small proline-rich protein 3	15.8
	435313	AI769400	Hs.189729	ESTs	15.7
	449635	AI989942	Hs.232150	ESTs	15.6
	424098	AF077374	Hs.139322	small proline-rich protein 3	15.4
55	411660	AW855718		*gb:RC1-CT0279-070100-021-a06 CT0279 Homo sapiens c	15.4
	442653	BE269247	Hs.170226	Homo sapiens clone 23579 mRNA sequence	15.4
	443534	AI076123		gb:oxy92e04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo	15.4
	458012	AI424899	Hs.188211	ESTs	15.3
	441018	AI809587	Hs.148782	ESTs	15.1
60	425972	BE391563	Hs.165433	*ESTs, Highly similar to T17342 hypothetical protein DKFZ	15.1
	418092	R45154	Hs.106604	ESTs	15.1
	410909	AW898161	Hs.53112	*ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	15.1
	458234	BE651408	Hs.127196	ESTs	15.0
	434208	T92641	Hs.127648	hypothetical protein PRO2176	15.0
65	403177			predicted exon	15.0
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	14.9
	425090	AA350552		*gb:EST57886 Infant brain Homo sapiens cDNA 5' end, mR	14.7
	409723	AW885757	Hs.257862	ESTs	14.6
	423735	AA330259		*gb:EST33963 Embryo, 12 week II Homo sapiens cDNA 5'	14.6
70	444266	AI424984	Hs.125465	ESTs	14.5
	443341	AW631480	Hs.8688	ESTs	14.4
	457336	AW969657	Hs.291029	ESTs	14.4
	440500	AA972165	Hs.150308	ESTs	14.4
	446292	AF081497	Hs.279682	Rh type C glycoprotein	14.3
75	438086	AA336519	Hs.301167	*Homo sapiens cDNA: FLJ21545 fls, clone COL06195"	14.3
	434715	BE005346	Hs.116410	ESTs	14.2
	409387	AW384900	Hs.123526	ESTs	14.2
	409272	AB014569	Hs.52526	KIAA0669 gene product	14.2
	454913	AW841462		*gb:RC6-CN0014-080300-012-B09 CN0014 Homo sapiens	14.0
80	439846	T63959	Hs.228320	*Homo sapiens cDNA: FLJ23537 fls, clone LNG07690"	14.0
	409695	AA296961		*gb:EST112514 Adrenal gland tumor Homo sapiens cDNA	13.9
	422897	AA679784	Hs.4290	ESTs	13.9
	404664			predicted exon	13.9
	458829	AI557388		*gb:PT2.1_6_G03.r tumor2 Homo sapiens cDNA 3', mRNA	13.8
	407327	AA487182	Hs.269414	ESTs	13.8

	455435	AW939445		"gb:QV1-DT0072-310100-056-b07 DT0072 Homo sapiens	13.7
	449327	AI638743	Hs.224672	ESTs	13.7
	411693	AW857271		"gb:CMO-CT0307-210100-158-g09 CT0307 Homo sapiens	13.7
5	407463	AJ272034		gb:Homo sapiens mRNA for putative capacitative calcium c	13.6
	446767	AI380107	Hs.158954	ESTs	13.6
	433040	H70423	Hs.300511	ESTs	13.5
	435209	AW027809	Hs.187698	"ESTs, Highly similar to cytomegalovirus partial fuson reco	13.5
	441459	AI919142	Hs.214233	ESTs	13.5
10	401269			predicted exon	13.4
	438663	AI199575	Hs.153070	ESTs	13.4
	426698	AA394104	Hs.97489	ESTs	13.4
	423637	AL137279	Hs.130187	Homo sapiens mRNA; cDNA DKFZp43401214 (from clon	13.2
	448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P1124 (from clon	13.2
15	456714	AW897265		"gb:CMO-NN0057-150400-335-a04 NN0057 Homo sapiens	13.2
	458356	AI024855	Hs.131575	ESTs	13.2
	431822	AA516049		"gb:ng65d01.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clo	13.1
	454822	AW833793		"gb:QV4-TT0008-130100-080-a06 TT0008 Homo sapiens c	13.1
	453358	AI990738	Hs.240066	ESTs	13.1
20	435542	AA687376	Hs.269533	ESTs	13.1
	421286	AA806584	Hs.187895	ESTs	13.0
	452799	AI948829	Hs.213786	ESTs	13.0
	444355	BE383686	Hs.191621	ESTs	13.0
	444271	AW452569	Hs.149804	ESTs	12.9
25	443860	AW866632		"gb:QV4-SN0024-210400-181-g04 SN0024 Homo sapiens	12.9
	428719	AA358193	Hs.193128	hypothetical protein FLJ10805	12.9
	418282	AA215535	Hs.98133	ESTs	12.8
	437308	AA749417	Hs.292353	ESTs	12.7
	400584			predicted exon	12.7
30	426306	AA447310	Hs.164059	"Homo sapiens cDNA FLJ13338 fis, clone OVARC100188	12.7
	448466	AI522109	Hs.171066	ESTs	12.7
	402738			predicted exon	12.7
	451531	AA018311	Hs.114762	ESTs	12.6
	435243	AW292886	Hs.261373	adenosine A2b receptor pseudogene	12.6
35	431725	X65724	Hs.2839	Narrie disease (pseudoglioma)	12.6
	425108	AI000489	Hs.96967	ESTs	12.5
	422330	D30783	Hs.115263	epiregulin	12.5
	432949	AA570749	Hs.298866	ESTs	12.5
	417009	AA191719	Hs.171872	DEAD/H (Asp-Glu-Ala-Asp/Hs) box polypeptide 8 (RNA	12.4
40	456378	AA843387	Hs.87279	ESTs	12.4
	432966	AA650114		"gb:ns92h09.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clon	12.4
	440571	AA904461	Hs.130798	ESTs	12.3
	411178	AW820852		"gb:RC2-ST0301-120200-011-f12 ST0301 Homo sapiens c	12.3
	445934	AF131737	Hs.13475	hypothetical protein	12.3
45	433917	AI809325	Hs.122814	Human DNA sequences from clone RP5-1028D15 on chrom	12.2
	402018			predicted exon	12.2
	424101	AA335394		"gb:EST39787 Eplididymus Homo sapiens cDNA 5' end, mR	12.2
	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	12.1
	458154	AW816379		"gb:QV4-ST0234-181199-035-g01 ST0234 Homo sapiens c	12.1
50	440919	AW291274	Hs.262826	ESTs	12.0
	415747	AA381209		"gb:EST94257 Activated T-cells I Homo sapiens cDNA 5' e	12.0
	411748	AW859920		"gb:QV1-CT0364-260100-052-g05 CT0364 Homo sapiens	12.0
	452975	M85521	Hs.69469	dendritic cell protein	12.0
	427276	AA400269	Hs.49598	ESTs	12.0
55	454315	AW373564	Hs.251928	nuclear pore complex interacting protein	12.0
	450786	H86632	Hs.33654	ESTs	12.0
	402578			predicted exon	11.9
	459591	AL037185		gb:DKFZp564A1169_r1 554 (synonym: hfbz2) Homo sapie	11.9
	433449	AW772282		"gb:hn71b05.x1 NCI_CGAP_Kd11 Homo sapiens cDNA c	11.9
60	429108	AA890521	Hs.126035	ESTs	11.8
	454556	AW807073		"gb:MR4-ST0062-031199-018-d06 ST0062 Homo sapiens	11.7
	443613	AI079355		gb:oz39b09.s1 Soares_NhHMPu_S1 Homo sapiens cDNA c	11.7
	400385	NM_020389	Hs.283104	putative capacitative calcium channel	11.6
	411725	AW858396		"gb:CMO-CT0341-181289-130-c06 CT0341 Homo sapiens	11.5
65	455174	AI694575	Hs.147801	ESTs	11.5
	412402	AW984788		"gb:RC1-HN0015-120400-021-c07 HN0015 Homo sapiens	11.5
	434205	AF119861	Hs.283032	hypothetical protein PRO2015	11.5
	450496	AW449251	Hs.257131	ESTs	11.5
	411149	N68715	Hs.269128	ESTs	11.5
70	414210	BE383592		"gb:601297871F1 NIH_MGC_19 Homo sapiens cDNA clon	11.4
	409994	D86864	Hs.57735	acetyl LDL receptor; SREC	11.3
	453845	AL157568		gb:DKFZp761F0816_r1 761 (synonym: hamy2) Homo sapi	11.3
	404849			predicted exon	11.3
	442824	BE178065	Hs.144081	ESTs	11.3
75	428548	AA430058	Hs.98649	EST	11.3
	434804	AA649530		"gb:ns44f05.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clo	11.3
	430486	BE062109	Hs.241551	"chloride channel, calcium activated, family member 2"	11.3
	400174			predicted exon	11.2
	424324	AA346316		"gb:EST52440 Greater omentum tumor Homo sapiens cDN	11.2
80	447724	AW296375	Hs.24477	ESTs	11.2
	457028	AW449838	Hs.97562	ESTs	11.2
	429900	AA460421	Hs.30875	ESTs	11.2
	452240	AI591147	Hs.61232	ESTs	11.2
	458067	AA393603	Hs.36752	"Homo sapiens cDNA: FLJ22834 fis, clone KIAA4314"	11.1
	402222			predicted exon	11.1

	446745	AW118189	Hs.156400	ESTs	11.1
	453060	AW294092	Hs.21594	ESTs	11.1
	443482	AW188093	Hs.250385	ESTs	11.1
5	436843	AA824588		"gboc83d02.s1 NCL_CGAP_GCB1 Homo sapiens cDNA c	11.0
	416320	HA7867	Hs.34024	ESTs	11.0
	435772	AA700019	Hs.132992	"ATP-binding cassette, sub-family G (WHITE), member 5 (11.0
	451542	AA018365	Hs.32713	ESTs	11.0
	408522	AI541214	Hs.46320	"Small proline-rich protein SPRK [human, odontogenic kera	11.0
10	414712	N88858.comp	Hs.77039	ribosomal protein S3A	10.9
	411940	AW876686		"gb:CM4-PT0031-180200-507-e05-PT0031 Homo sapiens c	10.9
	408733	AW264812	Hs.254290	ESTs	10.9
	452030	AL137578	Hs.27607	Homo sapiens mRNA; cDNA DKFZp564N2464 (from clon	10.9
	458175	AW296024	Hs.150434	ESTs	10.9
15	400812			predicted exon	10.9
	440159	AI637599	Hs.126127	ESTs	10.8
	429443	AB028967	Hs.202687	"potassium voltage-gated channel, Shal-related subfamily, m	10.8
	416319	AI815601	Hs.79197	"CD83 antigen (activated B lymphocytes, immunoglobulin s	10.8
	405783			predicted exon	10.7
20	405708			predicted exon	10.7
	433266	AI863224	Hs.288677	"Homo sapiens cDNA FLJ13872 fls, clone THYRO100132	10.6
	456900	AA355442	Hs.169054	ESTs	10.6
	432408	N39127	Hs.76391	"myxovirus (influenza) resistance 1, homolog of murine (int	10.6
	451702	AW665452	Hs.245503	ESTs	10.6
25	418179	X51630	Hs.1145	Wilms tumor 1	10.6
	408987	H85615		gb:yo03f11.r1 Soares retina N2b5HR Homo sapiens cDNA	10.6
	405285			predicted exon	10.5
	419276	BE165909	Hs.134682	"Homo sapiens cDNA: FLJ23161 fls, clone LNG09730"	10.5
	407287	AI678812	Hs.201658	"ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAM	10.5
30	403055			predicted exon	10.5
	414195	BE263293		"gb:G01144881F2 NIH_MGC_19 Homo sapiens cDNA clon	10.4
	454258	AI457286	Hs.143979	"ESTs, Weakly similar to KAA1276 protein [H.sapiens]"	10.4
	412951	BE018611	Hs.251948	"Homo sapiens cDNA: FLJ23107 fls, clone LNG07738"	10.4
	428888	AA437010	Hs.266584	ESTs	10.4
35	440834	AA907027	Hs.128608	ESTs	10.4
	437096	AA744406		"gb:ny51h02.s1 NCL_CGAP_Pr18 Homo sapiens cDNA clo	10.4
	400135			predicted exon	10.4
	447849	AI538147	Hs.164277	ESTs	10.3
40	400593			predicted exon	10.3
	427469	AA403084	Hs.269347	ESTs	10.3
	402794			predicted exon	10.2
	452743	AW965082	Hs.61455	ESTs	10.2
	448983	AI611654	Hs.224908	ESTs	10.2
45	422696	AF242524	Hs.26323	hypothetical nuclear factor SBB122	10.2
	428949	AA442153	Hs.104744	"ESTs, Weakly similar to AF208855 1 BM-013 [H.sapiens]	10.2
	409191	AW818390		"gb:RC1-ST0278-160200-014-d10 ST0278 Homo sapiens c	10.2
	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	10.2
	406076	AL390179	Hs.137011	Homo sapiens mRNA; cDNA DKFZp547P134 (from clone	10.2
	410628	BE407727		"gb:G01299771F1 NIH_MGC_21 Homo sapiens cDNA clon	10.1
50	445835	AW290999	Hs.145534	chromosome 21 open reading frame 23	10.1
	452507	AI904646		"gb:QV-BT065-020399-103 BT065 Homo sapiens cDNA, m	10.1
	433297	AV658581	Hs.282633	ESTs	10.1
	426724	AA383623	Hs.293616	ESTs	10.0
	436659	AI217900	Hs.144464	ESTs	10.0
55	405675			predicted exon	10.0
	413466	BE141737	Hs.254105	"enolase 1, (alpha)"	10.0
	447198	D61523	Hs.283435	ESTs	10.0
	403306	NM_006825	Hs.74368	"transmembrane protein (63kD), endoplasmic reticulum/Go	10.0
	413544	BE147225		"gb:PM2-HT0225-031299-003-f11 HT0225 Homo sapiens	9.9
60	437094	AW103746	Hs.136907	ESTs	9.9
	401497			predicted exon	9.9
	416203	H27794	Hs.269055	ESTs	9.9
	426882	AA393108	Hs.97365	ESTs	9.9
	454874	AW836407		"gb:PM3-LT0031-301299-002-b09 LT0031 Homo sapiens	9.9
65	406702	Z20656	Hs.278432	"myosin, heavy polypeptide 6, cardiac muscle, alpha (cardio	9.9
	404952			predicted exon	9.9
	430691	C14187	Hs.103538	ESTs	9.9
	444518	AI160278	Hs.146884	ESTs	9.8
	416665	H72974		"gb:yu28a10.s1 Soares fetal liver spleen 1NFLS Homo sapie	9.8
70	438691	AA906288	Hs.212184	ESTs	9.8
	405636			predicted exon	9.8
	437242	AA747538	Hs.187942	ESTs	9.8
	425627	AF019612	Hs.297007	ESTs	9.8
	452226	AA024898	Hs.296002	ESTs	9.8
	418986	AI123555	Hs.81796	ESTs	9.8
75	441139	AW449009	Hs.126647	ESTs	9.7
	427244	AA402400	Hs.178045	ESTs	9.7
	423756	AA828125		"gb:od71a09.s1 NCL_CGAP_Ov2 Homo sapiens cDNA clo	9.7
	457940	AL360159	Hs.30445	Homo sapiens mRNA full length insert cDNA clone EURO	9.6
80	443526	AW792804	Hs.134002	ESTs	9.6
	440576	AW449775	Hs.126008	ESTs	9.6
	419088	AI538323	Hs.77496	small nuclear ribonucleoprotein polypeptide G	9.6
	454707	AW814989		"gb:MR1-ST0206-170400-024-g05 ST0206 Homo sapiens	9.6
	446252	AI283125	Hs.150009	ESTs	9.6
	434374	AA631439		"gb:np85d02.s1 NCL_CGAP_Thy1 Homo sapiens cDNA cl	9.6

	403093		predicted exon	9.6
	454633	AW811380	"gb:IL3-ST0143-290999-019-005 ST0143 Homo sapiens c	9.6
	407291	AA001464	gb:ze45b01.r1 Soares retina N2b4HR Homo sapiens cDNA	9.5
5	455203	AW865450	"gb:PM4-SN0020-010400-008-b09 SN0020 Homo sapiens	9.5
	403647		predicted exon	9.5
	401530		predicted exon	9.5
	414281	BE269751	Hs.288995 hypothetical protein FLJ20813	9.5
	411057	AW815098	"gb:QV4-ST0212-091199-023-f10 ST0212 Homo sapiens c	9.5
10	416953	H14425	Hs.27947 ESTs	9.5
	450174	T82121	Hs.177285 ESTs	9.5
	422949	AA319435	"gb:EST21657 Adrenal gland tumor Homo sapiens cDNA 5	9.5
	402112	R58624	Hs.2186 eukaryotic translation elongation factor 1 gamma	9.5
	457888	AA742279	Hs.293346 ESTs	9.4
15	458145	AZ39457	Hs.130794 ESTs	9.4
	452332	AW014859	Hs.101657 ESTs	9.4
	434950	AW974892	"gb:EST386997 MAGE resequences, MAGN Homo sapien	9.3
	409601	AF237621	Hs.80828 keratin 1 (epidermolytic hyperkeratosis)	9.3
	418968	XD4430	Hs.93913 "interleukin 6 (interferon, beta 2)"	9.3
20	436211	AK001581	Hs.80961 "polymerase (DNA directed), gamma"	9.3
	428412	AA428240	Hs.126083 ESTs	9.3
	449441	AI656040	Hs.186532 ESTs	9.3
	458771	AW295151	Hs.163612 ESTs	9.3
	458543	AA213403	Hs.257542 ESTs	9.3
25	414257	AI828600	Hs.21124 "ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	9.3
	442826	AI018777	Hs.131241 ESTs	9.3
	446740	AI611635	Hs.192605 ESTs	9.2
	408938	AA059013	Hs.22607 ESTs	9.2
	434157	AI538316	Hs.158451 ESTs	9.2
30	408774	AW270899	Hs.254569 ESTs	9.2
	424268	AA397653	Hs.144339 Human DNA sequence from clone 495010 on chromosome	9.2
	415715	F30364	"gb:HSPD20786 HM3 Homo sapiens cDNA clone s400009	9.1
	405277		predicted exon	9.1
	412167	AW897230	"gb:CM0-NN0057-150400-335-a11 NN0057 Homo sapiens	9.1
35	442771	AW409608	Hs.101550 ESTs	9.1
	404898		predicted exon	9.1
	401230		predicted exon	9.1
	400623		predicted exon	9.1
	418808	AI821836	Hs.10359 ESTs	9.1
40	436396	AI683487	Hs.299112 "Homo sapiens cDNA FLJ11441 fis, clone HEMBA100132	9.1
	440466	AA885871	Hs.135727 ESTs	9.0
	437568	AI954795	Hs.156135 ESTs	9.0
	405382		predicted exon	9.0
	435673	AF202961	Hs.284200 "Homo sapiens uncharacterized gastric protein ZG12P mRNA	9.0
45	405848		predicted exon	9.0
	437229	AW976005	"gb:EST388114 MAGE resequences, MAGN Homo sapien	9.0
	417728	AW138437	Hs.24790 KIAA1573 protein	9.0
	454597	AW809648	"gb:MR4-ST0124-261099-015-d01 ST0124 Homo sapiens	9.0
	427093	AA398118	Hs.97579 ESTs	9.0
50	408000	L11690	Hs.620 bullous pemphigoid antigen 1 (230/240kD)	9.0
	440556	AW206958	Hs.125968 ESTs	9.0
	400163		predicted exon	8.9
	420120	AL049610	Hs.95243 transcription elongation factor A (SII)-like 1	8.9
	417549	AA203651	gb:z58f10.r1 Soares_fetal_liver_spleen_INFLS_S1 Homo	8.9
55	406163		predicted exon	8.9
	437918	AI761449	Hs.121629 ESTs	8.9
	449419	R34910	Hs.119172 ESTs	8.9
	434683	AW298724	Hs.202639 ESTs	8.9
	418432	M14156	Hs.85112 insulin-like growth factor 1 (somatomedin C)	8.9
60	454590	AW809762	Hs.222056 "Homo sapiens cDNA FLJ11572 fis, clone HEMBA100337	8.8
	454574	AW809109	"gb:MR4-ST0117-070100-027-a04 ST0117 Homo sapiens c	8.8
	441433	AA933809	Hs.42746 ESTs	8.8
	416858	AW979294	Hs.85634 ESTs	8.8
	421978	AJ243662	Hs.110196 NICE-1 protein	8.8
65	451528	AA018297	Hs.35493 ESTs	8.8
	408751	N91553	Hs.258343 ESTs	8.7
	401862		predicted exon	8.7
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	454455	AW752710	"gb:IL3-CT0219-281099-024-A03 CT0219 Homo sapiens c	8.7
70	455592	BE008002	"gb:QV0-BND147-290400-214-h04 BND147 Homo sapiens	8.7
	417650	T05870	Hs.100640 ESTs	8.7
	456309	AA225423	"gb:nc24a12.r1 NCL_CGAP_Pr1 Homo sapiens cDNA clon	8.7
	432030	AI908400	Hs.143789 ESTs	8.7
	421492	BE176990	Hs.104916 hypothetical protein FLJ21940	8.7
75	402576		predicted exon	8.7
	425874	N67325	Hs.247132 ESTs	8.7
	403334		predicted exon	8.7
	408562	AI436323	Hs.31141 "Homo sapiens mRNA for KIAA1568 protein, partial cds"	8.7
	439443	AF086261	Hs.127892 ESTs	8.7
80	428600	AW863261	Hs.15036 "ESTs, Highly similar to AF161358 1 HSPC095 [H.sapiens	8.7
	414539	BE379046	"gb:601236646F1 NIH_MGC_44 Homo sapiens cDNA clon	8.6
	432527	AW975028	Hs.102754 ESTs	8.6
	403273		predicted exon	8.6
	452077	BE144949	"gb:RC2-HT0187-041099-011-d12 HT0187 Homo sapiens	8.6
	444598	AI288830	Hs.149924 ESTs	8.6

	434066	AF116649	Hs.283944	"Homo sapiens PRO0566 mRNA, complete cds"	8.6
	429643	AA455889	Hs.187548	ESTs	8.6
	432340	AA534222		gb:J21d02.s1 NCL CGAP_AA1 Homo sapiens cDNA clone	8.6
5	446142	A1754693	Hs.145968	ESTs	8.6
	417412	X16886	Hs.82112	"interleukin 1 receptor, type I"	8.6
	416913	AW934714		"gb:RC1-DT0001-031299-011-a11 DT0001 Homo sapiens	8.5
	451318	AA029888	Hs.95071	ESTs	8.5
	405547			predicted exon	8.5
10	423843	AA332652		"gb:EST36627 Embryo, 8 week I Homo sapiens cDNA 5' end	8.5
	454145	AA046872	Hs.62798	ESTs	8.4
	401200			predicted exon	8.4
	404166			predicted exon	8.4
	412761	AW995092		"gb:QV0-BN0041-030300-145-a10 BN0041 Homo sapiens	8.4
15	412333	AW937485		"gb:QV3-DT0044-221299-045-b09 DT0044 Homo sapiens	8.4
	455092	BE152428		"gb:CM0-HT0323-151299-126-b04 HT0323 Homo sapiens	8.4
	419281	H96452	Hs.42189	ESTs	8.4
	446171	A374927		gb:ta66c04.x1 Soares fetal_fetus_Nb2HF8_9w Homo sapie	8.3
	437362	AL359561	Hs.16493	hypothetical protein DKFZp762N2316	8.3
20	402631			predicted exon	8.3
	458573	AV653838	Hs.295131	ESTs	8.3
	439185	AF087976	Hs.233343	ESTs	8.3
	445881	AI263029	Hs.210689	ESTs	8.3
	449737	AI668581	Hs.248316	ESTs	8.3
25	401830	AJ004832	Hs.5038	neuropathy target esterase	8.3
	421991	NM_014918	Hs.110488	KIAA0990 protein	8.3
	416998	W91892	Hs.59609	ESTs	8.2
	443626	AI540644	Hs.138479	"ESTs, Moderately similar to ALU7_HUMAN ALU SUBF	8.2
	407471	D55644		gb:Human spleen PABL (pseudautosomal boundary-like se	8.2
30	402664			predicted exon	8.2
	417682	W69561		gb:zd47a08.r1 Soares fetal_heart_NbHH19W Homo sapien	8.2
	424983	A1742434	Hs.169911	ESTs	8.2
	434353	AA630863	Hs.131375	"ESTs, Weakly similar to ALUB_HUMAN III ALU CLAS	8.2
	453448	AL036710	Hs.209527	ESTs	8.2
35	455121	BE155459		"gb:QV0-HT0368-040100-082-06 HT0368 Homo sapiens	8.2
	404270			predicted exon	8.1
	438297	AW515196	Hs.258238	"ESTs, Moderately similar to ALU1_HUMAN ALU SUBF	8.1
	418122	R42778	Hs.22217	ESTs	8.1
	419929	U90268	Hs.93810	cerebral cavernous malformations 1	8.1
40	400925			predicted exon	8.1
	403350			predicted exon	8.1
	426116	AA868729	Hs.144694	ESTs	8.1
	441518	AW161697	Hs.294150	ESTs	8.1
	421888	AA299780	Hs.121036	ESTs	8.1
45	402745			predicted exon	8.1
	402071			predicted exon	8.1
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated protein homolog	8.0
	430372	AJ206173	Hs.211375	ESTs	8.0
	449867	AJ672379	Hs.73919	"clathrin, light polypeptide (Lcb)"	8.0
50	422174	AL049325	Hs.112493	Homo sapiens mRNA; cDNA DKFZp554D036 (from clone	8.0
	413382	BE090689		"gb:RC1-BT0720-280300-011-08 BT0720 Homo sapiens c	8.0
	456502	A1798611	Hs.157277	ESTs	8.0
	405336			predicted exon	8.0
	405917			predicted exon	8.0
55	436007	AJ247716	Hs.232168	ESTs	8.0
	439192	AW970536	Hs.105413	ESTs	8.0
	437724	AW444828	Hs.184323	ESTs	8.0
	452755	AW138937	Hs.213436	ESTs	8.0
	401781			predicted exon	7.9
60	406057			predicted exon	7.9
	406289	AW068311	Hs.82582	"integrin, beta-like 1 (with EGF-like repeat domains)"	7.9
	421459	AJ821539	Hs.97249	ESTs	7.9
	448251	BE280486	Hs.84045	"Homo sapiens cDNA FLJ11979 fis, clone MEMBB100128	7.9
	429125	AA446854	Hs.271004	ESTs	7.9
65	440154	BE077129	Hs.126119	"Homo sapiens cDNA FLJ13273 fis, clone OVARC100101	7.9
	413233	AW578713	Hs.47534	"ESTs, Weakly similar to ORF YKL201c [S.cerevisiae]"	7.9
	438268	AA782163	Hs.293502	ESTs	7.9
	452468	N84635	Hs.29684	Human DNA sequence from clone 682J15 on chromosome 6	7.9
	441194	BE274581		"gb:60112087OF1 NIH_MGC_20 Homo sapiens cDNA clone	7.9
70	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	7.9
	445090	AW205208	Hs.147293	ESTs	7.9
	431292	AA370141	Hs.251453	Human DNA sequence from clone 967N21 on chromosome	7.9
	414266	BE267834		"gb:601124428F1 NIH_MGC_8 Homo sapiens cDNA clone	7.8
	407839	AA045144	Hs.161566	ESTs	7.8
75	456101	AA159478		gb:zo74d06.s1 Stratagene pancreas (937208) Homo sapiens	7.8
	455853	BE147225		"gb:PM2-HT0225-031299-003-411 HT0225 Homo sapiens	7.8
	414995	C18200		gb:C18200 Human placenta cDNA (TFujwara) Homo sapie	7.8
	447247	AW369351	Hs.287955	"Homo sapiens cDNA FLJ13090 fis, clone NTZRP3002142	7.8
	416161	T26661		"gb:AB65C7R Infant brain, LLNL array of Dr. M. Soares 1	7.8
80	446435	AW206737	Hs.253582	ESTs	7.8
	403698			predicted exon	7.8
	424914	AA348410	Hs.119065	ESTs	7.8
	409731	AA125985	Hs.56145	"thymosin, beta, identified in neuroblastoma cells"	7.8
	401604			predicted exon	7.8
	413025	AA805265	Hs.291646	ESTs	7.8

	405896		predicted exon	7.8
	454505	AW801365	"gb:IL5-UM0067-240300-050-a01 UM0067 Homo sapiens	7.7
	448283	A1340462	ribosomal protein L12	7.7
5	434098	AA625499	"gb:af69g08.r1 Soares_NhHMPu_S1 Homo sapiens cDNA	7.7
	431673	AW971302	ESTs	7.7
	421029	AW057782	ESTs	7.7
	408391	AW859276	"gb:MR1-CT0352-240200-105-d02 CT0352 Homo sapiens	7.7
	422529	AW015128	ESTs	7.7
10	454389	AW752571	"gb:IL3-CT0213-170100-055-F02 CT0213 Homo sapiens c	7.7
	427821	AA470158	ESTs	7.7
	434657	AA641876	ESTs	7.7
	445628	A1344166	ESTs	7.7
	424872	AA347923	"gb:EST54302 Fetal heart II Homo sapiens cDNA 5' end, m	7.7
15	439232	N46590	ESTs	7.7
	441417	A1733297	ESTs	7.7
	453598	AA441838	ESTs	7.7
	430440	X52599	"nerve growth factor, beta polypeptide"	7.7
	413306	AW303544	ESTs	7.7
20	400968		predicted exon	7.7
	446726	AW300144	"Homo sapiens cDNA FLJ11629 fis, clone HEMBA100424	7.7
	427504	AA776743	ESTs	7.7
	405621		predicted exon	7.6
	414127	A1431863	ESTs	7.6
25	409868	AW502152	gb:LI-HF-BR0p-efr-f-11-0-UI.r1 NIH_MGC_52 Homo sap	7.6
	446232	A1281848	ESTs	7.6
	403568		predicted exon	7.6
	451458	A1797558	ESTs	7.6
	439157	AA912737	ESTs	7.6
30	401793		predicted exon	7.6
	429839	A1190291	ESTs	7.6
	445672	A1907438	ESTs	7.6
	449444	AW818436	"solute carrier family 16 (monocarboxylic acid transporters)	7.6
	447499	AW262580	KIAA1621 protein	7.6
35	421773	W69233	ESTs	7.6
	439706	AW872527	ESTs	7.5
	432189	AA527941	"gb:nh30c04.s1 NCL_CGAP_Py3 Homo sapiens cDNA clone	7.5
	402050		predicted exon	7.5
	429687	A1675749	nucleoporin 153kD	7.5
40	423193	R07299	"Homo sapiens cDNA FLJ13502 fis, clone PLACE1004836	7.5
	416548	H62953	gb:yr4706.r1 Soares fetal liver spleen 1NFLS Homo sapien	7.5
	443236	A1079486	ESTs	7.5
	436053	A1057224	ESTs	7.4
	437191	NM_006846	"serine protease inhibitor, Kazal type, 5"	7.4
45	451829	AW964081	ESTs	7.4
	443151	A1827193	ESTs	7.4
	452055	A1377431	ESTs	7.4
	445265	A1218295	ESTs	7.4
	401032		predicted exon	7.4
50	448184	BE541249	ESTs	7.4
	414808	T95945	gb:ye42e02.r1 Soares fetal liver spleen 1NFLS Homo sapien	7.4
	418540	A1821597	"ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	7.4
	410449	AW748954	Ser/Arg-related nuclear matrix protein (plenty of prolines 1	7.4
	435568	AA688048	ESTs	7.4
55	459160	A1904723	"gb:CM-BT066-120299-092 BT066 Homo sapiens cDNA,	7.4
	419753	N42531	gb:yy11c12.r1 Soares melanocyte 2N6HM Homo sapiens cD	7.4
	432383	AK000144	"Homo sapiens cDNA FLJ20137 fis, clone COL07137"	7.4
	404893		predicted exon	7.4
	425349	AA425234	ribose 5-phosphate isomerase A (ribose 5-phosphate epimer	7.4
60	413864	BE175582	"gb:RCS-HT0580-100500-022-C01 HT0580 Homo sapiens	7.3
	426871	AA393041	ESTs	7.3
	415613	R20233	gb:yg18h11.r1 Soares infant brain 1NIB Homo sapiens cDN	7.3
	427025	AA397589	ESTs	7.3
	444683	A1375101	"ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	7.3
65	447700	AA201183	"ESTs, Weakly similar to similar to serine/threonine kinase	7.3
	412740	AW993984	"gb:RC1-BN0035-130400-013-a05 BN0035 Homo sapiens	7.3
	416642	T96118	"ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	7.3
	416506	H59879	ESTs	7.3
	426130	AA853282	gb:NHTBCae0407.r1 Normal Human Trabecular Bone Cell	7.3
70	407392	AB032369	"gb:Homo sapiens MIST mRNA, partial cds."	7.3
	432365	AK001106	hypothetical protein FLJ10244	7.3
	451221	A1949701	ESTs	7.3
	443161	A1038316	gb:zx48c08.x1 Soares_total_fetus_Nb2HF8_9w Homo sapi	7.3
	418186	BE541042	"Homo sapiens cDNA FLJ13496 fis, clone PLACE1004471	7.3
75	439152	H65014	gb:yu66f10.r1 Weizmann Olfactory Epithelium Homo sapie	7.2
	459534	BE386808	ESTs	7.2
	443326	BE156494	ESTs	7.2
	417351	T90278	ESTs	7.2
	454182	AW177335	"gb:CM1-CT0129-180899-005-b08 CT0129 Homo sapiens	7.2
80	402298		predicted exon	7.2
	458562	N34128	ESTs	7.2
	407021	U52077	"gb:Human mariner1 transposase gene, complete consensus	7.2
	449276	AW241510	ESTs	7.2
	418251	AA832123	ESTs	7.2
	420788	AA937957	ESTs	7.2

	401881			predicted exon	7.2
	456436	AA251079	Hs.158386	ESTs	7.2
	413425	F20956		"gbtHSPD05390 HM3 Homo sapiens cDNA clone 032-X4-	7.2
5	448966	AW372914	Hs.287462	"Homo sapiens cDNA FLJ11875 fis, clone HEMBA100707	7.2
	429340	N35938	Hs.199429	Homo sapiens mRNA; cDNA DKFZp434M2216 (from clon	7.2
	406053			predicted exon	7.2
	405851			predicted exon	7.2
	431009	BE149762	Hs.248213	"gap junction protein, beta 6 (connexin 30)"	7.2
10	426682	AA879474	Hs.122710	ESTs	7.2
	408536	AW381532	Hs.135188	ESTs	7.1
	455013	BE073250		"gbtMR0-BT0551-060300-102-e05 BT0551 Homo sapiens	7.1
	428910	W03667	Hs.193792	ESTs	7.1
	424634	NM_003613	Hs.151407	"cartilage intermediate layer protein, nucleotide pyrophosph	7.1
15	449794	AW444502	Hs.256982	"ESTs, Highly similar to AF116865 1 hedgehog-interacting	7.1
	423410	AF058989	Hs.128231	"G antigen, family B, 1 (prostate associated)"	7.1
	445460	AI797473	Hs.209468	ESTs	7.1
	447285	AI371849	Hs.200696	"ATPase, Class VI, type 11C"	7.1
	419750	AL079741	Hs.183114	"Homo sapiens cDNA FLJ14236 fis, clone NT2RP4000515	7.1
20	438986	AF085888	Hs.269307	ESTs	7.1
	420757	X78582	Hs.099915	androgen receptor (dihydrotestosterone receptor; testicular	7.1
	432479	AL042844	Hs.275575	katanin p80 (WD40-containing) subunit B 1	7.1
	449733	R74548	Hs.29438	"Homo sapiens cDNA FLJ12094 fis, clone HEMBB100260	7.1
	437846	AA773866	Hs.244569	ESTs	7.1
25	454834	AW846080		"gbtMR3-CT0176-081099-002-b09 CT0176 Homo sapiens	7.1
	421929	AA300543	Hs.247360	ESTs	7.1
	401780			predicted exon	7.0
	448106	AI800470	Hs.171941	ESTs	7.0
	448835	BE277929	Hs.11081	"ESTs, Weakly similar to S57447 HPBR1-7 protein [H.sap	7.0
30	400842			predicted exon	7.0
	428364	AA451797	Hs.201202	"ESTs, Moderately similar to Pro-Pol-dUTPase polyprotein	7.0
	454963	AW847647		"gbtIL3-CT0213-280100-056-A08 CT0213 Homo sapiens c	7.0
	423891	AK002042	Hs.134795	"Homo sapiens cDNA FLJ11180 fis, clone PLACE1007452	7.0
	407506	U71600		"gbtHuman zinc finger protein zfp31 (zfp31) mRNA, partial	7.0
35	413802	AW964490	Hs.32241	ESTs	7.0
	440051	BE555980		"gbt601345293F1 NIH_MGC_8 Homo sapiens cDNA clone	7.0
	446283	AI948801	Hs.171073	ESTs	7.0
	419236	AA330447	Hs.135159	"Homo sapiens cDNA FLJ11481 fis, clone HEMBA100180	7.0
	405472			predicted exon	7.0
40	435024	AI863518	Hs.127743	"ESTs, Weakly similar to V-ATPase G-subunit like protein	7.0
	453969	AW090783	Hs.301731	"Homo sapiens cDNA FLJ11738 fis, clone HEMBA100547	7.0
	404992			predicted exon	7.0
	428129	AI244311	Hs.26912	ESTs	7.0
	414315	Z24878		"gbtHS86SD052 STRATAGENE Human skeletal muscle cD	7.0
45	400491	H25530	Hs.50868	"solute carrier family 22 (organic cation transporter), memb	6.9
	459275	AI808913	Hs.118321	ESTs	6.9
	450853	AA479629	Hs.44243	ESTs	6.9
	457460	AI143312	Hs.164004	ESTs	6.9
	434168	AI204525	Hs.116156	ESTs	6.9
50	445153	AI214671		"gbtqm32d02x1 NCL_CGAP_Lu5 Homo sapiens cDNA clo	6.9
	450028	AI912012	Hs.200737	ESTs	6.9
	414954	DB1402		gbtHUM162A03B Human fetal brain (TFujwara) Homo sa	6.9
	459478	AW195566	Hs.263182	ESTs	6.9
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (from clon	6.9
55	401050			predicted exon	6.9
	447588	AI394154	Hs.279659	"ESTs, Weakly similar to unknown protein [H.sapiens]"	6.9
	449002	AI620018	Hs.117461	ESTs	6.9
	452759	AW590773	Hs.258996	ESTs	6.9
	443220	R85304	Hs.132032	"Homo sapiens cDNA FLJ11683 fis, clone HEMBA100490	6.9
60	400749			predicted exon	6.8
	406277			predicted exon	6.8
	433785	BE044593	Hs.112704	ESTs	6.8
	434129	AI807757	Hs.221041	ESTs	6.8
	453369	BE551550	Hs.232630	ESTs	6.8
65	411722	AW875942		"gbtCM1-PT0013-131299-067-b10 PT0013 Homo sapiens	6.8
	455152	AW858821		"gbtCM0-CT0342-021299-115-f04 CT0342 Homo sapiens	6.8
	412670	AA115456		gbtck89b05.r1 Soares_pregnant_uterus_NibHPU Homo sapi	6.8
	418054	N40340	Hs.191510	"ESTs, Weakly similar to ORF2 [M.musculus]"	6.8
	421316	AA287203	Hs.251397	SMA5	6.8
70	432363	AA534489		gbtMT6g11.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone	6.8
	458603	AW103046	Hs.6162	KIAA0771 protein	6.8
	439527	AW298119	Hs.202536	ESTs	6.8
	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane protein 2	6.8
	439127	AW978465	Hs.292368	ESTs	6.8
75	434890	AF161345	Hs.283930	"Homo sapiens HSPC082 mRNA, partial cds"	6.8
	429413	NM_014058	Hs.201877	DESC1 protein	6.7
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	6.7
	447252	RS0916		gbtym01e10.r1 Soares adult brain N2b4HB55Y Homo sapien	6.7
	455851	BE146879		"gbtQV4-HT0222-261099-014-c11 HT0222 Homo sapiens	6.7
80	439509	AF086332	Hs.58314	ESTs	6.7
	418858	AW961605	Hs.21145	"Homo sapiens cDNA: FLJ22489 fis, clone HRC10951"	6.7
	419323	AI092379	Hs.135275	ESTs	6.7
	415317	Z43388	Hs.5570	hypothetical protein FLJ10006	6.7
	418654	AA226334	Hs.154291	ESTs	6.7
	407413	AF067801		"gbtHomo sapiens HDCGC21P mRNA, complete cds."	6.7

	439694	AA843915	Hs.54707	ESTs	6.7
	451191	N67900	Hs.118446	ESTs	6.7
	454006	U12775	Hs.37006	agouti (mouse)-signaling protein	6.7
5	443657	R14973		gb:yf4210.s1 Soares fetal liver spleen 1N1LS Homo sapien	6.7
	455879	BE153275		*gb:PMO-HT0335-180400-008-e11 HT0335 Homo sapiens	6.7
	451368	BE242152	Hs.288417	protein serine threonine kinase Ctk4	6.7
	453509	AL040021		gb:DKFZp434N1812_r1 434 (synonym: htes3) Homo sapie	6.7
	420892	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cerevisiae PWP1	6.7
10	423372	AL246375	Hs.154458	ESTs	6.7
	450316	W84448	Hs.17850	ESTs	6.7
	447795	AW295151	Hs.163612	ESTs	6.7
	413252	BE074910		*gb:RCS-BT0580-170300-021-F12 BT0580 Homo sapiens	6.7
	405771			predicted exon	6.6
	411483	AW848115		*gb:IL3-CT0214-301299-048-C09 CT0214 Homo sapiens c	6.6
15	420271	A954365	Hs.42892	ESTs	6.6
	431948	AA917706	Hs.194616	ESTs	6.6
	409629	AW449589	Hs.279724	ESTs	6.6
	458841	W26965		gb:54d10 Human retina cDNA randomly primed sublibrary	6.6
20	416565	AW000950	Hs.44970	ESTs	6.6
	409097	AA677827	Hs.144269	ESTs	6.6
	441832	AL018249	Hs.128062	ESTs	6.6
	457285	AL038858	Hs.228780	*ESTs, Highly similar to AF199597 1 A-type potassium cha	6.6
	406504			predicted exon	6.6
25	414606	BE387771		*gb:601283251F1 NIH_MGC_44 Homo sapiens cDNA clon	6.6
	452956	AW003578	Hs.231872	ESTs	6.6
	410743	AA089474	Hs.272153	ESTs	6.6
	404599			predicted exon	6.6
	423575	C18863	Hs.163443	*Homo sapiens cDNA FLJ11576 fs, clone HEMBA100354	6.6
30	443027	AL027847	Hs.253550	ESTs	6.6
	458663	AV558444	Hs.280776	*Homo sapiens cDNA FLJ13684 fs, clone PLACE2000021	6.6
	431277	AA501806	Hs.249965	ESTs	6.6
	445232	BE294357		*gb:601172878F1 NIH_MGC_17 Homo sapiens cDNA clon	6.6
	459170	AL095518		*gb:RC-BT091-210199-098 BT091 Homo sapiens cDNA, m	6.6
35	437876	AA770151	Hs.126424	ESTs	6.6
	406752	AL285598	Hs.217493	annexin A2	6.6
	401245			predicted exon	6.6
	446102	AW168067	Hs.252956	ESTs	6.5
40	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	6.5
	421160	AL080215	Hs.102301	Homo sapiens mRNA; cDNA DKFZp586J0323 (from clone	6.5
	458831	H71739	Hs.200227	ESTs	6.5
	408914	AW450309		gb:UH-H-B13-alc-q-08-0-ULs1 NCI_CGAP_Sub5 Homo sa	6.5
	411018	AW813428		*gb:MR3-ST0192-010200-210-c05 ST0192 Homo sapiens c	6.5
	436562	H71937	Hs.169756	*complement component 1, s subcomponent	6.5
45	457620	AA602711		*gb:ncp03h06.s1 NCI_CGAP_P2 Homo sapiens cDNA clon	6.5
	438647	AA813118	Hs.163230	ESTs	6.5
	439570	T79925	Hs.269165	ESTs	6.5
	419273	BE271180	Hs.293490	ESTs	6.5
	443745	AB039670	Hs.9728	ALEX1 protein	6.5
50	431029	BE392725	Hs.248571	Homo sapiens PAC clone RP5-1163J12 from 7q21.2-q31.1	6.5
	458695	AV660159	Hs.282284	ESTs	6.5
	410966	AW812088		*gb:RC4-ST0173-191099-032-a07 ST0173 Homo sapiens c	6.4
	417135	AA422067	Hs.50547	ESTs	6.4
	416441	BE407197		*gb:601301552F1 NIH_MGC_21 Homo sapiens cDNA clon	6.4
55	413702	BE170313		*gb:QV4-HT0536-040500-193-g02 HT0536 Homo sapiens	6.4
	452563	AL070552		*gb:RC-BT147-120499-044 BT147 Homo sapiens cDNA, m	6.4
	408956	AK001868	Hs.295306	*ESTs, Highly similar to unnamed protein product [H.sapien	6.4
	406349			predicted exon	6.4
	425420	BE536911	Hs.234545	*ESTs, Weakly similar to AF155135 1 novel retinal pigmen	6.4
60	459430	AW662886		gb:h8zh11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDN	6.4
	425733	F13287	Hs.159388	Homo sapiens clone 23578 mRNA sequence	6.4
	458678	AL306162	Hs.170938	*ESTs, Weakly similar to KIAA0705 protein [H.sapiens]	6.4
	429695	AA835714	Hs.293556	ESTs	6.4
	426872	AA410446	Hs.112011	*ESTs, Weakly similar to unknown [H.sapiens]	6.4
65	437152	AL050027		gb:Homo sapiens mRNA; cDNA DKFZp566C0324 (from c	6.4
	440517	AW139632	Hs.132246	ESTs	6.4
	450877	AL799608	Hs.29178	ESTs	6.4
	410664	NM_006033	Hs.65370	*lipase, endothelial	6.4
	405793			predicted exon	6.4
70	418709	AA227394		gb:zr17c10.r1 Stratagene NT2 neuronal precursor 937230 H	6.4
	428684	AA431792	Hs.44784	ESTs	6.4
	448516	AW898595		*gb:RC1-NN0073-260400-011-g09 NN0073 Homo sapiens	6.4
	400983			predicted exon	6.3
	422365	AF035537	Hs.115521	*REV3 (yeast homolog)-like, catalytic subunit of DNA poly	6.3
75	425612	BE004257		*gb:CM0-BN0103-180300-296-c04 BN0103 Homo sapiens	6.3
	401521			predicted exon	6.3
	430290	AL734110	Hs.136355	ESTs	6.3
	414931	AK000342	Hs.77646	Homo sapiens mRNA; cDNA DKFZp761M0223 (from clon	6.3
	437939	AW298600	Hs.141840	*ESTs, Weakly similar to S59501 Interferon receptor JFNA	6.3
80	451842	AL820539	Hs.267087	*ESTs, Moderately similar to ALU4_HUMAN ALU SUBF	6.3
	405810			predicted exon	6.3
	443747	AV646352		*gb:AV646352 GLC Homo sapiens cDNA clone GLCAME	6.3
	427287	NM_014903	Hs.174188	KIAA0338 protein	6.3
	413521	BE145814		*gb:MR0-HT0208-101299-202-a04 HT0208 Homo sapiens	6.3
	429090	AW820278	Hs.99066	ESTs	6.3

	451488	H22999	Hs.208846	ESTs	6.3
	455713	BE069891		"gb:QV4-BT0401-201299-064-b01 BT0401 Homo sapiens	6.3
	452161	R43077	Hs.221747	ESTs	6.3
	428647	AA830050	Hs.124344	ESTs	6.3
5	445063	AI246275	Hs.149198	ESTs	6.3
	456671	AB011142	Hs.114293	KIAA0570 gene product	6.3
	401508			predicted exon	6.3
	412677	AW029608	Hs.17384	ESTs	6.3
10	441720	AJ346487	Hs.28739	ESTs	6.3
	418051	AW182535	Hs.19479	ESTs	6.3
	438014	N71183	Hs.121806	"Homo sapiens cDNA FLJ11971 fls, clone HEMBB100120	6.3
	432101	AI918950	Hs.11092	"Homo sapiens cDNA FLJ14290 fls, clone PLACE1006795	6.3
	421032	AW283133	Hs.101340	ESTs	6.3
15	436532	AA721622		"gb:mv54h12.r1 NCL CGAP_Ew1 Homo sapiens cDNA clo	6.3
	431318	AA502700	Hs.293147	ESTs	6.3
	413470	N20934		gb:yn54c11.s1 Soares melanocyte 2NbHM Homo sapiens c	6.3
	402425			predicted exon	6.3
	455993	BE179085		"gb:RC0-HT0613-140300-021-d06 HT0613 Homo sapiens	6.3
20	400160			predicted exon	6.3
	413795	AL040178	Hs.142003	ESTs	6.2
	405071			predicted exon	6.2
	403741			predicted exon	6.2
	432489	AJB04855	Hs.207530	ESTs	6.2
25	402298			predicted exon	6.2
	446091	AW022192	Hs.200197	ESTs	6.2
	444788	AI871122	Hs.202821	ESTs	6.2
	404972			predicted exon	6.2
	400227			predicted exon	6.2
30	433804	AI936561	Hs.112740	ESTs	6.2
	448807	AI571940	Hs.7549	ESTs	6.2
	404340			predicted exon	6.2
	424632	AB014523	Hs.151408	KIAA0623 gene product	6.2
	449547	H93543	Hs.117963	ESTs	6.2
35	406945	K01383	Hs.203967	metallothionein 1A (functional)	6.2
	433663	AF083131	Hs.229535	CATX-15 protein	6.2
	407809	AW082279	Hs.244106	ESTs	6.2
	418342	BE002723	Hs.293504	"ESTs, Moderately similar to ALU1_HUMAN ALU SUBF	6.2
	438007	AA133008	Hs.158675	ribosomal protein L14	6.2
40	410536	N39533		gb:yy27d04.s1 Soares fetal liver spleen 1NFLS Homo sapi	6.2
	448005	AW207437	Hs.170378	ESTs	6.2
	414083	AL121282	Hs.257786	ESTs	6.2
	405362			predicted exon	6.2
	410102	AW248508	Hs.279727	"Homo sapiens cDNA FLJ14035 fls, clone HEMBA100463	6.2
45	457868	AW975133		"gb:EST387239 MAGE resequences, MAGN Homo sapien	6.2
	407395	AF005082		"gb:Homo sapiens skin-specific protein (xp33) mRNA, part	6.2
	443603	BE502601	Hs.134289	"ESTs, Weakly similar to KIAA1063 protein [H.sapiens]"	6.2
	430051	AA464611	Hs.52515	transducin (beta)-like 2	6.1
	434569	AI311295	Hs.58609	ESTs	6.1
50	430481	AA479678	Hs.203269	"ESTs, Moderately similar to ALU8_HUMAN ALU SUBF	6.1
	402859			predicted exon	6.1
	401260			predicted exon	6.1
	406544			predicted exon	6.1
	428446	AJ024600	Hs.98612	ESTs	6.1
55	412246	AI160873	Hs.69233	"ESTs, Weakly similar to KIAA1064 protein [H.sapiens]"	6.1
	400420	AJ277247	Hs.287369	interleukin 22	6.1
	455652	BE065387		"gb:RC1-BT0314-030500-016-d03 BT0314 Homo sapiens	6.1
	428613	AB037749	Hs.186928	KIAA1328 protein	6.1
	443267	AW450630	Hs.133851	ESTs	6.1
60	433405	AW157568	Hs.156892	ESTs	6.1
	416795	AI497778	Hs.168053	"ESTs, Highly similar to AF227948 1 HBV pX associated p	6.1
	435706	W31254	Hs.7045	GL004 protein	6.1
	450769	AA057418	Hs.33654	ESTs	6.1
	427174	AA398848	Hs.97541	ESTs	6.1
65	425389	AW974499	Hs.192183	ESTs	6.1
	416875	H73802	Hs.35381	ESTs	6.1
	432749	NM_014438	Hs.278909	Interleukin-1 Superfamily e	6.1
	401809			predicted exon	6.1
	403041			predicted exon	6.0
70	408523	AW833259		"gb:RC2-TT0007-131099-011-c01 TT0007 Homo sapiens c	6.0
	416515	N91716	Hs.184140	ESTs	6.0
	452591	BE173164	Hs.1516	Insulin-like growth factor-binding protein 4	6.0
	437146	AA730977		"gb:mv55f05.s1 NCL CGAP_Ew1 Homo sapiens cDNA clo	6.0
	450094	AI174947	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1164 (from clon	6.0
	402529			predicted exon	6.0
75	430706	NM_003540	Hs.247816	"H4 histone family, member C"	6.0
	459186	AI908287		"gb:RC-BT168-020499-035 BT168 Homo sapiens cDNA, m	6.0
	452158	AI699120	Hs.61198	ESTs	6.0
	411237	AW833676		"gb:QV4-TT0008-181199-038-h04 TT0008 Homo sapiens	6.0
	400441	M15530	Hs.99879	B-cell growth factor 1 (12kD)	6.0
80	439398	AA284267	Hs.221504	ESTs	6.0
	440862	H39048	Hs.127432	ESTs	6.0
	415451	H19415	Hs.268720	"ESTs, Moderately similar to ALU1_HUMAN ALU SUBF	6.0
	459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbHPU Homo sapi	6.0
	456072	H54381		gb:yyq89e03.s1 Soares fetal liver spleen 1NFLS Homo sapi	6.0

	409954	AW512770	Hs.266457	ESTs	6.0
	443488	AJ073495	Hs.133912	"ESTs, Weakly similar to methyl-CpG binding domain-cont	6.0
	430825	AJ734186	Hs.185105	ESTs	6.0
5	454466	AA584138	Hs.279895	"Homo sapiens mRNA for KIAA1578 protein, partial cds"	6.0
	456506	AA278277	Hs.194212	ESTs	6.0
	449228	AJ403107	Hs.148590	"ESTs, Weakly similar to AF208846 1 BM-004 [H.sapiens]	6.0
	457727	AW974687		"gbtEST386776 MAGE resequences, MAGM Homo sapien	6.0
	442440	BE464435	Hs.146180	"ESTs, Weakly similar to non-receptor protein tyrosine kina	5.9
10	455110	BE154505		"gbtPMO-HT0343-281299-003-e06 HT0343 Homo sapiens	5.9
	402790			predicted exon	5.9
	409982	BE005839		"gbtRC2-BN0120-250400-012-f03 BN0120 Homo sapiens	5.9
	427635	BE397988	Hs.179982	tumor protein p53-binding protein	5.9
	408948	AW296713	Hs.221441	ESTs	5.9
	402046			predicted exon	5.9
15	416438	R89238	Hs.34262	ESTs	5.9
	403083			predicted exon	5.9
	402481			predicted exon	5.9
	409867	AW502161		gbtUL-HF-BR0p-ajr-g-12-0-ULr1 NIH_MGC_52 Homo sap	5.9
20	420362	U79734	Hs.97206	huntingtin interacting protein 1	5.9
	421375	AA489200	Hs.100595	"ESTs, Moderately similar to ALU1_HUMAN ALU SUBF	5.9
	437630	AI252782	Hs.153029	ESTs	5.9
	443500	AV646388	Hs.137071	ESTs	5.9
	448995	AJ613276	Hs.5662	"guanine nucleotide binding protein (G protein), beta polyp	5.9
25	438214	H06076	Hs.26320	TRABID protein	5.9
	428046	AW812795	Hs.155381	"ESTs, Moderately similar to I38022 hypothetical protein [H	5.9
	431941	AK000106	Hs.272227	"Homo sapiens cDNA FLJ20099 fts, clone COL04544"	5.9
	403358			predicted exon	5.9
	435031	AF075079		gbt:Homo sapiens full length insert cDNA YQ80A08	5.9
30	430032	AW936136	Hs.99610	ESTs	5.9
	423457	F08208	Hs.155606	paired mesoderm homeo box 1	5.9
	422158	L10343	Hs.112341	"protease inhibitor 3, skin-derived (SKALP)"	5.9
	406582			predicted exon	5.9
	418636	AW749855		"gbt:QV4-BT0534-281299-053-c05 BT0534 Homo sapiens	5.8
35	429399	AA452244	Hs.16727	ESTs	5.8
	408590	AW238162	Hs.253873	ESTs	5.8
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psoriasin 1)	5.8
	417421	AL138201	Hs.82120	"nuclear receptor subfamily 4, group A, member 2"	5.8
	401129			predicted exon	5.8
40	434745	AW974445	Hs.185155	"ESTs, Weakly similar to HuEMAP [H.sapiens]"	5.8
	402800			predicted exon	5.8
	436185	AW753380	Hs.49753	"Homo sapiens mRNA for KIAA1561 protein, partial cds"	5.8
	419519	AJ198719	Hs.176376	ESTs	5.8
	452542	AW812256		"gbt:RCO-ST0174-191099-031-a07 ST0174 Homo sapiens c	5.8
45	427166	AA431576	Hs.155658	ESTs	5.8
	416168	H23687		gbtyn72d12r1 Soares adult brain N2b5H855Y Homo sapie	5.8
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (from clon	5.8
	421558	AB011125	Hs.105749	KIAA0553 protein	5.8
	458055	AW979121	Hs.131375	"ESTs, Weakly similar to ALUB_HUMAN !!!! ALU CLAS	5.8
50	418345	AJ001696	Hs.241407	"serine (or cysteine) proteinase inhibitor, clade B (ovalbumi	5.8
	426544	AA492325		gbtng81b11.s1 NCL_CGAP_Pr6 Homo sapiens cDNA clone	5.8
	433544	AJ793211	Hs.165372	"ESTs, Moderately similar to ALU1_HUMAN ALU SUBF	5.8
	442007	AA301116	Hs.142838	"Homo sapiens cDNA: FLJ23444 fts, clone HSI01343"	5.8
	443422	R10288	Hs.301529	ESTs	5.8
55	434311	BE543469	Hs.266263	"Homo sapiens cDNA FLJ14115 fts, clone MAMMA10017	5.8
	424966	AJ077312	Hs.153985	"solute carrier family 7 (cationic amino acid transporter, y+	5.8
	441744	AA960922	Hs.200938	ESTs	5.8
	413101	BE065215		"gbt:RC1-BT0314-310300-015-f01 BT0314 Homo sapiens c	5.7
	445687	W80382	Hs.149297	ESTs	5.7
60	441369	AA931535		gbtzo056a04.s1 NCL_CGAP_Lu5 Homo sapiens cDNA clon	5.7
	414428	BE296906	Hs.182625	VAMP (vesicle-associated membrane protein)-associated pr	5.7
	431211	M86849	Hs.55566	"gap junction protein, beta 2, 26kD (connexin 26)"	5.7
	411541	W03940		gbtza62b02.r1 Soares fetal liver spleen 1NFLS Homo sapien	5.7
	448612	AI696363	Hs.171285	ESTs	5.7
65	419118	AA234223	Hs.139204	ESTs	5.7
	406322			predicted exon	5.7
	454690	AW854639		"gbt:MR1-CT0258-140100-203-d10 CT0258 Homo sapiens	5.7
	450313	AJ038989	Hs.24809	hypothetical protein FLJ10826	5.7
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility protein	5.7
70	449309	AW589823	Hs.224189	ESTs	5.7
	408418	AW963897	Hs.44743	KIAA1435 protein	5.7
	416100	H18700	Hs.268799	ESTs	5.7
	437845	AA769578	Hs.90488	ESTs	5.7
	443345	AJ052508	Hs.164482	"ESTs, Weakly similar to contains similarity to TPR domain	5.7
75	418407	AL044818	Hs.84928	"nuclear transcription factor Y, beta"	5.7
	434557	AW855468	Hs.271866	"ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	5.7
	431688	AA513906		"gbtng57c08.s1 NCL_CGAP_Lip2 Homo sapiens cDNA clo	5.7
	437641	AA811452	Hs.291911	ESTs	5.7
	409319	AW752736	Hs.33565	ESTs	5.7
80	403967	AF030107	Hs.17165	regulator of G-protein signalling 13	5.7
	445189	AI936450	Hs.147482	ESTs	5.7
	414418	H62943	Hs.154188	ESTs	5.7
	446563	BE326588	Hs.141454	ESTs	5.7
	446075	AW451457	Hs.279179	ESTs	5.7
	428068	AW016437	Hs.233482	ESTs	5.7

	438425	AW292922	Hs.293170	ESTs	5.7
	415532	R14780	Hs.12826	ESTs	5.7
	411442	AL043282	Hs.131824	ESTs	5.7
5	443380	A1792478	Hs.135377	ESTs	5.7
	445527	W39694	Hs.83288	ESTs	5.7
	414376	BE393856	Hs.68915	*ESTs, Weakly similar to 16.7Kd protein [H.sapiens]	5.7
	457960	AA771881	Hs.288149	ESTs	5.6
	453283	AA382267	Hs.10653	ESTs	5.6
10	452503	AB000509	Hs.29736	TNF receptor-associated factor 5	5.6
	405227			predicted exon	5.6
	442257	AW503831		gb:U-HF-BN0-atb-b-05-0-ULr1 NIH_MGC_50 Homo sap	5.6
	403403			predicted exon	5.6
	454377	AA076811		gb:7B03C12 Chromosome 7 Fetal Brain cDNA Library Hom	5.6
15	438656	H85310	Hs.209456	*ESTs, Weakly similar to NG22 [H.sapiens]	5.6
	419936	A1792788		*gb:col91d05.y5 NCLCGAP_K1d5 Homo sapiens cDNA clo	5.6
	437267	AW511443	Hs.258110	ESTs	5.6
	430563	AA481269	Hs.178381	ESTs	5.6
	444835	A198994	Hs.158479	ESTs	5.6
20	444902	AJ132099	Hs.12114	vanin 1	5.6
	451800	AW977435	Hs.31890	ESTs	5.6
	405465			predicted exon	5.6
	403891			predicted exon	5.6
	425557	A1694300	Hs.46730	ESTs	5.6
25	432162	AA584062	Hs.272798	hypothetical protein FLJ20413	5.6
	450152	A138635	Hs.22868	ESTs	5.6
	410053	AW579707	Hs.59332	ESTs	5.6
	421285	NM_000102	Hs.1363	*cytochrome P450, subfamily XVII (steroid 17-alpha-hydro	5.6
	425264	AA353953	Hs.20369	*ESTs, Weakly similar to gonadotropin inducible transcript	5.6
30	418844	M62982	Hs.1200	arachidonate 12-lipoxygenase	5.6
	429616	A1882722	Hs.120845	ESTs	5.6
	423528	AB011137	Hs.129740	KIAA0565 gene product	5.6
	403089			predicted exon	5.6
	414373	AW162907	Hs.75969	proline-rich protein with nuclear targeting signal	5.6
35	403687			predicted exon	5.6
	417079	U65690	Hs.81134	interleukin 1 receptor antagonist	5.5
	432501	BE546532	Hs.287329	Fas binding protein 1	5.5
	403691			predicted exon	5.5
	409545	BE296182		*gb:601177324F1 NIH_MGC_17 Homo sapiens cDNA clon	5.5
40	435990	A015862	Hs.131793	ESTs	5.5
	444409	A1792140	Hs.49265	ESTs	5.5
	435478	AA682622		gb:z20f09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo	5.5
	439981	A348408	Hs.124675	*ESTs, Weakly similar to unnamed protein product [H.sapie	5.5
	433644	AW342028	Hs.256112	ESTs	5.5
45	441541	AA938663	Hs.199828	ESTs	5.5
	400709			predicted exon	5.5
	407615	AW753085		*gb:PM1-CT0247-151299-005-a03 CT0247 Homo sapiens	5.5
	424153	AA451737	Hs.141496	MAGE-like 2	5.5
	452465	AA610211	Hs.34244	ESTs	5.5
50	406030			predicted exon	5.5
	431071	AA491379		*gb:aa65f05.r1 NCLCGAP_GCB1 Homo sapiens cDNA cl	5.5
	418088	AA211791	Hs.269668	*Homo sapiens cDNA FLJ13415 fis, clone PLACE1001799	5.5
	453034	BE246010	Hs.184109	ribosomal protein L37a	5.5
	412953	Z45794	Hs.238809	ESTs	5.5
55	425351	A1206234	Hs.155924	cAMP responsive element modulator	5.5
	406149			predicted exon	5.5
	416533	BE244053	Hs.79362	retinoblastoma-like 2 (p130)	5.5
	458378	AJ040535	Hs.150524	ESTs	5.5
	401213			predicted exon	5.5
60	405904			predicted exon	5.5
	445132	Z44811		gb:HSC29G031 normalized Infant brain cDNA Homo sapie	5.5
	405138			predicted exon	5.5
	442238	AW135374	Hs.270949	ESTs	5.5
	416852	AF283776	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (from clon	5.5
65	448691	AA481119	Hs.283558	hypothetical protein PRO1855	5.5
	452242	R50956	Hs.59503	*ESTs, Weakly similar to AF157318 1 AD-017 protein [H.s	5.5
	456994	AA383623	Hs.293616	ESTs	5.5
	440913	A1267491	Hs.160593	ESTs	5.5
	435380	AA679001	Hs.192221	ESTs	5.5
70	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain 12 (meltrin alph	5.5
	414035	Y00630	Hs.75716	*serine (or cysteine) proteinase inhibitor, clade B (ovalbumi	5.4
	459084	H01699	Hs.27289	CGI-125 protein	5.4
	405867			predicted exon	5.4
	414093	BE544867		*gb:601078872F1 NIH_MGC_12 Homo sapiens cDNA clon	5.4
75	447306	A1373163	Hs.170333	ESTs	5.4
	413083	BE064528		*gb:RC4-BT0311-250200-014-h06 BT0311 Homo sapiens	5.4
	404828			predicted exon	5.4
	402543			predicted exon	5.4
	421988	AW450481	Hs.161333	ESTs	5.4
	413404	BE503463	Hs.297431	ESTs	5.4
80	459043	A1806444	Hs.208113	*ESTs, Weakly similar to N-WASP [H.sapiens]	5.4
	404410			predicted exon	5.4
	430264	AA470519		*gb:nc71f10.s1 NCLCGAP_Pr1 Homo sapiens cDNA clon	5.4
	431499	NM_001514	Hs.258561	general transcription factor IIB	5.4
	412566	AW962574		*gb:EST374647 MAGE resequences, MAGG Homo sapten	5.4

	454239	BE176420	Hs.8177	ESTs	5.4
	458163	AA884304	Hs.131163	ESTs	5.4
	446205	AW172662	Hs.149479	ESTs	5.4
5	455275	AW977808		"gb:EST389810 MAGE resequences, MAGO Homo sapien	5.4
	415579	AA165232	Hs.222069	ESTs	5.4
	423200	AA323073	Hs.289083	ESTs	5.4
	440052	AI633744	Hs.195648	ESTs	5.4
	424717	H03754	Hs.152213	"wingless-type MMTV integration site family, member 5A"	5.4
10	420111	AA255652		gb:z21h11.1 NCI_CGAP_GCB1 Homo sapiens cDNA clo	5.4
	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	5.4
	414904	AA157881	Hs.143056	ESTs	5.4
	409479	BE163800	Hs.136912	ESTs	5.4
	404727			predicted exon	5.4
15	446011	AI623778	Hs.145809	ESTs	5.4
	456083	U46922	Hs.77252	fragile histidine triad gene	5.4
	424834	AK001432	Hs.153408	"Homo sapiens cDNA FLJ10570 fis, clone NT2RP2003117	5.4
	425071	NM_013989	Hs.154424	"delodilase, iodothyronine, type II"	5.4
	426065	N32049		gb:z21h11.1 NCI_CGAP_GCB1 Homo sapiens cDNA clo	5.4
20	415602	F12920	Hs.165575	ESTs	5.4
	432839	AA579465	Hs.287332	ESTs	5.4
	416879	H96899	Hs.42699	ESTs	5.4
	456088	BE177320	Hs.156148	"Homo sapiens cDNA: FLJ23082 fis, clone LNG06451"	5.4
	423175	W27595	Hs.18653	ESTs	5.4
25	424585	AA464840		gb:z21h11.1 NCI_CGAP_GCB1 Homo sapiens cDNA clo	5.3
	452281	T93500	Hs.28782	"Homo sapiens cDNA FLJ11041 fis, clone PLACE1004405	5.3
	424323	AA338791	Hs.146763	nascent-polyprotein-associated complex alpha polypeptide	5.3
	426701	AI968103	Hs.209461	"Homo sapiens cDNA FLJ12836 fis, clone NT2RP2003206	5.3
	447645	AW897321	Hs.159699	ESTs	5.3
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	436607	AW681783	Hs.211061	ESTs	5.3
	428873	AI701609	Hs.98908	ESTs	5.3
	405454			predicted exon	5.3
35	431867	AA523660	Hs.191727	ESTs	5.3
	442768	AL048534	Hs.48458	"ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	5.3
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40kD)	5.3
	435098	AF174394	Hs.177461	"Homo sapiens apoptotic-related protein PCAR mRNA, par	5.3
	421284	U62435	Hs.103128	"cholinergic receptor, nicotinic, alpha polypeptide 6"	5.3
	435711	AF226667	Hs.58553	CTP synthase II	5.3
40	405292			predicted exon	5.3
	410123	T16981	Hs.21963	ESTs	5.3
	435435	T89473	Hs.192328	ESTs	5.3
	417071	N58820	Hs.275133	ESTs	5.3
	438958	H50167	Hs.33113	ESTs	5.3
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	433868	AA612960		gb:z21h11.1 NCI_CGAP_GCB1 Homo sapiens cDNA clo	5.3
	444461	R53734	Hs.25978	ESTs	5.3
	427088	AA398085	Hs.142390	ESTs	5.3
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	403831			predicted exon	5.3
	402892			predicted exon	5.3
	433420	AI674093	Hs.293961	ESTs	5.3
55	455759	BE080469		"gb:QV1-BT0630-280200-086-d06 BT0630 Homo sapiens	5.3
	411379	AI816344	Hs.12554	"ESTs, Weakly similar to Nucleosome Assembly Protein 1-	5.3
	428483	AI908539	Hs.184592	KIAA0344 gene product	5.3
	429208	AA447990	Hs.190478	ESTs	5.3
	447572	AI631546	Hs.159732	ESTs	5.3
	434896	AW022054	Hs.136591	ESTs	5.3
60	417616	R07728	Hs.268668	ESTs	5.3
	411805	AW864183		"gb:PM0-SN0014-260400-002-d02 SN0014 Homo sapiens	5.3
	419000	T79855	Hs.268592	ESTs	5.3
	413488	BE144017	Hs.184693	"transcription elongation factor B (SIII), polypeptide 1 (15k	5.3
	400975			predicted exon	5.3
65	407453	AJ132087		gb:Homo sapiens mRNA for axonemal dynein heavy chain (5.3
	430757	AI458623		"gb:tk04g09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clo	5.3
	417793	AW405434	Hs.82575	small nuclear ribonucleoprotein polypeptide B"	5.2
	401877	AB011094	Hs.129892	KIAA0522 protein	5.2
	457122	AI026157	Hs.33728	"ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	5.2
70	410706	AI732404	Hs.68846	ESTs	5.2
	435807	AI033299	Hs.113614	ESTs	5.2
	428398	AI249368	Hs.98558	ESTs	5.2
	401088			predicted exon	5.2
	414501	NA3991	Hs.171984	ESTs	5.2
75	419083	AJ479560	Hs.98613	"Homo sapiens cDNA FLJ12292 fis, clone MAMMA10018	5.2
	421107	AA263822	Hs.55606	"ESTs, Weakly similar to ZN91_HUMAN ZINC FINGER P	5.2
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	419249	X14767	Hs.89768	"gamma-aminobutyric acid (GABA) A receptor, beta 1"	5.2
	430082	AW514083	Hs.190135	ESTs	5.2
80	425698	NM_016112	Hs.159241	polycystic kidney disease 2-like 1	5.2
	451686	AA059246	Hs.110293	ESTs	5.2
	453867	AI929383	Hs.108196	HSPC037 protein	5.2
	419985	H66373	Hs.15973	"ESTs, Highly similar to BA393J16.3 [Hsapiens]"	5.2
	426550	AA382614		"gb:EST96097 Testis I Homo sapiens cDNA 5' end, mRNA	5.2
	424115	AA335497	Hs.293965	ESTs	5.2

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	439155	H81076	Hs.269001 ESTs	5.2
	432267	AK000872	Hs.274227 *Homo sapiens cDNA FLJ10010 fis, clone HEMBA100030	5.2
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10	403525		predicted exon	5.2
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	448257	AW772070	Hs.253146 ESTs	5.2
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	456084	AA155859	Hs.79708 ESTs	5.2
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	434623	AB023163	Hs.4014 KIAA0946 protein; Huntingtin interacting protein H	5.2
	454484	AW795196	Hs.215857 ring finger protein 14	5.2
	402131		predicted exon	5.2
	438913	AI380429	Hs.172445 ESTs	5.2
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	415973	R24707	Hs.260201 ESTs	5.1
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	404638		predicted exon	5.1
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	439519	AA837118	Hs.118366 ESTs	5.1
	427335	AA448542	Hs.251677 G antigen 7B	5.1
	416450	AA180467	Hs.142556 ESTs	5.1
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	408968	AI652236	Hs.49376 hypothetical protein FLJ20644	5.1
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	412088	AI689496	Hs.108932 ESTs	5.1
	428785	AI015953	Hs.125265 ESTs	5.1
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	452502	AI904296	*gb:PM-BT046-220199-286_1 BT046 Homo sapiens cDNA	5.0
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	436084	AK000185	*gb:Homo sapiens cDNA FLJ20178 fis, clone COL09990	5.0
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	438490	AW593272	Hs.26261	ESTs	5.0
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	439152	46920_1	AF075079 H48601 H48785
75	439518	47334_1	H65014 AF086007 H65015
	440051	48426_2	W76326 AF086341 W72300
	441194	51193_1	BE559980 BE397203 BE268207 BE559764 BE267725 BE513654 BE267742 BE268219 BE267665 BE561356
	441369	515638_1	BE274581 BE275382 AA703515 BE166690
	442257	53699_1	AA931535 AA58601 Z44913
80	443161	561305_1	AW503831 AW503317 BE565665
	443175	561882_1	A1038316 A1344631 A1261653
	443198	562655_1	N57863 A1038952 W90167 N64103
	443534	572957_1	A1039813 A1684642 Z40121 A1951414 BE501049
	443613	575391_1	A1076123 A1244834 A1695239
			A1079356 W23287

5	443657	576685_1	R14973 R14967 AI081006
	443747	57918_1	AV646352 AV652121 AV652008
	443860	583216_1	AW866632 AI089351 D61942
	445132	63111_1	Z44811 R13709 AV652749 AW814906 AA084016
	445153	631644_1	AI214671 Z45244 H24136 R25934
	445232	633433_1	BE294357 N36568 AI217006
	446171	664826_1	AI374527 AI278380 AI301383
	447252	714160_1	R90916 AL120023 R18429 Z42095 AI369730 R90824
10	448516	766241_1	AW896595 AW898588 AW898590 AW898663 AW898952 AI525093
	449104	798149_1	R08702 R09864 AI630313
	450813	840016_1	AI702055 R89204 R86260
	452077	897051_1	BE144949 BE144991 BE144990 AI832199
	452502	919733_1	AI904296 BE007223 R30687
	452507	919998_1	AI904646 BE179494 BE179421
15	452542	921410_1	AW812256 AW812257 AI906423 AI906422
	452563	922265_1	AI907552 C03707 C02870
	452947	939810_1	AW130413 AI832362
	453509	969632_1	AL040021 AL040037
20	453845	983027_1	AL157568
	454182	1049569_1	AW177335 AW177352 AW177340 AW177378 AW177339 AW177388 AW177393
	454377	114781_1	AA076811 AW814764
	454389	115682_1	AW752571 AW847602 AA077979
	454455	1206965_1	AW752710 BE180336 BE180186
25	454505	1219564_1	AW801365 AW801435 AW801372
	454558	1223878_1	AW807073 AW807055 AW807087 AW807276 AW807030 AW807363 AW845892 AW807091 AW807275 AW807284 AW807287 AW845891
			AW807195 AW807271
	454574	1225636_1	AW809109 AW809112 AW809122 AW809126 AW809128 AW809133 AW809131 AW809113 AW809111 AW809132
	454597	1226059_1	AW809648 AW809704 AW809643 AW809653 AW809709 AW809949 AW809939 AW810010 AW809705 AW809950 AW809822 AW809667
30			AW810093 AW810076 AW809673 AW810349 AW809895
	454633	1227604_1	AW811380 AW811385
	454653	1228081_1	AW812227 AW812294 AW812092
	454690	1229106_1	AW854639 AW854719 AW854718 BE145880 AW854692 BE145866 AW816154 AW854698 AW854654 AW813335 AW854699
	454707	1230250_1	AW814989 AW814852 AW814808
35	454822	1236369_1	AW833793 AW833799 AW833346 AW833371 AW833795 AW833562 AW833667 AW833377
	454874	1238494_1	AW836407 BE175600 BE175579
	454913	1242238_1	AW841462 BE156657 BE156668 BE092475
	454934	1245577_1	AW846080 AW846074 AW846118 AW846130
	454963	1246752_1	AW847647 AW847659 AW847656 AW847653 AW847717 AW847786
40	455013	1248899_1	BE073250 BE073378 BE073379 AW850533 AW850529
	455092	1252971_1	BE152428 AW855572 AW855607
	455110	1253955_1	BE154505 BE154462 BE154454 BE154460 BE154489 BE154496 AW856909 BE154497 BE154565 BE154572 BE154500 BE154472
	455121	1254339_1	BE155459 BE156469 BE156468 AW857447
	455152	1255227_1	AW858621 AW937120
45	455203	1259973_1	AW865450 AW865119 AW865452 AW865461 AW865325 AW865114 AW865116 AW865321 AW865590 AW865390
	455275	1272255_1	AW977806 AW867923 AW866321
	455435	1290546_1	AW839445 AW939465 AW938604 AW939531 AW939530 AW939993
	455441	1291505_1	AW945964 AW946020 AW946034 AW946027 AW946041 AW946044 AW946033 AW946024 AW946021 AW946029 AW946015 AW946016
			AW946039 AW946045 AW946028 AW946036
50	455592	1335196_1	BE008002 BE007997 BE007998 BE008000
	455640	1348141_1	BE064059 BE063903 BE063838 BE063863 BE064056 BE063974 BE063904 BE063898 BE063896 BE063906 BE063980
	455662	1349206_1	BE065387 BE065310 BE065391
	455713	1352512_1	BE069891 BE158893 BE069898 BE158900
	455759	1359316_1	BE080469 BE080474 BE080477 BE080546 BE080545
55	455851	1375451_1	BE146879 BE146914 BE146918
	455853	1375671_1	BE147225 BE147205 BE147234
	455879	1380017_1	BE153275 BE153189 BE153329 BE153022 BE153030 BE152974
	455993	1398665_1	BE179085 BE179084 BE179086 BE179264
	456072	1470256_1	H54381 H54463 BE393262
60	456101	151654_1	AA159478 AW901089 AA160437 AW593155
	456212	1655565_1	N51636 T51874 T51829
	456309	177026_1	AA225423 AA225369 BE144153 AW801549
	456714	221500_1	AW897255 AW897274 AL119504 AW897275 AW897270 AW897312 AW897318 AW897317 AA317240 AW961361 T06241 AA326794
			AL138130 AW407975 AW999277
65	457405	333127_1	AA504860 AA504911
	457620	371514_1	AA602711 BE078290
	457727	393556_1	AW974687 AA649658 AA652145
	457868	426095_1	AW975133 AA729943 AA805813
	458154	491768_1	AW816379 AA888282 AA879046 AA879195
70	458804	75803_1	AL157625 N72696 BE622492
	458829	773443_1	AI557388 BE158938
	458841	784186_1	W28965 W28971
	459160	920051_1	AI904723 AI904725 AI904729 AI904722 AI904758 AI904736
	459170	920646_1	AI905518 AI905516 AI905457 AI905515 AW176013 AW176037
75	459186	922888_1	AI908287 BE064074 BE068820 BE068823 BE068822 BE068826

TABLE 1C:

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham et al." refers to the publication entitled "The DNA sequence of human chromosomes 22" Dunham, et al. (1999) *Nature* 402:489-495

Strand: Indicates DNA strand from which exons were predicted

Nt_position: Indicates nucleotide positions of predicted exons

Pkey	Ref	Strand	NL_position
400584	9887612	Minus	18398-18573
400593	9887642	Minus	25013-25127
400612	9929646	Minus	151513-151662
400613	9884507	Plus	92278-92472
400823	7228177	Plus	74185-74335,74653-74827
400709	7249204	Plus	153075-154680
400749	7331445	Minus	9162-9293
400842	1927148	Plus	90462-90673
400925	7651921	Plus	38183-38391,43900-44088
400964	7139719	Minus	155282-155403
400968	7923967	Plus	19938-20043
400975	7139779	Minus	108473-108847
400983	8081198	Plus	107803-108832
401032	8117525	Minus	68451-68555
401050	8117628	Minus	78449-79425
401088	8492704	Plus	194659-195179
401129	8699792	Minus	62022-62242,62326-62451,62543-62710,63072-63167
401200	9743387	Minus	111586-111806,114791-114916,115419-115583,116351-116446,116847-116907,122853-123067,124982-125407
401213	9858408	Plus	98243-98380,98489-98619
401230	9929527	Minus	33835-34006,34539-34592,36461-36745,48925-49098,52604-52758
401245	4827300	Minus	59373-59531
401260	8076883	Minus	88008-88355
401269	8954208	Plus	2259-2591
401283	9800093	Minus	47256-47456
401497	7381770	Plus	92607-92813
401508	7534110	Minus	110779-110983
401521	7705261	Plus	9127-9234
401530	7770649	Plus	41468-42406
401575	7228804	Minus	76253-76364
401604	7689963	Minus	119835-120185
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
401793	7263888	Minus	102945-103083
401809	7342191	Minus	107548-108298
401862	7770606	Minus	55839-55993,59145-59293
401881	8122429	Minus	148470-148651,153418-153618,154282-154438
402018	7528100	Plus	168728-168859
402046	8072415	Plus	166394-166556,168167-168395
402050	8076908	Minus	130105-130227
402071	8117361	Plus	85924-86039
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
402131	7704961	Minus	33114-33209,33498-33678
402203	8576119	Minus	8124-8285
402222	9958106	Plus	3261-3834,3939-4269
402296	6598824	Plus	22587-23723
402298	6598824	Plus	36758-37953
402421	9796341	Minus	46609-46662,46758-46811,86293-86346,89776-89829,90048-90101,102817-102924
402425	9796347	Minus	50224-50395
402481	9797406	Plus	87891-88991
402529	7630937	Minus	165-917
402543	9838066	Minus	89684-90893
402576	7230225	Minus	1857-2247
402578	9884928	Plus	66350-66496
402628	9931216	Plus	31753-31956
402631	9931231	Minus	115658-116580
402639	9958129	Minus	20167-22383
402664	8077024	Plus	70318-70846
402709	8901246	Minus	56847-57055
402738	7331557	Minus	8725-8859
402745	9212200	Minus	76516-76680
402790	4835258	Minus	147744-147861
402794	6136940	Minus	131034-131794
402800	6010175	Plus	43921-44049,46181-46273
402859	9588237	Minus	69821-75323
402892	8086844	Minus	194384-194645
402974	9663349	Plus	124035-124321
403041	3171152	Plus	70527-71019
403065	8954197	Minus	71615-71773,73930-74144
403083	8954241	Plus	163070-163351
403089	8954241	Plus	171964-172239
403093	8954241	Plus	177083-177373,177464-177751
403177	9838213	Minus	142560-142726
403273	8018055	Plus	133809-134099
403334	8568877	Minus	137205-137350
403350	8569775	Minus	135374-135523
403356	8569930	Plus	92839-93038
403403	9438460	Plus	21240-21399
403525	7960440	Plus	152431-153243
403568	8101145	Minus	85509-85658
403647	8699843	Minus	35849-36204
403687	7387384	Plus	9009-9534
403691	7387384	Minus	88280-88463
403698	4263532	Plus	10464-10907

	403741	7630932	Minus	2833-3468
	403747	7658395	Minus	20493-20621
	403786	8083636	Minus	73028-73217
5	403831	7249249	Minus	61468-61575
	403891	7331467	Minus	191508-193220
	403944	7711864	Minus	128213-129415
	403963	8568150	Plus	149466-149665
	404070	2996642	Plus	7210-7414,10043-10195
10	404088	9958257	Plus	184131-184295
	404097	7770701	Plus	55512-55781
	404166	7596822	Plus	86147-86509
	404270	9828129	Minus	3649-3750,4161-4306,5962-6049,6849-6965
	404340	7630856	Plus	10898-11506
15	404410	7342122	Plus	49062-49176,56177-56273,59384-59488
	404599	8705107	Plus	110443-110733
	404638	9796751	Minus	99433-99528,100035-100161
	404664	9797142	Minus	104257-105215
	404727	8081050	Plus	115534-115747
20	404767	7882827	Minus	23244-23759
	404828	6580415	Minus	26291-27253
	404849	7706886	Plus	144843-144964,149846-150121
	404893	6850447	Plus	65083-65223
	404898	7331420	Minus	177015-177328
25	404952	7382669	Minus	136326-136618
	404972	3213020	Plus	48711-49524
	404992	4682677	Minus	106104-106199,111659-111781
	405071	7708797	Minus	11115-11552
	405138	8576241	Plus	90303-90516
30	405198	7230083	Minus	135716-135851
	405227	6731245	Minus	22550-22802
	405277	3980473	Plus	23471-23572
	405285	6139075	Minus	55744-55903,57080-57170,61478-61560
	405292	3845420	Plus	33227-33442
35	405338	6094635	Plus	33267-33563
	405362	2337862	Minus	105008-105142,105980-106091,140445-140556,142519-142641
	405382	6552767	Plus	31923-32311
	405454	7656675	Plus	133807-134053
	405465	7767904	Plus	8935-9073,12242-12367,13364-13506,14965-15493
40	405472	8439781	Plus	106297-106447,108462-108596
	405547	1054740	Plus	124361-124520,124914-125050
	405576	4003382	Plus	84000-85009
	405621	5523811	Plus	59362-59607
	405636	5123990	Plus	56384-56587
45	405675	4557087	Plus	70304-70630
	405708	4156182	Plus	55030-55604
	405771	7018349	Plus	91191-91254,91510-91589
	405783	5738434	Minus	27238-27885
	405793	1405887	Minus	89197-89453
50	405800	2791346	Plus	19271-19813
	405810	4938307	Minus	64543-64966
	405848	7651809	Minus	28135-28244
	405851	6164995	Minus	26407-27151
	405867	6758731	Minus	74553-75173
55	405896	6758795	Plus	57311-57874
	405904	7705118	Minus	16375-16584
	405917	7712162	Minus	106829-107213
	405982	8247790	Minus	36028-36408
60	406030	8312328	Minus	96123-96547
	406053	6758997	Plus	30921-31532
	406057	6691254	Minus	20830-21222
	406149	7144791	Minus	44464-45164
	406163	7158901	Plus	66690-66835
	406277	5886030	Minus	4759-5490
65	406322	9212102	Minus	130230-130418
	406349	9256007	Minus	21251-21528
	406504	7711360	Minus	107068-107277
	406544	7711508	Plus	46576-46757
	406589	8224211	Plus	38806-38989
70	406592	4567182	Plus	352560-352963

TABLE 2A lists about 187 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to be extracellular or cell-surface proteins. These were selected as for Table 1A, except that the ratio was greater than or equal to 2.5, and the predicted protein contained a PFAM domain that is indicative of extracellular localization (e.g., Ig, fn3, egi, 7tm domains).

TABLE 2A: ABOUT 187 UP-REGULATED OVARIAN CANCER GENES ENCODING EXTRACELLULAR/CELL SURFACE PROTEINS

Key: Primekey
 Ex. Accr: Exemplar Accession
 UG ID: UniGene ID
 Title: Unigene Title
 PFAM domains
 ratio: tumor vs. normal tissues

	Pkey	Ex. Accn No.	UG ID	Title	PFAM domain	ratio
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor	serpin	63.6
	431938	AA938471	Hs.115242	developmentally regulated GTP-bind	SCP	32.0
5	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris ant	cadherin	30.0
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molec	EGF_tectin_csushi	24.5
	452947	AW130413		gbx50f04.x1 NCI_CGAP_Gas4 Hom	alpha-amylase	15.8
	418092	R45154	Hs.106604	ESTs	phkinase/Activin_rec	15.1
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	Cys_knot	12.6
10	422330	D30783	Hs.115263	epiregulin	EGF	12.5
	446745	AW118189	Hs.156400	ESTs	vwa	11.1
	416319	AJ15601	Hs.79197	CD83 antigen (activated B lymphocyt	Ig	10.8
	432408	N39127	Hs.76391	myxovirus (influenza) resistance 1, ho	ion_trans_K_tetra	10.6
	405285			predicted exon	A2M/A2M_N	10.5
15	405636			predicted exon	EGF_idl_recept_acidl_recept_b	9.8
	403093			predicted exon	fn3	9.6
	446740	AJ611635	Hs.192605	ESTs	RYDR_JTPR	9.2
	405547			predicted exon	ABC_tran/ABC_membrane	8.5
	412333	AW937485		gb:QV3-DT0044-221299-045-b09 DT	7tm_1	8.4
20	404270			predicted exon	SCP	8.1
	402745			predicted exon	EGF_idl_recept_b;thyroglobulin_1	8.1
	452755	AW138937	Hs.213436	ESTs	cystatin	8.0
	421459	AJ821539	Hs.97249	ESTs	disintegrin;Reprolysin	7.9
	416151	T26661		gb:AB65C7R Infant brain, LLNL arra	laminin_G;EGF	7.8
25	446232	AJ281848	Hs.165547	ESTs	7tm_3	7.6
	431009	BE149762	Hs.248213	gap junction protein, beta 6 (connexin	connexin	7.2
	424634	NM_003613	Hs.151407	cartilage intermediate layer protein, n	lg;isp_1	7.1
	400749			predicted exon	fn3_idl_recept_acidl_recept_b	6.8
	419054	N40340	Hs.191510	ESTs, Weakly similar to ORF2 [M.m	lg;SPRY	6.8
30	459170	AJ905518		gb:RC-BT091-210199-096 BT091 Ho	ABC_tran/ABC_membrane	6.6
	416441	BE407197		gb:601301552F1 NIH_MGC_21 Hom	SDF	6.4
	410664	NM_006033	Hs.65370	lipase, endothelial	Ribosomal_L22	6.4
	402425			predicted exon	ion_trans	6.3
	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_H	Ephrin	6.0
35	403083			predicted exon	fn3	5.9
	448995	AJ613276	Hs.5662	guanine nucleotide binding protein (G	SDF	5.9
	418345	AJ001696	Hs.241407	serine (or cysteine) proteinase inhibito	serpin	5.8
	424966	AJ077312	Hs.153985	solute carrier family 7 (cationic amino	aa_permeases	5.8
	431211	M86849	Hs.55566	gap junction protein, beta 2, 26kD (co	connexin	5.7
40	430563	AA481269	Hs.178381	ESTs	ABC_tran/ABC_membrane	5.6
	450152	AJ138635	Hs.22968	ESTs	lg;pklnase	5.6
	418844	M62982	Hs.1200	arachidonate 12-lipoxygenase	lipoxygenase;PLAT	5.6
	403089			predicted exon	fn3	5.6
	403687			predicted exon	tsp_1;Reprolysin	5.6
45	403691			predicted exon	tsp_1;Reprolysin	5.5
	414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibito	serpin	5.4
	421284	U62435	Hs.103128	cholesterol receptor, nicotinic, alpha p	neur_chan	5.3
	435435	T89473	Hs.192328	ESTs	lipase;PLAT	5.3
	457122	AJ026157	Hs.33728	ESTs, Weakly similar to ALU1_HUM	lipoxygenase;PLAT	5.2
50	419249	X14767	Hs.89769	gamma-aminobutyric acid (GABA) A	neur_chan	5.2
	425698	NM_016112	Hs.159241	polycystic kidney disease 2-like 1	ion_trans	5.2
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	EGF;DSL	5.1
	457948	AJ498640	Hs.159354	ESTs	G-alpha;ar	5.1
	435174	AA687378	Hs.194624	ESTs	SPRY	5.0
55	408170	AW204516	Hs.31835	ESTs	artras	5.0
	434351	AW974991	Hs.191852	ESTs, Weakly similar to ALU1_HUM	artras	4.9
	430708	U76308	Hs.278485	olfactory receptor, family 1, subfamily	7tm_1	4.8
	422597	BE245909	Hs.118634	ATP-binding cassette, sub-family B (M	ABC_tran/ABC_membrane	4.8
	405545			predicted exon	ABC_tran/ABC_membrane	4.8
60	426471	M22440	Hs.170009	transforming growth factor, alpha	EGF	4.7
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	serpin	4.7
	420208	M91463	Hs.95958	solute carrier family 2 (facilitated gluc	sugar_tr	4.6
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2	Kunitz_BPTI;G-gamma	4.6
	424402	M63108	Hs.1769	lutinizing hormone/choriogonadotrop	7tm_1	4.5
65	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	ASC	4.5
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	7tm_1	4.4
	436126	AW449757	Hs.163036	ESTs	SNF	4.4
	406812	AF000575	Hs.67846	leukocyte immunoglobulin-like recep	Ig	4.4
	409385	AA071267		gb:zm61g01.r1 Stratagene fibroblast (TIMP	4.3
70	449184	AW296295	Hs.196491	ESTs	TNFR_c6	4.3
	410555	U92649	Hs.64311	a disintegrin and metalloproteinase do	disintegrin;Reprolysin	4.3
	422389	AF240635	Hs.115897	protocadherin 12	cadherin	4.3
	405281			predicted exon	A2M/A2M_N	4.3
	413548	BE147555	Hs.288541	Homo sapiens mRNA for KIAA1558	EGF_idl_recept_acidl_recept_b	4.3
75	449535	W15267	Hs.23672	low density lipoprotein receptor-relate	idl_recept_acidl_recept_b	4.3
	425864	U56420	Hs.159903	olfactory receptor, family 5, subfamily	7tm_1	4.3
	410611	AW954134	Hs.20924	KIAA1628 protein	Peptidase_S9	4.2
	430686	NM_001942	Hs.2633	desmoglein 1	cadherin;Cadherin_C_term	4.1
	418693	AJ750878	Hs.87409	thrombospondin 1	vwc;TSPN	4.0
80	445924	AJ264571	Hs.164166	ESTs	sugar_tr	3.9
	457148	AF091035	Hs.184627	KIAA0118 protein	artras	3.9
	428568	AC004755	Hs.184922	one cut domain, family member 3	E1-E2_ATPase	3.9
	412170	D16532	Hs.73729	very low density lipoprotein receptor	EGF_idl_recept_acidl_recept_b	3.8
	442566	R37337	Hs.12111	ESTs	ank;death;RH;D;TIG	3.8
	403763			predicted exon	7tm_1	3.8

	403074			predicted exon	fn3	3.8
	413505	BE152644		gb:CM1-HT0329-250200-128-f09 HT	alpha-amylase	3.8
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, c	Collagen;COL1	3.7
5	403681			predicted exon	7tm_3;ANF_receptor	3.7
	407305	AA715284		gb:mv35f03.r1 NCL CGAP.Br5 Hom	pklnase;Sema;Plexin_repeat;TIG	3.7
	457353	X65633	Hs.248144	melanocortin 2 receptor (adrenocortic	7tm_1	3.7
	431176	AI026984	Hs.293662	ESTs	laminin_EGF;laminin_B	3.6
	436233	AI742878	Hs.124116	ESTs	lg	3.6
10	431808	M30703	Hs.270833	amphiregulin (schwannoma-derived g	EGF	3.6
	445788	NM_012421	Hs.13321	rearranged L-myc fusion sequence	zf-C2H2	3.6
	400380	NM_018485	Hs.283079	G protein-coupled receptor CSL2	7tm_1	3.6
	453893	NM_000835	Hs.36451	glutamate receptor, ionotropic, N-met	lg_chan	3.5
	409402	AF208234	Hs.695	cystatin B (sterin B)	cystatin	3.5
15	421166	AA305407	Hs.102308	potassium inwardly-rectifying channe	IRK	3.5
	445575	Z25368	Hs.172004	tin	fn3	3.5
	428957	NM_003881	Hs.194679	WNT1 inducible signaling pathway p	tsp_1;wvc;IGFBP	3.5
	403909	NM_016255	Hs.95260	Homo sapiens mRNA; cDNA DKFZp	Na_H_Exchange	3.5
	403077			predicted exon	fn3	3.5
20	455612	BE042696	Hs.274848	ESTs	ABC_tran;ABC_membrane	3.5
	424091	AF235097	Hs.139263	calcium channel, voltage-dependent, a	ion_trans	3.5
	403956	W26077	Hs.79389	nel (chicken)-like 2	cadherin;Cadherin_C_term	3.4
	457470	AB040973	Hs.272385	G protein-coupled receptor 72	7tm_1	3.4
	401522	NA7812	Hs.81360	CGI-35 protein	disintegrin;Reprolysin	3.4
25	404886			predicted exon	ion_trans	3.4
	437692	AA176959	Hs.172004	tin	fn3	3.4
	407944	R34008	Hs.239727	desmocollin 2	cadherin	3.4
	407393	AB038237		gb:Homo sapiens mRNA for G protel	7tm_1	3.3
	436936	AL134451	Hs.197478	ESTs	EGF;laminin_G	3.3
30	423309	BE006775	Hs.126782	sushi-repeat protein	sushi;HYR	3.3
	402172			predicted exon	lg	3.3
	447420	AI378628		gb:tc72g07.x1 Soares_NhHMPu_S1 H	ank;pklnase;death	3.3
	438901	AF085834	Hs.29038	ESTs	sushi	3.3
	424362	AL137646	Hs.146001	Homo sapiens mRNA; cDNA DKFZp	trypsin;sushi;CUB	3.3
35	430453	BE387060	Hs.3903	Cdc42 effector protein 4; binder of Rh	fn3	3.3
	416631	H69466		gb:yr88f07.r1 Soares fetal liver spleen	ldl_recept_alpha;MACPF	3.3
	453174	AI633529	Hs.135238	ESTs	7tm_1	3.3
	433848	AF095719	Hs.93754	carboxypeptidase A3	Zn_carbOpept;Propep_M14	3.2
	408546	W49512	Hs.46348	bradykinin receptor B1	7tm_1	3.2
40	423573	AA328504		gb:EST31993 Embryo, 12 week I Hom	7tm_1	3.2
	458662	AI823410	Hs.169149	karyopherin alpha 1 (importin alpha 5	7tm_3;ANF_receptor	3.2
	433430	AI863735	Hs.186755	ESTs	thyroglobulin_1;IGFBP	3.2
	438850	R33727	Hs.24688	EST	ank;pklnase;death	3.2
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	Gal-bind_lectin	3.2
45	409668	U56102	Hs.57699	adhesion glycoprotein	lg	3.1
	430630	AW269920	Hs.2621	cystatin A (stafin A)	7tm_3;ANF_receptor	3.1
	420737	L08096	Hs.99899	tumor necrosis factor (ligand) superfa	TNF	3.1
	422279	H69644	Hs.114231	C-type lectin-like receptor-2	lectin_c	3.1
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromely	hemopexin;Peptidase_M10	3.1
50	412597	AU077051	Hs.74561	alpha-2-macroglobulin	A2M;A2M_N	3.1
	453420	AJ003459		gb:AJ003459 Selected chromosome 2	IRK	3.1
	404243			predicted exon	zf-C3HC4;SPRY;zf-B_box	3.1
	449987	AW079749	Hs.184719	ESTs, Weakly similar to AF116721 1	ABC_tran;ABC_membrane	3.1
	422471	AA311027	Hs.271894	ESTs	lg	3.0
55	400464			predicted exon	Peptidase_S9	3.0
	458713	BE044496	Hs.282707	ESTs	EGF	3.0
	421340	F07783	Hs.1369	decay accelerating factor for complem	sushi	3.0
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	7tm_1	3.0
	400704			predicted exon	lg_chan;ANF_receptor	3.0
60	416239	AL038450	Hs.48948	ESTs	E1-E2_ATPase;Hydrolase	3.0
	433664	AW292176	Hs.245834	ESTs	Ricin_B_lectin	3.0
	423994	X01057	Hs.1724	interleukin 2 receptor, alpha	rm	2.9
	447726	AL137638	Hs.19368	Homo sapiens mRNA; cDNA DKFZp	vwa	2.9
	425483	AF231022	Hs.301273	Homo sapiens protocadherin Fat 2 (FA	EGF;cadherin;laminin_G	2.9
65	423513	AF035960	Hs.129719	transglutaminase 5	Transglut_core;Transglutamin_N	2.9
	401537			predicted exon	lg;pklnase;LRRNT;LRRCT	2.9
	405790			predicted exon	Sema;Plexin_repeat;TIG	2.9
	422669	H12402	Hs.119122	ribosomal protein L13a	arfrs;Ribosomal_S17	2.9
	430793	M83181	Hs.247940	5-hydroxytryptamine (serotonin) recep	7tm_1	2.9
70	403411			predicted exon	ABC_tran;ABC_membrane	2.8
	428188	M98447	Hs.22	transglutaminase 1 (K polypeptide ep	Transglutamin_N;Transglut_core	2.8
	414482	S57498	Hs.76252	endothelin receptor type A	7tm_1	2.8
	427223	BE208189	Hs.174031	cytochrome c oxidase subunit Vlb	COX6B	2.8
	404187			predicted exon	lg	2.8
75	443537	D13305	Hs.203	cholecystokinin B receptor	7tm_1	2.8
	428701	NM_013276	Hs.190207	carbohydrate kinase-like	vwa;integrin_A;P2X_receptor	2.7
	411213	AA676939	Hs.69285	neuropilin 1	CUB;MAM;F5_F8_type_C	2.7
	453999	BE328153	Hs.240087	ESTs	kazal	2.7
	401244			predicted exon	vwa;vwd;TIL	2.7
80	458930	NM_003612	Hs.24640	sema domain, immunoglobulin domai	Sema	2.7
	434411	AA632649	Hs.201372	ESTs	sushi	2.7
	400421	AF263537	Hs.287370	fibroblast growth factor 23	FGF	2.7
	448999	AF179274	Hs.22791	transmembrane protein with EGF-like	kazal	2.7
	417350	U50928	Hs.82001	polycystic kidney disease 2 (autosoma	ion_trans	2.6
	419452	U33635	Hs.90572	PTK protein tyrosine kinase 7	pklnase;lg	2.6

	401657			predicted exon	7m_1	2.6
	456711	AA033699	Hs.83938	ESTs, Moderately similar to MASP-2	sushi;trypsin;CUB	2.6
	432042	AW971345	Hs.292715	ESTs	sugar_tr	2.6
5	433138	AB029496	Hs.59729	semaphorin sem2	lg;Sema	2.6
	452530	AI905518		gb:RC-BT091-210199-098 BT091 Ho	ABC_tran;ABC_membrane	2.6
	426418	M90464	Hs.169825	collagen, type IV, alpha 5 (Alport syn	Collagen;C4	2.6
	403786			predicted exon	cadherin	2.6
	431728	NM_007351	Hs.268107	multimerin	EGF;C1q	2.6
10	441595	AW205035	Hs.192123	ESTs	sugar_tr	2.6
	445537	AJ245671	Hs.12844	EGF-like domain, multiple 6	EGF;MAM	2.6
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2H	SDF	2.5
	428785	X54150	Hs.193122	Fc fragment of IgA, receptor for	lg	2.5
	450245	AA007536	Hs.271767	ESTs, Moderately similar to ALU1_H	lg	2.5
15	416429	H54658	Hs.268942	ESTs	E1-E2_ATPase;Hydrolase	2.5
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneurona	sugar_tr	2.5
	433182	AB039920	Hs.127821	BWRT protein	ion_trans	2.5
	403092			predicted exon	fn3	2.5
	406850	AI624300	Hs.172928	collagen, type I, alpha 1	vwc;Collagen;COLFI	2.5
20	438698	AW297855	Hs.125815	ESTs	lipoxigenase;PLAT	2.5
	456815	NM_013348	Hs.144011	potassium inwardly-rectifying channe	IRK	2.5

TABLE 2B:

Pkey: Unique Eos probeset Identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

25	Pkey	CAT Number	Accession
	409385	112523_1	AA071267 T65940 T64515 AA071334
	412333	1289037_1	AW937485 AW937589 AW937658 AW937654 AW937492
30	413605	1379792_1	BE152644 BE152712 BE152668 BE152659 BE152810 BE152811 BE152816 BE152643 BE152706 BE152656 BE152660 BE152715 BE152662 BE152669 BE152661 BE152672 BE152653 BE152716 BE152651 BE152767 BE152677 BE152652 BE152714 BE152708 BE152665 BE152679 BE152771 BE152775 BE152666 BE152768 BE152813 BE152684 BE152676 BE152681 BE152709 BE152667 BE152814 BE152808 BE152711 BE152707 BE152815 BE152678 BE152673 BE152782 BE152671 BE152682 BE152760 BE152809 BE152778 BE152780 BE152762 BE152776 BE152781 BE152774 BE152763 BE152769
35	416151	1573926_1	T26661 Z44135 H23016
	416441	159480_1	BE407197 AA182474 AA180369 BE275628 BE276131
	416631	1605019_1	H69466 H93884 N59684
	423573	229714_1	AA328504 AA327783 AW962370
40	447197	711623_1	R36075 AJ366546 R36167
	447420	721207_1	AJ378628 N32350 H85772
	452530	920646_1	AI905518 AI905516 AI905457 AI905515 AW176013 AW176037
	452947	939810_1	AW130413 AJ932362
	453420	965433_1	AJ003459 AJ003461
45	459170	920646_1	AI905518 AI905516 AI905457 AI905515 AW176013 AW176037

TABLE 2C:

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495

Strand: Indicates DNA strand from which exons were predicted

NL_position: Indicates nucleotide positions of predicted exons

50	Pkey	Ref	Strand	NL_position
	400464	8929670	Plus	22074-22214
55	400704	8118864	Minus	63110-63241
	400749	7331445	Minus	9162-9293
	401244	4827300	Minus	55359-56376
	401537	7960358	Minus	186786-187029,190607-190779,198218-198348
60	401657	9100664	Minus	7312-8163
	402172	8575911	Minus	143378-143671
	402425	9796347	Minus	50224-50395
	402745	9212200	Minus	76516-76690
	403074	8954241	Plus	143375-143561
	403077	8954241	Plus	146923-147222,147326-147628
65	403083	8954241	Plus	163070-163351
	403089	8954241	Plus	171964-172239
	403092	8954241	Plus	174720-175016,175104-175406,175508-175813
	403093	8954241	Plus	177083-177373,177464-177751
	403411	8438835	Minus	104247-104420
70	403661	8705027	Minus	30268-30482
	403687	7387384	Plus	9009-9534
	403691	7387384	Minus	88280-88463
	403763	7229888	Minus	43575-43887
75	403796	8096896	Minus	75073-77664
	404187	4481839	Plus	7644-7991
	404243	5672609	Plus	74695-75123
	404270	9828129	Minus	3649-3750,4161-4306,5962-6049,6849-6965
	404886	4884062	Plus	30058-30596
80	405281	6139075	Minus	34202-34351,35194-35336,45412-45475,45731-45958,47296-47457,49549-49658,49790-49904,50231-50342,53583-53667,54111-54279
	405285	6139075	Minus	55744-55903,57080-57170,61478-61560
	405545	1054740	Plus	118677-118807,119091-119296,121626-121823
	405547	1054740	Plus	124361-124520,124914-125050
	405636	5123990	Plus	56384-56587

405790 1203968 Plus 136364-136509,136579-136699,136805-136941

5 TABLE 3A lists about 1643 genes up-regulated in ovarian cancer compared to normal ovaries. These were selected as for Table 1A, except that the ratio was greater than or equal to 15, and the denominator was the arithmetic mean value for various non-malignant ovary specimens obtained.

TABLE 3A: ABOUT 1643 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY

Pkey: Primkey

Ex. Accn: Exemplar Accession

UG ID: UniGene ID

Title: Unigene Title

PFAM domains

ratio: tumor vs. normal tissues

Pkey	Ex. Accn No.	UG ID	Title	ratio
420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgranulin A)	219.9
422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgranulin B)	180.2
422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKALP)	165.0
424799	BE550723	Hs.153179	fatty acid binding protein 5 (psoriasis-associated)	161.5
442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	150.2
408522	AU541214	Hs.46320	Small proline-rich protein SPRK [human, odontogenic k	149.5
431369	BE184456	Hs.251754	secretory leukocyte protease inhibitor (antileukoprotein	144.9
430520	NM_016190	Hs.242057	chromosome 1 open reading frame 10	136.6
428471	X57348	Hs.184510	stratfin	129.5
421978	AJ243662	Hs.110196	NICE-1 protein	108.7
437191	NM_006846	Hs.5476	serine protease inhibitor, Kazal type, 5	105.2
407788	BE514982	Hs.38991	S100 calcium-binding protein A2	105.5
441565	AW953575	Hs.169902	solute carrier family 2 (facilitated glucose transporter),	103.6
431211	M86849	Hs.5566	gap junction protein, beta 2, 26kD (connexin 26)	102.1
419329	AY007220	Hs.288998	S100-type calcium binding protein A14	95.3
430572	U33114	Hs.245188	tissue inhibitor of metalloproteinase 3 (Sorsby fundus d	87.0
417079	U65590	Hs.81134	Interleukin 1 receptor antagonist	86.1
412636	NM_004415	Hs.74316	desmoplakin (DPI, DPL)	85.0
417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated protein	84.8
426295	AW367283	Hs.75839	zinc finger protein 6 (CMPX1)	84.5
452669	AA216363	Hs.262958	ESTs, Weakly similar to alternatively spliced product u	84.4
406711	N25514	Hs.77385	myosin, light polypeptide 6, alkali, smooth muscle and n	83.8
406712	M31212	Hs.77385	myosin, light polypeptide 6, alkali, smooth muscle and n	81.0
432680	T47364	Hs.278613	Interferon, alpha-inducible protein 27	81.0
416889	AW250318	Hs.80395	mal, T-cell differentiation protein	77.8
409453	AJ885516	Hs.95612	ESTs	75.3
424670	W61215	Hs.116651	epithelial V-like antigen 1	67.5
417130	AW276858	Hs.81256	S100 calcium-binding protein A4 (calcium protein, calv	67.0
423634	AW959908	Hs.1690	heparin-binding growth factor binding protein	65.7
442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, protein-glutamine-g	64.7
456898	NM_001928	Hs.155597	D component of complement (adipsin)	64.6
423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor, clade B (ovalbu	63.6
447950	BE048821	Hs.20144	small inducible cytokine subfamily A (Cys-Cys), memb	60.7
424362	AL137646	Hs.146001	Homo sapiens mRNA; cDNA DKFZp586F0824 (from	60.3
414438	AJ879277	Hs.76136	thioredoxin	59.9
420136	AW801090	Hs.195851	actin, alpha 2, smooth muscle, aorta	58.9
433336	AF017986	Hs.31386	ESTs, Highly similar to JE0174 fizzled protein-2 [H.s.a	58.8
403741			predicted exon	57.0
430637	BE160081	Hs.256290	S100 calcium-binding protein A11 (calgizzarin)	56.1
424098	AF077374	Hs.139322	small proline-rich protein 3	55.8
441591	AF055992	Hs.183	Duffy blood group	55.6
426521	AF161445	Hs.170219	hypothetical protein	55.5
406713	U02629	Hs.77385	myosin, light polypeptide 6, alkali, smooth muscle and n	55.3
406725	D51245	Hs.288061	actin, beta	54.1
422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psoriasin 1)	54.1
406755	N80129	Hs.94360	metallothionein 1L	54.0
425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	53.3
442257	AW503831		gb:U1-HF-BNO-aly-b-05-0-U1r1 NIH_MGC_50 Homo	53.1
421957	AW068637	Hs.109857	hypothetical protein DKFZp434H0820	52.3
447526	AL048753	Hs.340	small inducible cytokine A2 (monocyte chemotactic pro	51.2
406722	H27498	Hs.283305	Homo sapiens SNC73 protein (SNC73) mRNA, comple	51.0
427223	BE208189	Hs.174031	cytochrome c oxidase subunit VIb	51.0
414420	AA043424	Hs.76095	Immediate early response 3	50.9
417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (versican)	50.3
414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	49.5
436906	H95990	Hs.181244	major histocompatibility complex, class I, A	49.0
408000	L11690	Hs.620	bulbous pemphigoid antigen 1 (Z30/240kD)	49.0
414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibitor, clade B (ovalbu	48.8
432706	NM_013230	Hs.286124	CD24 antigen (small cell lung carcinoma cluster 4 antig	48.8
421948	L42583	Hs.111758	keratin 6A	48.7
414662	AL036058	Hs.76807	major histocompatibility complex, class II, DR alpha	48.5
425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	48.5
404767			predicted exon	48.4
418327	U70370	Hs.84136	paired-like homeodomain transcription factor 1	48.2
436729	BE621807	Hs.3337	transmembrane 4 superfamily member 1	47.7
414183	AW957446	Hs.301711	ESTs	47.2
400163			predicted exon	47.0
433423	BE407127	Hs.8997	heat shock 70kD protein 1A	46.9
423457	F08208	Hs.155606	paired mesoderm homeo box 1	46.6

	414085	AA114016	Hs.75746	aldehyde dehydrogenase 6	46.0
	423189	M59371	Hs.171596	EphA2	45.6
	438240	N92638	Hs.124004	ESTs	45.5
5	417366	BE185289	Hs.1076	small proline-rich protein 18 (cornifin)	45.3
	412774	AA120865	Hs.23136	ESTs	45.1
	407242	M18728		gbHuman nonspecific crossreacting antigen mRNA, co	44.8
	431292	AA370141	Hs.251453	Human DNA sequence from clone 967N21 on chromos	44.8
	403695			predicted exon	43.5
10	417365	D50683	Hs.82028	transforming growth factor, beta receptor II (70-80kD)	43.4
	432331	W37862	Hs.274368	Homo sapiens mRNA; cDNA DKFZp586i1524 (from c	43.4
	424479	AF064238	Hs.149098	smoothelin	43.3
	444726	NM_006147	Hs.11801	interferon regulatory factor 6	43.2
	432314	AA533447	Hs.285173	ESTs	43.2
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxin)	43.1
15	441406	Z45957	Hs.7837	Homo sapiens cDNA FLJ10457 fis, clone NT2RP1001	42.7
	412959	AI373162	Hs.75103	tyrosine 3-monooxygenase/tryptophan 5-monooxygenas	42.6
	423720	AL044191	Hs.23388	Homo sapiens cDNA: FLJ21310 fis, clone COL02160	42.5
	400111			predicted exon	42.4
20	407207	T03651	Hs.179661	tubulin, beta polypeptide	42.4
	417164	AA338283	Hs.81361	heterogeneous nuclear ribonucleoprotein A/B	42.2
	424971	AA479005	Hs.154036	tumor suppressing subtransferable candidate 3	41.9
	439394	AA149250	Hs.56105	ESTs, Weakly similar to WDNM RAT WDNM1 PROT	41.9
	406657	AI678644	Hs.277477	major histocompatibility complex, class I, C	41.8
25	451092	AI207256	Hs.13766	Homo sapiens mRNA for FLJ00074 protein, partial cds	41.6
	412596	AA161219	Hs.799	diphtheria toxin receptor (heparin-binding epidermal gro	41.6
	422103	AA984330	Hs.111676	protein kinase H11; small stress protein-like protein HS	41.5
	428785	AK015953	Hs.125265	ESTs	41.3
	450988	BE618571	Hs.429	ATP synthase, H+ transporting, mitochondrial F0 comp	41.0
30	414622	AI752666	Hs.76669	nicotinamide N-methyltransferase	40.8
	405022			predicted exon	40.8
	408221	AA912183	Hs.47447	ESTs	40.8
	446500	U78093	Hs.16154	sushi-repeat-containing protein, X chromosome	40.7
	421416	BE302950	Hs.104125	adenylyl cyclase-associated protein	40.6
35	412247	AF022375	Hs.73793	vascular endothelial growth factor	40.5
	410541	AA065003	Hs.64179	hypothetical protein	40.5
	406658	AI920965	Hs.77961	major histocompatibility complex, class I, B	40.0
	420225	AW243046	Hs.94789	ESTs	40.0
	406825	AI982529	Hs.84298	CD74 antigen (invariant polypeptide of major histocom	39.4
40	443623	AA345519	Hs.9641	complement component 1, q subcomponent, alpha poly	39.4
	404201	AF059566	Hs.103983	solute carrier family 5 (sodium iodide symporter), mem	39.3
	405138			predicted exon	39.1
	408733	AW264812	Hs.254290	ESTs	39.0
	414044	BE614194	Hs.76721	profilin 1	38.9
45	430152	AB001325	Hs.234642	aquaporin 3	38.8
	428121	AB006622	Hs.182536	Homo sapiens cDNA: FLJ21370 fis, clone COL03092	38.8
	434311	BE543469	Hs.266263	Homo sapiens cDNA FLJ14115 fis, clone MAMMA10	38.7
	406140			predicted exon	38.5
	432918	AF077200	Hs.279813	hypothetical protein	38.4
50	420107	AL043980	Hs.7886	pellino (Drosophila) homolog 1	38.4
	427693	BE546832	Hs.180370	cofilin 1 (non-muscle)	38.1
	448835	BE277929	Hs.11081	ESTs, Weakly similar to S57447 HPBRIL-7 protein [H.	38.1
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PLACE1010	37.9
	428383	BE616599	Hs.184029	hypothetical protein DKFZp761A052	37.7
55	436258	AW867491	Hs.107125	ESTs, Weakly similar to S57447 HPBRIL-7 protein [H.	37.7
	420798	W93774	Hs.99936	keratin 10 (epidermolytic hyperkeratosis; keratosis palm	37.7
	400327	M18679	Hs.247942	Human variant 5S rRNA-like gene and ORF, complete	37.6
	401781			predicted exon	37.6
	448257	AW772070	Hs.253146	ESTs	37.3
60	428415	AA337211	Hs.184222	Down syndrome critical region gene 1	37.2
	424208	NM_003734	Hs.188241	amine oxidase, copper containing 3 (vascular adhesion p	37.2
	406812	AF000575	Hs.67846	leukocyte immunoglobulin-like receptor, subfamily B (37.2
	425882	U83115	Hs.161002	absent in melanoma 1	37.2
	432501	BE546532	Hs.287329	Fas binding protein 1	37.1
65	421786	AI188653	Hs.21351	ESTs	37.1
	427981	BE275986	Hs.181311	asparaginyl-tRNA synthetase	37.0
	410143	AA188169	Hs.288819	Homo sapiens cDNA: FLJ21022 fis, clone CAE06383	36.8
	451328	AW853606	Hs.109012	ESTs	36.7
	414135	NM_004419	Hs.2128	dual specificity phosphatase 5	36.7
70	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (from	36.7
	401785			predicted exon	36.5
	411469	T09997	Hs.70327	cysteine-rich protein 2	36.2
	419693	AA133749	Hs.92323	FXYD domain-containing ion transport regulator 3	36.1
	417039	AA302180	Hs.80986	ATP synthase, H+ transporting, mitochondrial F0 comp	36.1
75	406718	AA505525	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	36.0
	402543			predicted exon	36.0
	408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molecule (CD31 anti	35.9
	414987	AA524394	Hs.165544	ESTs	35.9
	445810	AW265700	Hs.155660	ESTs	35.9
80	406653	AA574074	Hs.77961	major histocompatibility complex, class I, B	35.7
	407498	U28131		gbHuman HMG1-C chimeric transcript mRNA, partial	35.6
	412524	AA417813	Hs.111177	ESTs	35.5
	401521			predicted exon	35.4
	408948	AW296713	Hs.221441	ESTs	35.1
	406728	AI986345	Hs.183704	ubiquitin C	34.9

5	440669	AI206964		gbrq30g06.x1 NCL CGAP_GC6 Homo sapiens cDNA	34.8
	422658	AF231981	Hs.250175	homolog of yeast long chain polyunsaturated fatty acid	34.8
	452924	AW580939	Hs.97199	complement component C1q receptor	34.7
	428600	AW863261	Hs.15036	ESTs, Highly similar to AF161358 1 HSPC095 [Hsapi	34.7
	409828	AW501137		gb:U1HF-BP0p-alt-e-12-D-ULr1 NIH_MGC_51 Homo	34.6
	459390	BE385725		gb:601276347F1 NIH_MGC_20 Homo sapiens cDNA	34.5
	445055	BE512856	Hs.109051	glycoprotein, synaptic 2	34.3
	411789	AF245505	Hs.72157	Homo sapiens adican mRNA, complete cds	34.3
10	410628	BE407727		gb:601299771F1 NIH_MGC_21 Homo sapiens cDNA	34.2
	410706	AF732404	Hs.68846	ESTs	34.2
	419273	BE271180	Hs.293490	ESTs	34.2
	407839	AA045144	Hs.161566	ESTs	34.0
	444286	AI625304	Hs.190312	ESTs	34.0
15	449226	AB002365	Hs.23311	KIAA0367 protein	34.0
	414290	AI568801	Hs.71721	ESTs	33.9
	401245			predicted exon	33.9
	425222	M85430	Hs.155191	villin 2 (ezrin)	33.8
	409950	RA2678	Hs.301669	KIAA0564 protein	33.8
20	437201	F29279	Hs.177486	amyloid beta (A4) precursor protein (protease nexin-II,	33.7
	406566	AF088886	Hs.11590	cathepsin F	33.7
	405071			predicted exon	33.7
	455426	AW937792		gb:CV3-DT0045-140200-082-b07 DT0045 Homo sapi	33.6
	415160	T82802		gbyd38a04r1 Soares fetal liver spleen 1NFLS Homo s	33.5
25	424985	Z45023		gb:HC2FA041 normalized infant brain cDNA Homo s	33.5
	453870	AW385001	Hs.8042	Homo sapiens cDNA: FLJ23173 fs, clone LNG10019	33.5
	433470	AW960564	Hs.3337	transmembrane 4 superfamily member 1	33.4
	428188	M98447	Hs.22	transglutaminase 1 (K polypeptide epidermal type I, pro	33.3
	417409	BE272506	Hs.82109	syndecan 1	33.3
30	425389	AW974499	Hs.192183	ESTs	33.3
	434658	AI624436	Hs.194488	ESTs	33.2
	456562	AA306049	Hs.102669	DKFZP434O125 protein	33.1
	447111	AI017574	Hs.17409	cysteine-rich protein 1 (intestinal)	33.0
	432360	BE045243	Hs.274416	NADH dehydrogenase (ubiquinone) 1 alpha subcomple	32.9
35	424125	M31669	Hs.1735	inhibin, beta B (activin AB beta polypeptide)	32.7
	419968	XD4430	Hs.93913	interleukin 6 (interferon, beta 2)	32.7
	429415	NM_002593	Hs.202097	procollagen C-endopeptidase enhancer	32.6
	451541	BE279383	Hs.26557	plakophilin 3	32.6
	424499	N90344	Hs.149436	kinesin family member 5B	32.4
40	402144			predicted exon	32.4
	422511	AU076442	Hs.117838	collagen, type XVII, alpha 1	32.4
	400231			predicted exon	32.3
	437712	XD4588	Hs.85844	neurotrophic tyrosine kinase, receptor, type 1	32.3
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	32.2
45	419659	AB023206	Hs.92186	Leman coiled-coil protein	32.0
	428582	BE336699	Hs.185055	BENE protein	32.0
	421401	AW410478	Hs.104019	transforming, acidic coiled-coil containing protein 3	32.0
	414064	BE245289	Hs.16165	expressed in activated TLAK lymphocytes	32.0
	431938	AA938471	Hs.115242	developmentally regulated GTP-binding protein 1	32.0
50	411930	F06485		gb:HC19G051 normalized infant brain cDNA Homo s	31.9
	428150	AW950547	Hs.182684	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)	31.8
	401887			predicted exon	31.8
	412570	AA033517	Hs.74047	electron-transfer-flavoprotein, beta polypeptide	31.7
	422738	X80915	Hs.1573	growth differentiation factor 5 (cartilage-derived morph	31.6
55	453092	X64838	Hs.31638	resin (Reed-Stenberg cell-expressed intermediate filam	31.5
	413924	AL119954	Hs.75618	KIAA0018 gene product	31.4
	420231	R06866	Hs.19813	ESTs	31.3
	434715	BE005346	Hs.116410	ESTs	31.3
	422831	R02504		gbye86f06.r1 Soares fetal liver spleen 1NFLS Homo sa	31.2
60	416854	HA0164	Hs.80296	Purkinje cell protein 4	31.2
	422976	AU076657	Hs.1600	sec61 homolog	31.1
	426356	BE536836		gb:601064837F1 NIH_MGC_10 Homo sapiens cDNA	31.0
	433935	AF112208	Hs.44163	13kDa differentiation-associated protein	30.8
	430040	AW503115	Hs.227823	pM5 protein	30.8
65	406340	AA299679	Hs.180370	cofilin 1 (non-muscle)	30.8
	426050	AF017307	Hs.166096	E74-like factor 3 (ets domain transcription factor, epith	30.7
	425105	BE280066	Hs.24956	hypothetical protein FLJ22056	30.7
	402066			predicted exon	30.7
	429538	BE182592	Hs.139322	small proline-rich protein 3	30.6
70	418371	M13560	Hs.84298	CD74 antigen (invariant polypeptide of major histocom	30.4
	421251	Z28913	Hs.102948	enigma (LIM domain protein)	30.3
	456084	AA155859	Hs.79708	ESTs	30.3
	402023			predicted exon	30.3
	404356			predicted exon	30.2
75	415973	R24707	Hs.260201	ESTs	30.2
	445983	AI269107	Hs.132219	ESTs	30.1
	450440	AB024334	Hs.25001	tyrosine 3-monooxygenase/tryptophan 5-monooxygenas	30.1
	458789	AI157468	Hs.20157	Homo sapiens cDNA FLJ20848 fs, clone ADKA01732	30.1
	400842			predicted exon	30.1
80	406828	AA419202	Hs.84298	CD74 antigen (invariant polypeptide of major histocom	30.0
	423267	AL137416	Hs.126177	Homo sapiens mRNA: cDNA DKFZp434O192 (from c	30.0
	451383	AW239384	Hs.20242	hypothetical protein FLJ12788	30.0
	437042	AK000702	Hs.5420	hypothetical protein FLJ20695	30.0
	459399	BE407712		gb:601299745F1 NIH_MGC_21 Homo sapiens cDNA	30.0
	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen)	30.0

	416511	NM_005762	Hs.79356	Lysosomal-associated multispinning membrane protein	29.9
	431009	BE149762	Hs.248213	gap junction protein, beta 6 (connexin 30)	29.7
	436651	BE045962	Hs.275998	ESTs	29.6
5	419766	BE243101	Hs.22391	chromosome 20 open reading frame 3	29.5
	420747	BE294407	Hs.99910	phosphofructokinase, platelet	29.5
	436895	AF037335	Hs.5338	carbonic anhydrase XII	29.5
	412765	AK000620	Hs.74571	ADP-ribosylation factor 1	29.4
	419223	X60111	Hs.1244	CD9 antigen (p24)	29.4
10	413796	AW408094	Hs.75545	interleukin 4 receptor	29.4
	447795	AW295151	Hs.163612	ESTs	29.4
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth factor 8, neurite g	29.4
	415314	N88802	Hs.5422	glycoprotein M6B	29.3
	428411	AW291464	Hs.10338	ESTs	29.3
15	430580	AA806105	Hs.140	immunoglobulin heavy constant gamma 3 (Gm marker)	29.3
	430451	AA836472	Hs.249982	cathepsin B	29.2
	453949	AJ077146	Hs.36927	heat shock 105kD	29.2
	413859	AW992356	Hs.8354	pyruvate dehydrogenase kinase, isoenzyme 4	29.2
	407845	AL036518	Hs.118598	ESTs	29.1
20	453500	AJ478427	Hs.43125	ESTs	29.1
	456054	BE313241		gb:601151545F1 NIH_MGC_19 Homo sapiens cDNA	29.0
	453467	AI535997	Hs.30089	ESTs	29.0
	411794	AL118577	Hs.75658	phosphorylase, glycogen; brain	28.9
	421773	W69233	Hs.112457	ESTs	28.9
25	423621	BE002904		gb:QV4-BN0090-070400-163-c07 BN0090 Homo sapi	28.8
	408935	BE539708	Hs.285363	ESTs	28.8
	450847	NM_003155	Hs.25580	stanniocalcin 1	28.8
	431243	U46455	Hs.252189	syndecan 4 (amphiglycan, ryudocan)	28.7
	423225	AA852604	Hs.125359	Thy-1 cell surface antigen	28.7
30	433469	F12741		gb:HSC3DG061 normalized Infant brain cDNA Homo	28.7
	405783			predicted exon	28.7
	417308	H60720	Hs.81892	KIAA0101 gene product	28.7
	400749			predicted exon	28.7
	413442	BE140643		gb:RCO-HT0015-310599-016 HT0015 Homo sapiens c	28.6
35	404828			predicted exon	28.6
	407453	AJ132087		gb:Homo sapiens mRNA for axonemal dynein heavy ch	28.6
	418529	AW005695	Hs.250897	TRK-fused gene (NOTE: non-standard symbol and nam	28.6
	413787	AI352558	Hs.75544	tyrosine 3-monooxygenase/tryptophan 5-monooxygenas	28.5
	450690	AA296696	Hs.25334	FXD domain-containing ion transport regulator 5	28.5
40	402430			predicted exon	28.4
	413929	BE501689	Hs.75617	collagen, type IV, alpha 2	28.2
	423803	NM_005709	Hs.132945	PDZ-73 protein	28.2
	406086			predicted exon	28.2
	416585	X54162	Hs.79386	telomodin 1 (smooth muscle)	28.2
45	417055	N39489	Hs.7258	Homo sapiens cDNA: FLJ22021 fs, clone HEP08253	28.1
	449184	AW296295	Hs.196491	ESTs	28.1
	446542	NM_004281	Hs.15259	BCL2-associated athanogene 3	28.1
	412793	AW997986		gb:RC1-BN0056-230200-021-e11 BN0056 Homo sapie	28.0
	452818	W21909	Hs.8372	ubiquinol-cytochrome c reductase (6.4kD) subunit	28.0
50	402869			predicted exon	27.9
	436810	AA353044	Hs.5321	ARP3 (actin-related protein 3, yeast) homolog	27.9
	402075			predicted exon	27.9
	410480	R97457	Hs.63984	cadherin 13, H-cadherin (heart)	27.8
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell adhesion molecu	27.8
55	439766	A8033492	Hs.301241	Homo sapiens mRNA: cDNA DKFZp586A0424 (from	27.7
	424482	BE268621	Hs.149155	voltage-dependent anion channel 1	27.6
	420737	L08096	Hs.99899	tumor necrosis factor (ligand) superfamily, member 7	27.6
	414663	BC396326		gb:601289258F1 NIH_MGC_8 Homo sapiens cDNA c	27.6
	409703	NM_006187	Hs.56009	Z'-5'-oligoadenylate synthetase 3	27.6
60	446108	AL036596	Hs.102773	ESTs	27.5
	428144	BE269243	Hs.182625	VAMP (vesicle-associated membrane protein)-associate	27.5
	445688	AI248205	Hs.153244	ESTs	27.5
	405411			predicted exon	27.5
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activating enhancer-b	27.5
65	424675	NM_005512	Hs.151641	glycoprotein A repetitions predominant	27.3
	450455	AL117424	Hs.25035	chloride intracellular channel 4	27.3
	414855	AA156986	Hs.104640	HIV-1 inducer of short transcripts binding protein	27.2
	433578	BE336886	Hs.3416	adipose differentiation-related protein	27.2
	401994			predicted exon	27.2
70	445033	AV652402	Hs.155145	ESTs	27.2
	402277			predicted exon	27.1
	428106	BE620016	Hs.182470	PTD010 protein	27.1
	448625	AW970786	Hs.178470	Homo sapiens cDNA: FLJ22662 fs, clone HSI08080	27.1
	422587	AI879352	Hs.118625	hexokinase 1	27.0
	457204	BE264152	Hs.221894	ESTs	27.0
75	444094	AI695764	Hs.202394	ESTs	27.0
	414053	BE391635	Hs.75725	transgelin 2	26.9
	430511	BE018158	Hs.2575	calpain 1, (mu/f) large subunit	26.9
	434039	L32977	Hs.3712	ubiquinol-cytochrome c reductase, Rieske iron-sulfur po	26.9
80	424939	AK000059	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, partial cds	26.9
	414539	BE379046		gb:501236646F1 NIH_MGC_44 Homo sapiens cDNA	26.9
	404675			predicted exon	26.8
	401597	AA172106	Hs.110950	Rag C protein	26.8
	401405			predicted exon	26.8
	411541	W03940		gb:ca62b02r1 Soares fetal liver spleen 1NFLS Homo sa	26.8

5	412025	A1827451	Hs.24143	ESTs	26.7
	414276	BE297862		gb:601174780F1 NIH_MGC_17 Homo sapiens cDNA	26.7
	444065	AW449415	Hs.10260	Homo sapiens cDNA FLJ11341 fis, clone PLACE1010	26.7
	447981	R53772	Hs.8929	hypothetical protein FLJ11362	26.7
	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein)	26.5
	400982			predicted exon	26.5
	452833	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone HRC08688	26.5
	407233	X16354	Hs.50964	carcinoembryonic antigen-related cell adhesion molecule	26.4
10	430127	AA219498	Hs.233952	proteasome (prosome, macropain) subunit, alpha type, 7	26.3
	448218	A188489		gb:q09b12.x1 Soares_placenta_8to9weeks_2NbHP8to	26.3
	413511	A1627178	Hs.75412	Arginine-rich protein	26.2
	459511	A1142379		gb:qg64c01.r1 Soares_testis_NHT Homo sapiens cDNA	26.2
	410668	BE379794	Hs.65403	hypothetical protein	26.2
15	458662	A1823410	Hs.169149	karyopherin alpha 1 (importin alpha 5)	26.2
	451219	AA054209	Hs.167804	ESTs	26.2
	448939	BE267795	Hs.22595	hypothetical protein FLJ10637	26.2
	400800	Y10262	Hs.46925	eyes absent (Drosophila) homolog 3	26.2
	446342	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (from c	26.2
20	421177	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (from	26.1
	433848	AF095719	Hs.93764	carboxypeptidase A3	26.1
	448497	BE613269	Hs.21893	ESTs, Weakly similar to glycerol 3-phosphate permease	26.1
	415279	FO4237	Hs.1447	glial fibrillary acidic protein	26.0
	419323	A1092379	Hs.135275	ESTs	26.0
25	430265	L36033	Hs.237356	stromal cell-derived factor 1	25.9
	437679	NM_014214	Hs.5753	inositol(myo)-[or 4]-monophosphatase 2	25.9
	425535	AB007937	Hs.158287	KIAA0468 gene product	25.8
	412923	AA179922	Hs.75056	adaptor-related protein complex 3, delta 1 subunit	25.8
	447980	A1703397	Hs.202355	ESTs	25.8
30	419118	AA234223	Hs.139204	ESTs	25.8
	421224	AW402154	Hs.125812	ESTs	25.8
	414890	BE281095	Hs.77573	uridine phosphorylase	25.8
	447330	BE279949	Hs.18141	ladinin 1	25.7
	405610			predicted exon	25.7
35	447604	AW089933	Hs.293674	ESTs	25.7
	445677	H96577	Hs.6838	ras homolog gene family, member E	25.7
	456088	BE177320	Hs.156148	Homo sapiens cDNA: FLJ23082 fis, clone LNG06451	25.7
	417120	N79687	Hs.46616	ESTs	25.6
	405194			predicted exon	25.6
40	410687	U24389	Hs.65436	lysyl oxidase-like 1	25.6
	421888	AA299780	Hs.121036	ESTs	25.6
	420459	AF016045	Hs.97905	ovo (Drosophila) homolog-like 1	25.5
	416323	N72630	Hs.33981	Homo sapiens genomic DNA, chromosome 21q, section	25.5
	446292	AF081497	Hs.279682	Rh type C glycoprotein	25.5
45	416274	AW180404	Hs.79126	guanine nucleotide binding protein 10	25.5
	430028	BE564110	Hs.227750	NADH dehydrogenase (ubiquinone) 1 beta subcomplex	25.5
	438450	A1050866	Hs.65853	nodal, mouse, homolog	25.5
	400215			predicted exon	25.4
	430014	H59354	Hs.182485	actinin, alpha 4	25.4
50	453582	AW854339	Hs.33476	hypothetical protein FLJ11937	25.4
	405867			predicted exon	25.4
	459170	A1905518		gb:RC-BT091-210199-098 BT091 Homo sapiens cDNA	25.4
	407944	R34008	Hs.239727	desmocollin 2	25.4
	415748	D90086	Hs.979	pyruvate dehydrogenase (liponamide) beta	25.3
55	423287	H38340		gb:yp70h07.r1 Soares adult brain N2b4HB55Y Homo s	25.3
	450944	AA554989	Hs.209061	sudD (suppressor of bldD6, Aspergillus nidulans) homo	25.3
	432906	BE265489	Hs.3123	lethal giant larvae (Drosophila) homolog 2	25.3
	400104			predicted exon	25.3
	449019	A1949095	Hs.67776	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFA	25.3
60	406897	M57417		gb:Homo sapiens mucin (mucin) mRNA, partial cds.	25.3
	402639			predicted exon	25.3
	447147	AA910353	Hs.292815	ESTs	25.3
	453379	AA035261	Hs.61753	ESTs	25.3
	414217	A1309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone LNG09846	25.3
65	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	25.3
	406685	M18728		gb:Human nonspecific crossreacting antigen mRNA, co	25.3
	444747	AW450407	Hs.257291	ESTs, Weakly similar to PSS8_HUMAN PROSTASIN	25.2
	417883	R22519	Hs.23398	ESTs	25.2
	430235	BE268048	Hs.236494	RAB10, member RAS oncogene family	25.2
70	459001	A1761313	Hs.204605	ESTs	25.2
	434368	AW519020	Hs.212840	Homo sapiens cDNA FLJ13265 fis, clone OVARC1000	25.2
	415917	Z43912		gb:HSC10A111 normalized infant brain cDNA Homo	25.2
	444409	A1792140	Hs.49265	ESTs	25.2
	428578	BE391797	Hs.82148	hypothetical protein	25.1
75	433417	AA587773	Hs.136494	ESTs	25.1
	426372	BE304680	Hs.169531	DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 21	25.1
	402131			predicted exon	25.1
	450545	AW135582	Hs.201767	ESTs	25.0
	434162	A1221214	Hs.116136	ESTs	25.0
80	406571			predicted exon	24.9
	427600	AW630918	Hs.179774	proteasome (prosome, macropain) activator subunit 2 (P	24.9
	409402	AF208234	Hs.695	cystatin B (stafin B)	24.9
	400135			predicted exon	24.9
	428403	A1393048	Hs.239894	leucine rich repeat (in FLN) interacting protein 1	24.9
	403223			predicted exon	24.8

5	435236	T03890	Hs.157208	ESTs, Highly similar to Anx homeoprotein [M.musculu	24.8
	457439	AW410408	Hs.271167	L-pipecolic acid oxidase	24.8
	448667	Z78394	Hs.4898	Homo sapiens cDNA: FLJ22046 fis, clone HEP09276	24.8
	440605	Z40094	Hs.185698	ESTs	24.8
	426724	AA383623	Hs.293616	ESTs	24.8
10	403359			predicted exon	24.7
	442826	A1018777	Hs.131241	ESTs	24.7
	411503	AW190338	Hs.28029	purinergic receptor P2X, ligand-gated ion channel, 4	24.6
	414540	BE379050	gb:601236655F1 NIH_MGC_44 Homo sapiens cDNA	24.6	
	421595	AB014520	Hs.105958	Homo sapiens cDNA: FLJ22735 fis, clone HUV00180	24.5
15	438802	AA825976	Hs.136954	ESTs	24.5
	400491	H25530	Hs.50868	solute carrier family 22 (organic cation transporter), me	24.5
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecule 1)	24.5
	426383	BE537380	gb:601064570F1 NIH_MGC_10 Homo sapiens cDNA	24.4	
	418408	AA219321	Hs.173294	ESTs	24.4
20	416186	W87575	Hs.269177	ESTs	24.4
	416908	AA333990	Hs.80424	coagulation factor XII, A1 polypeptide	24.4
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	24.4
	439706	AW872527	Hs.59761	ESTs	24.4
	441619	NM_014056	Hs.7917	DKFZP564K247 protein	24.4
25	417198	F11533	Hs.81634	ATP synthase, H+ transporting, mitochondrial F0 comp	24.3
	433662	W07162	Hs.150828	CATX-8 protein	24.3
	453968	M13232	Hs.36989	coagulation factor VII (serum prothrombin conversion a	24.3
	457123	AA770021	Hs.16332	ESTs	24.3
	433864	AA931550	Hs.192785	ESTs	24.3
30	409865	AW502208	gb:U1-HF-BR0p-aj-e-09-0-ULr1 NIH_MGC_52 Hom	24.3	
	448175	BE296174	Hs.225160	Homo sapiens cDNA FLJ13102 fis, clone NT2RP3002	24.3
	406277			predicted exon	24.3
	451957	A1796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PLACE1006	24.3
	408802	AL048269	Hs.288544	Homo sapiens cDNA: FLJ20882 fis, clone ADKA0320	24.2
35	401757			predicted exon	24.2
	444751	A1207406	Hs.11866	hypothetical protein PRO1197	24.2
	408647	AW245831		gb:2822937.5prime NIH_MGC_7 Homo sapiens cDNA	24.2
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fusin)	24.2
	436913	AA789074	Hs.187478	ESTs	24.2
40	434745	AW974445	Hs.185155	ESTs, Weakly similar to HuEMAP [H.sapiens]	24.2
	451743	AW074266	Hs.23071	ESTs	24.2
	421853	AL117472	Hs.108924	DKFZP586P1422 protein	24.2
	407926	AW956382	Hs.59771	ESTs	24.1
	413973	BE279858	Hs.128417	Homo sapiens cDNA FLJ14009 fis, clone Y79AA1002	24.1
45	439078	AF085936		gb:Homo sapiens full length insert cDNA clone YR58F	24.1
	401913			predicted exon	24.1
	435138	BE314734		gb:601152976F1 NIH_MGC_19 Homo sapiens cDNA	24.0
	405311			predicted exon	24.0
	413127	BE066529	Hs.83484	SRY (sex determining region Y)-box 4	24.0
50	430793	M83181	Hs.247940	5-hydroxytryptamine (serotonin) receptor 1A	24.0
	434445	A1349306	Hs.11782	ESTs	24.0
	418168	A1754416	Hs.260024	Cdc42 effector protein 3	24.0
	431971	BE274907	Hs.77385	myosin, light polypeptide 6, alkali, smooth muscle and n	23.9
	401167			predicted exon	23.9
55	454163	AW175997		gb:QV0-BT0078-190899-005-E02 BT0078 Homo sapi	23.9
	403306	NM_005825	Hs.74368	transmembrane protein (63kD), endoplasmic reticulum/	23.9
	410627	AA181339	Hs.929	myosin, heavy polypeptide 7, cardiac muscle, beta	23.9
	450796	NM_001988	Hs.25482	envoplakin	23.8
	442199	BE277633	Hs.286027	etoposide-induced mRNA	23.8
60	402599			predicted exon	23.8
	426143	BE379836	Hs.167106	proteasome (prosome, macropain) subunit, alpha type, 3	23.8
	437592	NM_003851	Hs.5710	cellular repressor of E1A-stimulated genes	23.8
	433598	A1762836	Hs.271433	ESTs, Moderately similar to ALU2_HUMAN ALU SU	23.8
	401088			predicted exon	23.8
65	445924	A1264671	Hs.164166	ESTs	23.8
	420902	AA742277		gb:ny28e09.s1 NCI_CGAP_GCB1 Homo sapiens cDN	23.8
	426369	AF134157	Hs.169487	Kreisler (mouse) maf-related leucine zipper homolog	23.8
	458698	AW452189	Hs.257528	ESTs	23.7
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	23.7
70	413460	R61610	Hs.21527	ESTs, Weakly similar to KIAA0918 protein [H.sapiens]	23.6
	401575			predicted exon	23.6
	431822	AA516049		gb:mg65d01.s1 NCI_CGAP_Lip2 Homo sapiens cDNA	23.6
	427276	AA400269	Hs.49598	ESTs	23.6
	417059	AA442192	Hs.81097	cytochrome c oxidase subunit VIII	23.5
75	400161			predicted exon	23.5
	417190	NM_001359	Hs.81548	2,4-dienoyl CoA reductase 1, mitochondrial	23.5
	443667	A1129066	Hs.135457	ESTs	23.5
	413544	BE147225		gb:PM2-HT0225-031299-003-f11 HT0225 Homo sapie	23.5
	400685			predicted exon	23.5
80	422090	W05345	Hs.293884	ESTs	23.4
	432517	AF275816	Hs.283096	PR domain containing 9	23.4
	405307			predicted exon	23.4
	416328	H48389	Hs.268886	ESTs	23.4
	427174	AA398848	Hs.97541	ESTs	23.4
	426148	A1751071	Hs.167135	Homo sapiens cDNA FLJ10728 fis, clone NT2RP3001	23.3
	452544	AW851888		gb:QV0-CT0225-131099-034-d05 CT0225 Homo sapie	23.3
	404890			predicted exon	23.3
	408725	AA131539	Hs.15569	ESTs	23.3
	408725	AA131539	Hs.15569	ESTs	23.3

	428362	AA426555	Hs.169333	ESTs	23.3
	425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5-phosphate ep	23.3
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B11 (aldose redu	23.3
5	410982	BE273749	Hs.752	FK506-binding protein 1A (12kD)	23.2
	411796	AA807197	Hs.6918	ESTs	23.2
	458954	AW379075	Hs.141742	Homo sapiens cDNA FLJ12211 fis, clone MAMMA10	23.2
	408896	AI610447	Hs.48778	riban protein	23.2
	457024	AA397546	Hs.119151	ESTs	23.2
10	414591	AI888490	Hs.55902	ESTs	23.2
	437846	AA773866	Hs.244569	ESTs	23.2
	401220			predicted exon	23.1
	421747	AI816224	Hs.107747	DKFZP566C243 protein	23.1
	452950	AA428123	Hs.7745	17kD fetal brain protein	23.1
	414327	BE408145	Hs.185254	ESTs, Moderately similar to NAC-1 protein [R]norvegic	23.1
15	405256			predicted exon	23.1
	452416	AA026115	Hs.114777	ESTs	23.1
	440684	AI253123	Hs.127356	ESTs, Highly similar to NEST_HUMAN NEST1 [H.sap	23.1
	445603	H08345	Hs.106234	ESTs	23.1
	436306	AA805939	Hs.117927	ESTs	23.1
20	434887	AF159442	Hs.103382	phospholipid scramblase 3	23.0
	404727			predicted exon	23.0
	407317	AI204033	Hs.271461	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFA	23.0
	405580			predicted exon	23.0
25	437898	W81260	Hs.43410	ESTs	22.9
	448781	AW243419	Hs.254048	ESTs	22.9
	457297	AW968188	Hs.290999	ESTs	22.9
	405545			predicted exon	22.9
	431562	AI884334	Hs.11637	ESTs	22.9
30	440703	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (from c	22.9
	439848	AW979249		gb:EST391359 MAGE resequences, MAGP Homo sap	22.9
	418149	AA811473	Hs.291877	ESTs	22.9
	439332	AW842747	Hs.293314	ESTs, Highly similar to unnamed protein product [H.s	22.8
	401566			predicted exon	22.8
35	425078	NM_002599	Hs.154437	phosphodiesterase 2A, cGMP-stimulated	22.8
	406684	X16354	Hs.50964	carcinoembryonic antigen-related cell adhesion molecu	22.8
	421651	AW860612	Hs.283566	ESTs	22.8
	421064	AI245432	Hs.101382	tumor necrosis factor, alpha-induced protein 2	22.8
	441249	AA971585	Hs.166250	ESTs	22.8
40	457624	AA809159	Hs.287581	Homo sapiens cDNA FLJ13544 fis, clone PLACE1006	22.8
	407395	AF005082		gb:Homo sapiens skin-specific protein (xp33) mRNA, p	22.8
	459008	AW298631	Hs.27721	hypothetical protein FLJ20353	22.8
	436827	H72187	Hs.5322	guanine nucleotide binding protein (G protein), gamma	22.7
	418174	L20588	Hs.83656	Rho GDP dissociation inhibitor (GDI) beta	22.7
45	418307	U70867	Hs.83974	solute carrier family 21 (prostaglandin transporter), mem	22.7
	456035	N54956	Hs.271726	ESTs	22.7
	457867	AA045767	Hs.5300	bladder cancer associated protein	22.7
	440401	AI126341	Hs.143887	ESTs	22.7
	400126			predicted exon	22.7
50	414931	AK000342	Hs.77646	Homo sapiens mRNA; cDNA DKFZp761M0223 (from	22.7
	406719	AI832962	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	22.6
	439675	W95357	Hs.138860	Rho GTPase activating protein 1	22.6
	456058	N94587	Hs.55063	ESTs	22.6
	441926	AI015051	Hs.130953	ESTs	22.6
55	428423	AI076517	Hs.184276	solute carrier family 9 (sodium/hydrogen exchanger), is	22.6
	438518	BE561958	Hs.285823	immunoglobulin heavy constant mu	22.6
	420674	NM_000055	Hs.1327	butyrylcholinesterase	22.6
	422160	AW582898		gb:aa07e04.y1 Human Pancreatic islets Homo sapiens c	22.5
	412408	DS1103	Hs.73851	ATP synthase, H+ transporting, mitochondrial F0 comp	22.5
	400964			predicted exon	22.5
60	434360	AW015415	Hs.127780	ESTs	22.5
	427977	AW630727	Hs.181307	H3 histone, family 3A	22.4
	450339	AI693281	Hs.54547	ESTs	22.4
	424059	AW451266	Hs.107418	ESTs	22.4
65	414626	BE410589		gb:601303308F1 NIH_MGC_21 Homo sapiens cDNA	22.4
	401991			predicted exon	22.4
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	22.3
	457952	U25750	Hs.210783	Human chromosome 17q21 mRNA clone 1046:1-1	22.3
	422597	BE245909	Hs.118634	ATP-binding cassette, sub-family B (MDR/TAP), mem	22.3
70	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	22.3
	447306	AI373163	Hs.170333	ESTs	22.3
	424966	AI077312	Hs.153985	solute carrier family 7 (cationic amino acid transporter,	22.3
	422739	H20106	Hs.119591	adaptor-related protein complex 2, sigma 1 subunit	22.2
	432504	AL121015	Hs.277704	oxygen regulated protein (150kD)	22.2
75	423804	AW403448	Hs.1706	interferon-stimulated transcription factor 3, gamma (48k	22.2
	404683	AI924294	Hs.173259	uncharacterized bone marrow protein BM033	22.2
	441624	AF220191	Hs.179666	uncharacterized hypothalamus protein HSMNP1	22.2
	425751	T19239	Hs.1940	crystallin, alpha B	22.2
	452976	R44214	Hs.101189	ESTs	22.2
80	414642	AA150350		gb:z03h01.r1 Soares_pregnant_uterus_NbHPU Homo	22.2
	437452	AL390127	Hs.7104	Homo sapiens mRNA; cDNA DKFZp761P06121 (from	22.2
	417426	NM_002291	Hs.82124	laminin, beta 1	22.2
	414774	X02419	Hs.77274	plasminogen activator, urokinase	22.1
	424631	AA688021	Hs.179808	ESTs	22.1
	413987	AW204431	Hs.117853	ESTs	22.1

	400174		predicted exon	22.1
	431837	T79326	Hs.298262 ESTs, Weakly similar to dJ88J8.1 [H.sapiens]	22.1
	401628		predicted exon	22.1
5	418374	AJ011916	Hs.84359 hypothetical protein	22.0
	429297	X82494	Hs.198862 fibulin 2	22.0
	403508		predicted exon	22.0
	432638	AJ017717	Hs.126525 chromosome 21 open reading frame 15	22.0
	407382	AA503620	gb:49b08.s1 NCI_CGAP_Co3 Homo sapiens cDNA	22.0
10	411492	T46848	Hs.70337 immunoglobulin superfamily, member 4	22.0
	420185	AL044056	Hs.158047 ESTs	22.0
	409545	BE286182	gb:501177324F1 NIH_MGC_17 Homo sapiens cDNA	22.0
	426662	AA879474	Hs.122710 ESTs	22.0
	424247	X14008	Hs.234734 lysozyme (renal amyloidosis)	22.0
15	443062	N77999	Hs.8963 Homo sapiens mRNA full length insert cDNA clone EU	21.9
	422447	AA310711	Hs.124340 ESTs	21.9
	421574	AJ000152	Hs.105924 defensin, beta 2	21.9
	435302	AJ076259	Hs.190337 ESTs	21.9
	414527	BE241739	Hs.76359 catalase	21.9
20	441436	AW137772	Hs.185980 ESTs	21.9
	454178	AW177274	gb:CM2-CT0128-230899-005-a02 CT0128 Homo sapie	21.8
	448838	BE614761	gb:501281335F1 NIH_MGC_39 Homo sapiens cDNA	21.8
	427889	AA00968	Hs.181048 dual specificity phosphatase 3 (vaccinia virus phosphat	21.8
	441114	AA917466	Hs.126600 ESTs	21.8
25	451831	NM_001674	Hs.460 activating transcription factor 3	21.8
	405600		predicted exon	21.8
	446981	AI652743	Hs.197497 ESTs	21.8
	432839	AA579465	Hs.287332 ESTs	21.8
	405208		predicted exon	21.8
30	435025	T08990	Hs.4742 anchor attachment protein 1 (Gaa1p, yeast) homolog	21.7
	413976	BE285452	Hs.75655 procollagen-proline, 2-oxoglutarate 4-dioxygenase (pro	21.7
	423515	AA327017	Hs.162204 ESTs	21.7
	452329	N36626	Hs.29106 mitogen-activated protein kinase phosphatase x	21.7
	423050	AA320946	gb:EST23529 Adipose tissue, brown Homo sapiens cD	21.7
35	413679	BE158765	gb:RC1-HT0370-120100-012-c09 HT0370 Homo sapie	21.7
	442168	AW845280	Hs.204723 ESTs	21.6
	445585	AI243836	Hs.147068 ESTs	21.6
	406160		predicted exon	21.6
40	433025	AA374743	Hs.279920 tyrosine 3-monooxygenase/tryptophan 5-monooxygenas	21.6
	446598	AW250546	gb:2821774.5prime NIH_MGC_7 Homo sapiens cDNA	21.6
	434493	AA635305	Hs.121574 ESTs	21.6
	429582	AI569068	Hs.22247 ESTs	21.6
	403798		predicted exon	21.6
	405028		predicted exon	21.6
45	426597	AA382250	Hs.145601 ESTs	21.6
	437308	AA749417	Hs.292353 ESTs	21.6
	447384	AI377221	Hs.40528 ESTs	21.6
	429060	AW139155	Hs.194995 hypothetical protein DKFZp434C0320	21.6
	437068	AA743643	Hs.291427 ESTs	21.6
50	418509	AB028524	Hs.85539 ATP synthase, H+ transporting, mitochondrial F0 comp	21.5
	432899	BE294029	Hs.279903 Ras homolog enriched in brain 2	21.5
	407663	NM_016429	Hs.37482 COP22 for nonclathrin coat protein zeta-COP	21.5
	446627	AI973016	Hs.15725 hypothetical protein SBBI48	21.5
	413605	BE152644	gb:CM1-HT0329-250200-128-f09 HT0329 Homo sapie	21.5
55	427286	AW732802	Hs.2132 epidermal growth factor receptor pathway substrate 8	21.5
	405226		predicted exon	21.4
	402570		predicted exon	21.4
	457960	AA771881	Hs.298149 ESTs	21.4
	400684		predicted exon	21.4
60	425943	H46986	Hs.31861 ESTs	21.4
	434240	AF119912	Hs.258119 hypothetical protein PRO3073	21.4
	448376	AM94332	Hs.196963 ESTs	21.4
	408089	H59799	Hs.42644 thioredoxin-like	21.4
	400304	AF005082	Hs.113261 Homo sapiens skin-specific protein (xp33) mRNA, part	21.4
65	412652	AI801777	Hs.6774 ESTs	21.4
	426373	AI751656	Hs.183986 poliovirus receptor-related 2 (herpesvirus entry mediato	21.3
	416138	C18946	Hs.79026 myeloid leukemia factor 2	21.3
	425184	BE278288	Hs.155048 Lutheran blood group (Auberger b antigen included)	21.3
	411028	AW813703	gb:RC3-ST0197-130100-014-h09 ST0197 Homo sapien	21.3
70	417438	Z43989	Hs.82141 Human clone Z3612 mRNA sequence	21.3
	417534	NM_004998	Hs.82251 myosin IC	21.3
	427767	AI879283	Hs.180714 cytochrome c oxidase subunit VIa polypeptide 1	21.2
	433300	AA582307	gb:mn49d09.s1 NCI_CGAP_Kd6 Homo sapiens cDNA	21.2
	452061	AI074259	Hs.469 succinate dehydrogenase complex, subunit A, flavoprot	21.2
75	411939	AI365585	Hs.146246 ESTs	21.2
	435060	AM22719	Hs.233349 ESTs, Weakly similar to fork head like protein [H.saple	21.2
	432412	AM70549	Hs.162201 ESTs	21.2
	407491	S82769	gb:GABAA receptor gamma 3 subunit [human, fetal bra	21.2
	418960	NM_004494	Hs.89525 hepatoma-derived growth factor (high-mobility group p	21.1
80	426254	BE018103	Hs.168541 Homo sapiens mRNA full length insert cDNA clone EU	21.1
	458188	AW297226	Hs.137840 ESTs, Moderately similar to SIX1_HUMAN HOME0B	21.1
	406215		predicted exon	21.1
	425481	AK000602	Hs.157938 hypothetical protein FLJ20595	21.1
	448296	BE622756	Hs.10949 Homo sapiens cDNA FLJ14162 fis, clone NT2RM4002	21.1
	409415	AA579258	Hs.6083 Homo sapiens cDNA: FLJ21028 fis, clone CAE07155	21.1

5	408546	W49512	Hs.46348	bradykinin receptor B1	21.1
	450008	H52870	Hs.36688	WAP four-disulfide core domain 1	21.1
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	21.1
	438901	AF085834	Hs.29038	ESTs	21.1
	440500	AA972165	Hs.150308	ESTs	21.1
	413101	BE065215		gb:RC1-BT0314-310300-015-01 BT0314 Homo sapie	21.1
	447452	BE618258	Hs.102480	ESTs	21.1
	412446	AI768015	Hs.92127	ESTs	21.1
10	418975	T75496	Hs.296980	ESTs	21.0
	454961	AW847807		gbl:LL3-CT0213-190200-040-E12 CT0213 Homo sapien	21.0
	401072			predicted exon	21.0
	401204			predicted exon	21.0
	433626	AF078859	Hs.86347	hypothetical protein	21.0
15	418047	R37633	Hs.4847	ESTs	21.0
	443380	AJ792478	Hs.135377	ESTs	21.0
	427424	AA402453	Hs.113011	ESTs	21.0
	433412	AV653729	Hs.8185	CGI-44 protein; sulfide dehydrogenase like (yeast)	21.0
	422599	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A) expressed in	20.9
20	435656	R93409	Hs.120759	ESTs	20.9
	413745	AW247252	Hs.75514	nucleoside phosphorylase	20.9
	418874	T60872		gb:yb72h11.s1 Stralagene ovary (937217) Homo sapien	20.9
	452574	AF127481	Hs.35093	lymphoid blast crisis oncogene	20.9
	400332	S66407	Hs.248032	FLT4	20.9
25	402421			predicted exon	20.9
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	20.9
	432038	AA524746	Hs.162110	ESTs	20.8
	423711	AF059194	Hs.131953	v-maf musculoaponeurotic fibrosarcoma (avian) oncoge	20.8
	402297			predicted exon	20.8
	405133			predicted exon	20.8
30	436661	AI125270	Hs.128069	ESTs, Weakly similar to similar to collagen [C.elegans]	20.8
	437836	BE269291	Hs.292458	ESTs	20.8
	437329	AA811977	Hs.291761	ESTs	20.8
	445830	H10451	Hs.42656	Homo sapiens cDNA FLJ12667 fis, clone NT2RM4002	20.8
35	406824	AW515961	Hs.84298	CD74 antigen (invariant polypeptide of major histocom	20.7
	421271	AW170057	Hs.133179	ESTs	20.7
	400256			predicted exon	20.7
	414028	AA782576	Hs.4944	Homo sapiens cDNA FLJ12783 fis, clone NT2RP2001	20.7
	456728	AL120077	Hs.122967	kelch (Drosophila)-like 2 (Mayven)	20.7
40	417707	AL035786	Hs.82425	actin related protein 2/3 complex, subunit 5 (16 kD)	20.7
	438713	H16902	Hs.6749	ESTs	20.7
	450306	AL080080	Hs.24768	DKFZP564E1962 protein	20.7
	438898	AI819863	Hs.106243	ESTs	20.7
	403273			predicted exon	20.7
45	414605	BE390440		gb:601263601F1 NIH_MGC_44 Homo sapiens cDNA	20.7
	401283			predicted exon	20.7
	403703			predicted exon	20.6
	416969	AI815443	Hs.283404	organic cation transporter	20.6
	442400	AW381148	Hs.3593	ESTs	20.6
50	447563	BE536115	Hs.160983	ESTs	20.5
	419754	H52299	Hs.75243	bromodomain-containing 2	20.5
	408204	AA454501	Hs.43666	protein tyrosine phosphatase type IVA, member 3	20.5
	450507	AW295603	Hs.250891	ESTs	20.5
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	20.5
55	413758	BE162391		gb:PM2-HT0451-090100-002-004 HT0451 Homo sapie	20.5
	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	20.5
	400642			predicted exon	20.4
	431582	F07136	Hs.261828	G protein-coupled receptor kinase 7	20.4
	442724	AA355525	Hs.159604	cysteinyl-tRNA synthetase	20.4
60	417861	AA334551	Hs.82767	sperm specific antigen 2	20.4
	402948			predicted exon	20.4
	411004	AW813242		gb:MR3-ST0191-020200-207-g10 ST0191 Homo sapie	20.4
	435478	AA682622		gb:cj20f09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Ho	20.4
	447955	BE544271	Hs.288390	Homo sapiens cDNA: FLJ22795 fis, clone KAI2543	20.3
65	433592	NM_004642	Hs.3436	deleted in oral cancer (mouse, homolog) 1	20.3
	420865	N73241	Hs.100001	solute carrier family 17 (sodium phosphate), member 1	20.3
	449482	AI784266	Hs.28774	ESTs	20.3
	400807			predicted exon	20.3
	419942	U25138	Hs.93841	potassium large conductance calcium-activated channel	20.3
70	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7 (galectin 7)	20.3
	402986	BE244588	Hs.6456	chaperonin containing TCP1, subunit 2 (beta)	20.3
	451375	AI792066	Hs.283902	Homo sapiens BAC clone RP11-481J13 from 2	20.3
	453586	AA248089	Hs.50841	ESTs, Weakly similar to tubulin [M.musculus]	20.3
	433090	AI720050	Hs.145362	immortalization-upregulated protein	20.3
75	425053	AF046024	Hs.154320	ubiquitin-activating enzyme E1C (homologous to yeast	20.3
	412602	U41518	Hs.74602	aquaporin 1 (channel-forming integral protein, 28kD)	20.3
	409738	BE222975	Hs.56205	insulin induced gene 1	20.3
	428245	AF151048	Hs.183180	hypothetical protein	20.2
	412582	BE270631	Hs.74077	proteasome (prosome, macropain) subunit, alpha type, 6	20.2
80	406207			predicted exon	20.2
	400931			predicted exon	20.2
	410709	AL122109	Hs.65735	Homo sapiens mRNA; cDNA DKFZp434M1827 (from	20.2
	428438	NM_001955	Hs.2271	endothelin 1	20.2
	446918	AL135125	Hs.13913	KIAA1577 protein	20.2
	417821	BE245149	Hs.82643	protein tyrosine kinase 9	20.2

	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (prostaglandin G	20.2
	414511	AA148725	Hs.12969	hypothetical protein	20.2
	451548	AF051782	Hs.26584	Homo sapiens clone CDABP0038 mRNA sequence	20.1
5	441899	AI372588	Hs.8022	TU3A protein	20.1
	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	20.1
	411014	AW816072		gb:MF3-ST0220-070100-021-h07 ST0220 Homo sapie	20.1
	451400	BE160479		gb:QV1-HT0413-210200-081-g05 HT0413 Homo sapi	20.1
	459247	N46243	Hs.110373	ESTs	20.1
10	441633	AW858544	Hs.112242	ESTs	20.1
	427466	AA523543	Hs.7678	cellular retinoic acid-binding protein 1	20.0
	406893	M22406		gb:Human Intestinal mucin mRNA, partial cds, clone SM	20.0
	406268			predicted exon	20.0
	403348			predicted exon	20.0
	400970			predicted exon	20.0
15	414045	NM_002951	Hs.75722	ribophorin II	20.0
	427169	AA398823	Hs.97549	EST	20.0
	405586			predicted exon	20.0
	445834	AI913290	Hs.145532	ESTs, Weakly similar to Gag polyprotein [M.musculus	20.0
20	422525	AA758797	Hs.192807	ESTs	20.0
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-like 1	20.0
	454590	AW809762	Hs.222056	Homo sapiens cDNA FLJ11572 fis, clone HEMBA100	20.0
	411529	AA430348	Hs.288837	Homo sapiens cDNA FLJ12927 fis, clone NT2RP2004	20.0
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kd)	20.0
	403234			predicted exon	19.9
25	427267	AI201185	Hs.119164	ESTs	19.9
	400203			predicted exon	19.9
	449296	AL137257	Hs.23458	Homo sapiens mRNA; cDNA DKFZp434C1613 (from	19.9
	406704	M21665	Hs.829	myosin, heavy polypeptide 7, cardiac muscle, beta	19.9
30	423083	AA321774	Hs.10941	ESTs, Weakly similar to IPP1_HUMAN PROTEIN PH	19.9
	422112	BE540240	Hs.111783	Lsm1 protein	19.9
	413282	BE076159		gb:CMD-BT0615-140200-175-e06 BT0615 Homo sapie	19.9
	453702	AA037637	Hs.42128	ESTs	19.9
	403085			predicted exon	19.9
35	440633	AI140686	Hs.263320	ESTs	19.9
	456994	AA383623	Hs.293616	ESTs	19.9
	458260	R41782	Hs.22279	ESTs	19.9
	452388	BE019696	Hs.29287	retinoblastoma-binding protein 8	19.9
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	19.9
40	441889	AA306207	Hs.286241	Homo sapiens cDNA: FLJ22698 fis, clone HSI12044	19.9
	418758	AW959311	Hs.87019	ESTs	19.9
	405848	M33600	Hs.180255	major histocompatibility complex, class II, DR beta 1	19.8
	433053	BE301909	Hs.279952	glutathione S-transferase subunit 13 homolog	19.8
	414194	BE175494	Hs.75811	N-acylsphingosine amidohydrolase (acid ceramidase)	19.8
45	452321	AW844498	Hs.289052	Homo sapiens LENG8 mRNA, variant C, partial sequen	19.8
	449713	AW027025	Hs.239262	ESTs	19.8
	458827	AW970786	Hs.178470	Homo sapiens cDNA: FLJ22662 fis, clone HSI08080	19.8
	414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	19.8
	441730	AI243276	Hs.149017	ESTs	19.8
50	420701	N42919	Hs.88630	ESTs, Weakly similar to AC007228.1 R31665.2 [H.sapi	19.8
	403642			predicted exon	19.8
	408987	H85615		gb:y03f11.1 Soares retina N2b5HR Homo sapiens cD	19.8
	446712	AW204789	Hs.209828	ESTs	19.8
	403286			predicted exon	19.8
55	434439	AI022360	Hs.190583	ESTs	19.8
	404067			predicted exon	19.7
	455694	BE067300		gb:PM2-BT0349-161299-001-h10 BT0349 Homo sapie	19.7
	403287			predicted exon	19.7
	434633	AI189587	Hs.120915	ESTs	19.7
60	408199	AA132637	Hs.15396	ESTs	19.7
	420080	M94065	Hs.94925	dihydroorotate dehydrogenase	19.7
	408852	AW291435	Hs.254961	ESTs	19.7
	403786			predicted exon	19.7
	416839	H94900	Hs.17882	ESTs	19.7
65	434385	AA631946	Hs.259580	ESTs	19.7
	446845	AI343645	Hs.156108	ESTs	19.7
	425612	BE004257		gb:CMD-BN0103-180300-296-c04 BN0103 Homo sapi	19.7
	402520			predicted exon	19.6
	436098	R20597	Hs.9739	ESTs	19.6
70	438974	AF089816	Hs.6454	chromosome 19 open reading frame 3	19.6
	447751	AA339541	Hs.24956	hypothetical protein FLJ22056	19.6
	451310	AW250651	Hs.26213	ESTs, Moderately similar to dJ447F3.3 [H.sapiens]	19.6
	435961	BE293127	Hs.283722	GTT1 protein	19.6
	452937	BE410390	Hs.288940	five-span transmembrane protein M83	19.6
	404850			predicted exon	19.6
75	438360	H74149	Hs.288193	hypothetical protein FLJ10375	19.6
	436508	AW604381	Hs.121121	ESTs	19.6
	430486	BE062109	Hs.241551	chloride channel, calcium activated, family member 2	19.6
	407824	AA147884	Hs.9812	ESTs	19.6
	406388			predicted exon	19.6
80	430204	AA618335	Hs.146137	ESTs, Weakly similar to putative [C.elegans]	19.5
	457560	AI801934	Hs.163909	ESTs	19.5
	429521	BE048708	Hs.50949	ESTs	19.5
	429758	AW137722	Hs.246804	ESTs	19.5
	441473	AA934995	Hs.184846	ESTs, Weakly similar to R28830.1 [H.sapiens]	19.5

	411724	AA770559	Hs.71618	polymerase (RNA) II (DNA directed) polypeptide L [7.	19.5
	450453	AA009883	Hs.50186	ESTs	19.5
	419687	AI638859	Hs.227699	ESTs, Weakly similar to Yhr217cp [S.cerevisiae]	19.5
5	442162	AW294956	Hs.150849	ESTs	19.5
	435056	AW023337	Hs.5422	glycoprotein M6B	19.5
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	19.5
	413825	BE299181	Hs.75564	CD151 antigen	19.4
	422687	AW068823	Hs.119206	insulin-like growth factor binding protein 7	19.4
10	435551	AF212365	Hs.5470	IL-17B receptor	19.4
	440069	BE617892	Hs.6895	actin related protein 2/3 complex, subunit 3 (21 kD)	19.4
	432277	AI669790	Hs.161825	ESTs	19.4
	428044	AA093322	Hs.182225	RNA binding motif protein 3	19.4
	456064	AA256213	Hs.72010	ESTs	19.4
	424897	D63216	Hs.153684	frizzled-related protein	19.4
15	424673	AA345051	Hs.294092	ESTs	19.4
	403852			predicted exon	19.3
	405699			predicted exon	19.3
	433096	AU076803	Hs.282975	carboxylesterase 2 (intestine, liver)	19.3
20	400344	NM_012368	Hs.258574	olfactory receptor, family 2, subfamily C, member 1	19.3
	417501	AL041219	Hs.82222	sema domain, immunoglobulin domain (Ig), short basic	19.3
	400449			predicted exon	19.3
	453801	AL134751	Hs.23450	mRNA for FLJ00023 protein	19.3
	435849	BE305242	Hs.112442	ESTs, Weakly similar to CLDE_HUMAN CLAUDIN-	19.3
	454181	AW177377		gb:CM4-CT0129-190899-007-e09 CT0129 Homo sapie	19.3
25	414807	AI738816	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(NAD)	19.3
	406326			predicted exon	19.3
	421821	H83363	Hs.109571	translocase of inner mitochondrial membrane 10 (yeast)	19.3
	416700	AW498958	Hs.79572	cathepsin D (lysosomal aspartyl protease)	19.2
30	458857	AI627342	Hs.224601	ESTs	19.2
	405501			predicted exon	19.2
	416601	R08652	Hs.20205	hemoglobin, beta pseudogene 1	19.2
	426600	NM_003378	Hs.171014	VEGF nerve growth factor inducible	19.2
	425590	A954686	Hs.158321	beaded filament structural protein 2, phakdin	19.2
35	428151	AA422028		gb:zv26g06.r1 Soares_NhiMPu_S1 Homo sapiens cDN	19.2
	426420	BE383808	Hs.169829	KIAA1180 protein	19.2
	414428	BE296906	Hs.182625	VAMP (vesicle-associated membrane protein)-associate	19.2
	404601			predicted exon	19.2
	403861			predicted exon	19.2
40	448363	BE174595	Hs.366	6-pyruvoyltetrahydropterin synthase	19.2
	406655	M21533	Hs.181244	major histocompatibility complex, class I, A	19.1
	435372	AA809591	Hs.106486	ESTs, Highly similar to CIKG_HUMAN VOLTAGE-G	19.1
	413154	BE067870		gb:RC0-BT0362-021299-031-b06 BT0362 Homo sapie	19.1
	443021	AA368546	Hs.8904	Ig superfamily protein	19.1
45	412975	T70956	Hs.75106	clusterin (complement lysis inhibitor, SP-40,40, sulfated	19.1
	412633	AF001691	Hs.74304	periplakin	19.1
	402071			predicted exon	19.1
	410387	AI277367	Hs.47094	ESTs	19.1
	423961	D13666	Hs.136348	osteoblast specific factor 2 (fasciadin I-like)	19.1
50	407032	U73799		gb:Human dynactin mRNA, partial cds.	19.0
	404034			predicted exon	19.0
	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudogene	19.0
	446599	Z97832	Hs.15476	differentially expressed in FDCP (mouse homolog) 6	19.0
	426410	BE298446	Hs.180372	BCL2-like 1	19.0
55	419618	AA528295		gb:zh26e06.s1 NC1_CGAP_Pr3 Homo sapiens cDNA c	19.0
	457632	AW292151	Hs.112689	ESTs	19.0
	417138	AA193646	Hs.65771	Homo sapiens chromosome 19, BAC CIT-HSPC_204F	19.0
	417933	X02308	Hs.82982	thymidylate synthetase	19.0
	458808	AW134832	Hs.246295	ESTs	19.0
60	415860	D56051	Hs.78888	diazepam binding inhibitor (GABA receptor modulator	18.9
	440919	AW291274	Hs.262826	ESTs	18.9
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	18.9
	401747			predicted exon	18.9
	454209	AW179083		gb:MRA-ST0065-270899-006-A07 ST0065 Homo sapi	18.8
65	417661	T84155	Hs.15464	Homo sapiens cDNA: FLJ21351 fis, clone COL02762	18.8
	426499	C14937	Hs.11169	Gene 33/Mig-6	18.8
	404240			predicted exon	18.8
	439718	AA307634	Hs.6650	vacuolar protein sorting 45B (yeast homolog)	18.8
	401789			predicted exon	18.8
70	456952	AW445081	Hs.301469	ESTs	18.8
	439739	AI199391	Hs.124464	ESTs	18.8
	437974	T74445	Hs.5957	Homo sapiens clone 24416 mRNA sequence	18.8
	427490	Z95152	Hs.178695	mitogen-activated protein kinase 13	18.8
	443482	AW188093	Hs.250385	ESTs	18.8
75	411420	BE390652		gb:601286820F1 NIH_MGC_44 Homo sapiens cDNA	18.8
	435196	F35675	Hs.188128	ESTs, Moderately similar to ALUB_HUMAN III ALU	18.8
	417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain family 2	18.8
	413531	AL036958	Hs.75416	DAZ associated protein 2	18.7
	428981	BE313077	Hs.93135	ESTs	18.7
80	421598	AW630942	Hs.106061	RD RNA-binding protein	18.7
	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding protein	18.7
	406754	AA477223	Hs.75922	brain protein I3	18.7
	400661			predicted exon	18.7
	442838	AJ088742	Hs.134713	ESTs	18.7
	434169	AA883752	Hs.179724	ESTs	18.7

	424126	AA335635	Hs.96917	ESTs	18.7
	408473	BE259039	Hs.129953	Ewing sarcoma breakpoint region 1	18.7
	401862			predicted exon	18.7
5	447326	AW002252	Hs.201395	ESTs	18.7
	459053	AI807052	Hs.210361	ESTs	18.7
	403362			predicted exon	18.7
	427697	T18997	Hs.180372	BCL2-like 1	18.7
	402061	H83363	Hs.109571	translocase of inner mitochondrial membrane 10 (yeast)	18.7
10	433785	BE044593	Hs.112704	ESTs	18.7
	405423			predicted exon	18.6
	429259	AA420450	Hs.292911	ESTs	18.6
	444071	AI627808	Hs.110524	ESTs	18.6
	410512	AA085603	Hs.250570	ESTs	18.6
	440376	AI024452	Hs.236816	ESTs	18.6
15	457353	X65633	Hs.248144	melanocortin 2 receptor (adrenocorticotrophic hormone)	18.6
	432749	NM_014438	Hs.278909	Interleukin-1 Superfamily s	18.6
	415602	F12920	Hs.165575	ESTs	18.6
	407891	AA486620	Hs.41135	endomucin-2	18.6
	455910	Z43712		gb:HSC1JA121 normalized infant brain cDNA Homo s	18.6
20	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig), short basic	18.6
	444246	H93281	Hs.10710	hypothetical protein FLJ20417	18.6
	428125	AA393071	Hs.182579	leucine aminopeptidase	18.6
	408457			predicted exon	18.5
	446625	AI333070	Hs.156141	ESTs	18.5
25	423334	AK000906	Hs.127273	hypothetical protein FLJ10044	18.5
	423103	AA322029		gb:EST24685 Cerebellum II Homo sapiens cDNA 5' en	18.5
	443549	T89508	Hs.16601	ESTs	18.5
	419299	AI311085	Hs.62406	Homo sapiens cDNA: FLJ22573 fis, clone HSI02387	18.5
30	411842	AW877015		gb:QV2-PT0010-250300-096-f12 PT0010 Homo saplen	18.5
	442440	BE464435	Hs.146180	ESTs, Weakly similar to non-receptor protein tyrosine k	18.5
	454574	AW809109		gb:MR4-ST0117-070100-027-a04 ST0117 Homo saple	18.5
	454377	AA075811		gb:7B03C12 Chromosome 7 Fetal Brain cDNA Library	18.5
	422365	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic subunit of DNA p	18.5
	421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (achondroplasia, tha	18.5
35	420603	AB042636	Hs.4775	junctophilin 3	18.4
	401373			predicted exon	18.4
	402292			predicted exon	18.4
	444118	AA458542	Hs.10326	coatomer protein complex, subunit epsilon	18.4
40	408310	AW179023		gb:PM3-ST0036-170899-001-e08 ST0036 Homo saple	18.4
	411236	AW833752		gb:QV4-TT0008-130100-077-b07 TT0008 Homo saple	18.4
	431405	AI470895	Hs.252574	ribosomal protein L10a	18.4
	441408	AI733249	Hs.126897	ESTs	18.4
	453994	BE180964	Hs.165590	ribosomal protein S13	18.4
	444518	AI160278	Hs.146884	ESTs	18.4
45	402407			predicted exon	18.4
	404270			predicted exon	18.4
	409103	AF251237	Hs.112208	XAGE-1 protein	18.4
	415198	AW009480	Hs.943	natural killer cell transcript 4	18.3
50	430771	BE387244	Hs.2664	flavin containing monooxygenase 4	18.3
	432636	AA340864	Hs.278562	claudin 7	18.3
	433504	NM_014874	Hs.3363	KIAA0214 gene product	18.3
	415606	W70022		gb:zd51e10.r1 Soares fetal heart_NbHH19W Homo sa	18.3
	401401	BE047878	Hs.99093	Homo sapiens chromosome 19, cosmid R26379	18.3
55	420758	AW287536	Hs.33053	ESTs	18.3
	457520	AA553495	Hs.182264	ESTs	18.3
	432323	AK001409	Hs.274356	hypothetical protein FLJ10547	18.3
	404750			predicted exon	18.3
	450645	AL117441	Hs.25264	DKFZP434N126 protein	18.3
60	445160	AI299144	Hs.150797	ESTs	18.3
	418461	BE242781	Hs.286037	Homo sapiens cDNA FLJ12999 fis, clone NT2RP3000	18.3
	401809			predicted exon	18.3
	458121	S42416	Hs.74647	Human T-cell receptor active alpha-chain mRNA from	18.3
	435106	AA100847	Hs.193380	ESTs, Highly similar to AF174600 1 F-box protein Fbx	18.3
65	448398	AW444655	Hs.170838	ESTs	18.3
	428145	BE243327	Hs.182626	chromosome 22 open reading frame 5	18.2
	445302	AK001537	Hs.12488	hypothetical protein FLJ10575	18.2
	407352	H47860		gb:yp76h12.r1 Soares fetal liver spleen 1NFLS Homo s	18.2
	413190	AA151802	Hs.40368	adaptor-related protein complex 1, sigma 2 subunit	18.2
70	436371	AI821912	Hs.113912	ESTs	18.2
	400965			predicted exon	18.2
	433427	AI816449	Hs.171889	cholinephosphotransferase 1	18.2
	427504	AA776743	Hs.191589	ESTs	18.2
	426759	AI590401	Hs.21213	ESTs	18.2
75	423792	AW135866	Hs.245854	ESTs	18.2
	406826	AW516005	Hs.84298	CD74 antigen (invariant polypeptide of major histocom	18.1
	406659	AA663985	Hs.277477	major histocompatibility complex, class I, C	18.1
	437453	AI761350	Hs.181391	hypothetical protein DKFZp761G2113	18.1
	409276	AW372097	Hs.278429	hepatocellular carcinoma-associated antigen 59	18.1
80	449628	AI697676	Hs.197713	ESTs	18.1
	421043	BE379455	Hs.89072	ESTs	18.1
	442344	AI022925	Hs.301212	ESTs	18.1
	448744	AL135424	Hs.9469	phosphoinositol 3-phosphate binding protein-1	18.1
	416062	AA724811	Hs.74427	p53-induced protein	18.1
	414500	W24087	Hs.76285	DKFZP564B167 protein	18.1

	427272	NM_001096	Hs.174140	ATP citrate lyase	18.1
	403964			predicted exon	18.1
	433217	AB040914	Hs.278628	KIAA1481 protein	18.1
5	427502	A1809202	Hs.208343	ESTs, Weakly similar to cerebroside sulfoltransferase [H	18.1
	449586	A1863918	Hs.195078	ESTs	18.1
	430826	U10061	Hs.248019	POU domain, class 4, transcription factor 3	18.1
	414195	BE263293		gb:G01144881F2 NIH_MGC_19 Homo sapiens cDNA	18.1
	416305	AU076628	Hs.79187	coxsackie virus and adenovirus receptor	18.1
10	411088	BE247593	Hs.145053	ESTs	18.1
	419407	AW410377	Hs.41502	Homo sapiens cDNA: FLJ21276 fis, clone COL01829	18.1
	407938	AA905097	Hs.85050	phospholamban	18.1
	449360	A1640623	Hs.252720	ESTs	18.1
	417286	AA122237	Hs.81874	microsomal glutathione S-transferase 2	18.0
	405515			predicted exon	18.0
15	439319	AW016401	Hs.233476	ESTs	18.0
	419387	BE379356	Hs.90107	cell membrane glycoprotein, 110000M(r) (surface anti	18.0
	414016	AA340987	Hs.75693	prolylcarboxypeptidase (angiotensinase C)	18.0
	447778	BE620592	Hs.71190	ESTs	18.0
	435523	T62849	Hs.11090	high affinity immunoglobulin epsilon receptor beta sub	18.0
20	429230	AF088991	Hs.198274	NADH dehydrogenase (ubiquinone) 1 beta subcomplex	18.0
	457822	AA970001	Hs.150319	ESTs	18.0
	442424	A1342715	Hs.129569	ESTs, Moderately similar to B34087 hypothetical prote	18.0
	418394	AF132818	Hs.84728	Kruppel-like factor 5 (intestinal)	18.0
	413477	A1815825	Hs.48756	ESTs, Moderately similar to neuronal-STOP protein [M	18.0
25	405277			predicted exon	18.0
	450192	AA263143	Hs.24596	RAD51-interacting protein	18.0
	442191	W95186	Hs.8136	endothelial PAS domain protein 1	18.0
	429490	A1971131	Hs.293684	ESTs, Weakly similar to alternatively spliced product u	18.0
	406744	AA554082	Hs.279860	hypothetical protein FLJ20030	17.9
30	425205	NM_005854	Hs.155106	receptor (calcitonin) activity modifying protein 2	17.9
	414387	AL043148	Hs.186257	ESTs	17.9
	411811	AW864370		gb:PM4-SN0016-100500-004-h09 SN0016 Homo sapie	17.9
	433882	U90441	Hs.3622	procollagen-proline, 2-oxoglutarate 4-dioxygenase (pro	17.9
	414333	BE274897		gb:G01122959F1 NIH_MGC_20 Homo sapiens cDNA	17.9
35	403747			predicted exon	17.9
	435542	AA687376	Hs.269533	ESTs	17.9
	403093			predicted exon	17.9
	412088	A1689496	Hs.108932	ESTs	17.9
40	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	17.9
	404763			predicted exon	17.9
	454633	AW811380		gb:IL3-ST0143-290999-019-D05 ST0143 Homo sapien	17.9
	440788	A1806594	Hs.128577	ESTs	17.9
	411800	N39342	Hs.5184	TH1 drosophila homolog	17.9
45	441361	BE263308	Hs.7797	TERF1 (TRF1)-interacting nuclear factor 2	17.8
	422033	AW245805	Hs.110903	claudin 5 (transmembrane protein deleted in velocardiof	17.8
	405333			predicted exon	17.8
	408297	R17710	Hs.113314	ESTs	17.8
	403036			predicted exon	17.8
50	417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatosis 1)	17.8
	417091	AA193283	Hs.291990	ESTs	17.8
	440789	AB007857	Hs.7416	KIAA0397 gene product	17.8
	438397	AA806478	Hs.123206	ESTs	17.8
	435948	AA702675	Hs.114135	ESTs	17.8
55	450273	AW296454	Hs.24743	hypothetical protein FLJ20171	17.8
	435969	W85773	Hs.191386	ESTs	17.8
	427031	AA397601	Hs.125147	ESTs	17.8
	454505	AW801365		gb:IL5-UM0067-240300-050-a01 UM0067 Homo sapi	17.8
	403447			predicted exon	17.8
60	433297	AV658581	Hs.282633	ESTs	17.8
	443326	BE156494	Hs.188478	ESTs	17.8
	448283	A1340462	Hs.182979	ribosomal protein L12	17.8
	458067	AA393603	Hs.36752	Homo sapiens cDNA: FLJ22834 fis, clone KALA4314	17.8
	452359	BE167229	Hs.29206	Homo sapiens clone 24659 mRNA sequence	17.8
65	434098	AA625499		gb:af69g08.r1 Soares_NhHMPu_S1 Homo sapiens cDN	17.8
	450911	AA011586	Hs.272097	ESTs	17.7
	410342	R31350	Hs.743	Fc fragment of IgE, high affinity I, receptor for; gamma	17.7
	407082	Z47055		gb:Human partial cDNA sequence, farnesyl pyrophosph	17.7
	415271	X94232	Hs.78335	microtubule-associated protein, RP/EB family, member	17.7
70	417413	AA197072	Hs.86092	Human DNA sequence from clone RP11-243J16 on chr	17.7
	408937	AA210734	Hs.291386	ESTs	17.7
	433459	AA593498		gb:mn27b05.s1 NCI_CGAP_Gas1 Homo sapiens cDNA	17.7
	459536	A1254723	Hs.145496	ESTs	17.7
	428500	A1815395	Hs.184641	delta-6 fatty acid desaturase	17.7
75	433463	R41963	Hs.4197	ESTs	17.7
	406537			predicted exon	17.7
	410003	AA079487		gb:zm97f08.s1 Stralagene colon HT29 (937221) Homo	17.7
	440857	AA907808	Hs.135556	ESTs	17.7
	451072	AA013451	Hs.117929	ESTs	17.7
	418693	A1750878	Hs.87409	thrombospondin 1	17.7
80	443624	BE616129	Hs.9651	related RAS viral (r-ras) oncogene homolog	17.6
	422626	AA344932	Hs.118786	metallothionein 2A	17.6
	410756	AB037820	Hs.66159	KIAA1399 protein	17.6
	436621	A1266254	Hs.132929	ESTs	17.6
	453317	NM_002277	Hs.41696	keratin, hair, acidic, 1	17.6

	456828	AF156889	Hs.148427	LIM homeobox protein 3	17.6
	421486	AW408800	Hs.104859	hypothetical protein DKFZp762E1312	17.6
	428834	AW899713	Hs.10338	ESTs	17.6
5	451419	R36309	Hs.174369	EST	17.6
	448413	AJ745379	Hs.42911	ESTs	17.6
	424323	AA338791	Hs.146763	nascent-polypeptide-associated complex alpha polypept	17.6
	423943	AF163570	Hs.135756	polymerase (DNA-directed) kappa	17.6
	439423	BE536678	Hs.147099	ESTs	17.6
10	434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mRNA	17.6
	408246	N55669	Hs.43946	L13 protein	17.6
	441579	AW468847	Hs.127194	ESTs	17.5
	420867	NM_014183	Hs.100002	HSPC162 protein	17.5
	453680	AL079647	Hs.14485	ESTs	17.5
	400202			predicted exon	17.5
15	410788	AF038185	Hs.66187	Homo sapiens clone 23700 mRNA sequence	17.5
	409932	AJ376750	Hs.57600	adaptor-related protein complex 1, sigma 1 subunit	17.5
	425563	AF084199	Hs.298337	ESTs	17.5
	440476	AJ807671	Hs.128343	ESTs	17.5
20	452767	AW014195	Hs.61472	ESTs, Weakly similar to unknown [S.cerevisiae]	17.5
	410570	AJ133096	Hs.64593	ATP synthase, H+ transporting, mitochondrial F1F0, su	17.4
	419600	AA448958	Hs.91481	NEU1 protein	17.4
	419588	AJ347205	Hs.91375	Human clone 23614 mRNA sequence	17.4
	428975	NM_004672	Hs.194694	mitogen-activated protein kinase kinase kinase 6	17.4
25	448928	AJ350260	Hs.5384	Homo sapiens cDNA FLJ11743 fis, clone HEMBA100	17.4
	403924			predicted exon	17.4
	419889	AA251600		gbcs10d12.r1.NCI_CGAP_GCB1 Homo sapiens cDNA	17.4
	405023	AW408800	Hs.104859	hypothetical protein DKFZp762E1312	17.4
	426065	N32049		gb:yrw56g08.a1 Soares_placenta_8to9weeks_2NbHP8to	17.4
30	453199	AJ336266	Hs.301854	Homo sapiens PRO0412 mRNA, complete cds	17.4
	455132	AW857955		gb:PM0-CT0325-151299-002-A12 CT0325 Homo sapi	17.4
	442932	AA457211	Hs.8858	bromodomain adjacent to zinc finger domain, 1A	17.4
	432065	AA401039	Hs.2903	protein phosphatase 4 (formerly X), catalytic subunit	17.3
	444652	BE513613	Hs.11538	actin related protein 2/3 complex, subunit 1A (41 kD)	17.3
35	417935	R53697	Hs.170044	ESTs	17.3
	430050	AA430993	Hs.227913	API5-like 1	17.3
	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn substrate 1	17.3
	425996	W67330	Hs.81258	S100 calcium-binding protein A4 (calcium protein, calv	17.3
	416984	D87467	Hs.80620	guanine nucleotide exchange factor for Rap1; M-Ras-ra	17.3
40	437418	AJ478954	Hs.59459	ESTs	17.3
	447255	AJ884908	Hs.158607	ESTs	17.3
	402203			predicted exon	17.3
	417611	AW993983		gb:RC1-BN0035-130400-013-a04 BN0035 Homo sapie	17.3
	426560	AA381661	Hs.119878	ESTs	17.3
45	446163	AA026880	Hs.25252	Homo sapiens cDNA FLJ13603 fis, clone PLACE1010	17.3
	445017	AJ205493	Hs.176860	ESTs	17.3
	438658	AJ222068	Hs.123571	ESTs	17.3
	442238	AW135374	Hs.270949	ESTs	17.3
	443195	BE148235	Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone NT2RP3002	17.3
50	442609	AL020996	Hs.8518	selenoprotein N	17.2
	416591	AA091976	Hs.78387	proteasome (prosome, macropain) 26S subunit, ATPase	17.2
	403674			predicted exon	17.2
	430514	AA318501	Hs.241587	megakaryocyte-enhanced gene transcript 1 protein	17.2
	411696	AW857404		gb:CM3-CT0313-291199-046-c11 CT0313 Homo sapie	17.2
55	434560	R13052	Hs.3964	Homo sapiens clone 24877 mRNA sequence	17.2
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced, 68kD	17.2
	414364	D38521	Hs.75935	KIAA0077 protein	17.2
	409119	AA531133	Hs.4253	G protein-coupled receptor 44	17.2
	425640	U34051	Hs.299204	ESTs, Highly similar to CD55_HUMAN CYCLIN-DE	17.2
60	436044	BE247571	Hs.15627	Nit protein 2	17.2
	401657			predicted exon	17.2
	449763	AJ822112	Hs.118241	ESTs	17.2
	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	17.2
	449636	AJ656608	Hs.281328	ESTs	17.2
65	444958	AW292643	Hs.167047	ESTs	17.2
	429978	AA249027	Hs.241507	ribosomal protein S6	17.2
	453043	AW136440	Hs.224277	ESTs	17.2
	458640	AJ284935		gb:qk55g09.x1 NCI_CGAP_Co8 Homo sapiens cDNA	17.1
	456329	T41418		gb:ph1h3_19/1TV Outward Alu-primed hncDNA librar	17.1
70	414839	X83692	Hs.77462	DNA (cytosine-5-)-methyltransferase 1	17.1
	403662			predicted exon	17.1
	411651	AW855392		gb:CM3-CT0275-191099-024-e12 CT0275 Homo sapie	17.1
	404097			predicted exon	17.1
	447252	R90916		gb:ym01e10.r1 Soares adult brain N2b4HB55Y Homo s	17.1
75	430024	AJ808780	Hs.227730	integrin, alpha 6	17.1
	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob disease, Gerst	17.1
	444558	AW181975	Hs.165892	ESTs	17.1
	420869	X58964	Hs.123638	regulatory factor X, 1 (influences HLA class II expressi	17.1
	448812	H30775	Hs.22140	BM88 antigen	17.0
80	431777	AA570296	Hs.105470	found in inflammatory zone 1	17.0
	422007	AJ739435	Hs.39168	ESTs	17.0
	403051			predicted exon	17.0
	402427			predicted exon	17.0
	417408	F17211	Hs.86092	Human DNA sequence from clone RP11-243J16 on chr	17.0
	450598	AF151076	Hs.25199	hypothetical protein	17.0

	421121	AA459028	Hs.86228	TRIAD3 protein	17.0
	458488	AL040565	Hs.209544	ESTs	17.0
	417158	AW965223	Hs.110062	ESTs, Weakly similar to ACR3_HUMAN 30 KD ADIP	17.0
5	439318	AW837046	Hs.6527	G protein-coupled receptor 56	17.0
	428758	AA433988	Hs.98502	Homo sapiens cDNA FLJ14303 fis, clone PLACE2000	17.0
	447572	AI631546	Hs.159732	ESTs	17.0
	434434	AA633516	Hs.157201	ESTs	17.0
	408994	D86864	Hs.57735	acetyl LDL receptor, SREC	17.0
10	408927	AW295650	Hs.255453	ESTs	17.0
	439093	AA534163	Hs.5476	serine protease inhibitor, Kazal type, 5	17.0
	454466	AA984138	Hs.278895	Homo sapiens mRNA for KIAA1578 protein, partial cd	17.0
	426998	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone HEP03447,	17.0
	436659	AI217900	Hs.144464	ESTs	17.0
15	422731	AL138411		gb:DKFZp434A1229_r1 434 (synonym: hies3) Homo s	17.0
	429294	AA095971	Hs.198793	KIAA0750 gene product	17.0
	432847	BE265941	Hs.278554	prolaser (prosome, macropain) 26S subunit, non-AT	16.9
	416977	AW130242	Hs.293476	ESTs	16.9
	406827	AA971409	Hs.84298	CD74 antigen (invariant polypeptide of major histocom	16.9
20	453758	U83527		gb:HSU83527 Human fetal brain (M.Lovett) Homo sap	16.9
	431314	AI732204	Hs.105423	ESTs	16.9
	423185	BE299590	Hs.125078	ornithine decarboxylase antizyme 1	16.9
	435086	AW975243	Hs.122596	ESTs	16.9
	447383	N24231		gb:yx22a11.r1 Soares melanocyte 2NblHM Homo sapie	16.9
25	456251	R13326	Hs.21303	ESTs	16.9
	456327	H68741	Hs.38774	ESTs	16.9
	450594	N31036		gb:yx51g04.r1 Soares melanocyte 2NblHM Homo sapie	16.9
	428177	AA423967	Hs.178113	ESTs, Moderately similar to kinesin like protein 9 [Mm	16.9
	453250	AI346520	Hs.121619	chromosome 11 open reading frame 15	16.9
30	418294	AF081739	Hs.83954	protein associated with PRK1	16.9
	446546	BE167687	Hs.156628	ESTs	16.9
	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone COLF6967	16.9
	455993	BE179085		gb:RCO-HT0613-140300-021-d06 HT0613 Homo sapie	16.9
	459375	BE251770		gb:601112470F1 NIH_MGC_16 Homo sapiens cDNA	16.9
35	454803	AW860148		gb:RCO-CT0379-290100-032-b10 CT0379 Homo sapie	16.9
	445474	AI240014	Hs.259558	ESTs	16.9
	443198	AI039813		gb:xx49d06.x1 Soares_tetal_fetus_Nb2HF8_9w Homo	16.9
	441557	AW452847	Hs.270482	ESTs	16.9
	420208	M91463	Hs.95958	solute carrier family 2 (facilitated glucose transporter),	16.9
40	442202	BE272862	Hs.106534	Homo sapiens cDNA: FLJ22625 fis, clone HSI06009	16.9
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo sapie	16.9
	419355	AA428520	Hs.90061	progesterone binding protein	16.9
	452975	M85521	Hs.69469	dendritic cell protein	16.9
	432525	AI796096	Hs.109414	ESTs	16.8
45	453718	AL119317	Hs.120360	phospholipase A2, group VI (cytosolic, calcium-indepe	16.8
	437270	R18087	Hs.11282	ESTs, Weakly similar to cleft lip and palate transmemb	16.8
	408007	AW135965	Hs.246783	ESTs	16.8
	450954	AI904740	Hs.25691	receptor (calcitonin) activity modifying protein 3	16.8
	402958			predicted exon	16.8
50	445658	W22050	Hs.21299	ESTs, Weakly similar to AF151840 1 CGI-82 protein [H	16.8
	410684	AA088500	Hs.170298	ESTs	16.8
	437669	AI358105	Hs.123164	ESTs, Weakly similar to match to ESTs AA667999 [H.	16.8
	447869	AW139113	Hs.164307	ESTs	16.8
	458025	AI275408		gb:qlf53c10.x1 Soares_NhlMPu_S1 Homo sapiens cDN	16.8
55	445614	AV660763	Hs.110675	apolipoprotein C-IV	16.8
	454610	AW810224		gb:MR4-ST0125-021199-017-e07 ST0125 Homo sapie	16.8
	449303	AK001495	Hs.23467	hypothetical protein FLJ10633	16.8
	422105	AI929700	Hs.111680	endostuffin alpha	16.8
	444788	AI871122	Hs.202821	ESTs	16.8
60	414057	AI815559	Hs.75730	signal recognition particle receptor (docking protein)	16.8
	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OVARC1000	16.8
	433379	AA586368	Hs.190232	ESTs	16.8
	441552	AA937975		gb:oc06e12.s1 NCI_CGAP_GCB1 Homo sapiens cDN	16.8
	403582			predicted exon	16.8
65	433871	W02410	Hs.205555	ESTs	16.8
	439509	AF086332	Hs.58314	ESTs	16.8
	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	16.8
	430129	BE301708	Hs.233955	hypothetical protein FLJ20401	16.8
	401465			predicted exon	16.8
70	448913	AA194422	Hs.22564	myosin VI	16.8
	410261	AF145713	Hs.61490	schwannomin interacting protein 1	16.8
	421199	BE244219	Hs.102497	paxillin	16.7
	450489	AI697990	Hs.224375	ESTs	16.7
	410186	AW602528		gb:RCS-BT0562-260100-011-A02 BT0562 Homo sapi	16.7
75	447224	BE617125		gb:601441664F1 NIH_MGC_65 Homo sapiens cDNA	16.7
	403010			predicted exon	16.7
	404881			predicted exon	16.7
	445572	AI243445	Hs.189654	ESTs	16.7
	419440	AB020689	Hs.90419	KIAA0882 protein	16.7
80	443406	AK056238	Hs.143316	ESTs	16.7
	457901	AW207023	Hs.250497	ESTs, Highly similar to dJ745C22.1 [H.sapiens]	16.7
	448364	T08958	Hs.16561	HSPC141 protein	16.6
	407239	AA076350	Hs.67846	leukocyte immunoglobulin-like receptor, subfamily B (16.6
	401847			predicted exon	16.6
	429523	AK000788	Hs.205280	Homo sapiens cDNA FLJ20781 fis, clone COL04235	16.6

	432845	AI989751	Hs.150378	ESTs	16.6
	400246			predicted exon	16.6
	404971			predicted exon	16.6
5	422954	AW998605	Hs.32399	ESTs, Weakly similar to Similar to Ena-VASP like prot	16.6
	415042	NM_006759	Hs.77837	UDP-glucose pyrophosphorylase 2	16.6
	432201	AI538613	Hs.135657	ESTs	16.6
	456993	AL134577	Hs.200302	ESTs	16.6
	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgranulin A)	16.6
10	444060	AA340277	Hs.10248	Homo sapiens cDNA FLJ20167 fis, clone COL09512	16.6
	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epithelial)	16.6
	448199	AI953278	Hs.170557	ESTs	16.6
	443422	R10288	Hs.301529	ESTs	16.6
	401117			predicted exon	16.6
	400613			predicted exon	16.6
15	431214	AA294921	Hs.250811	v-rat simian leukemia viral oncogene homolog B (ras re	16.6
	431649	AL133077	Hs.266746	Homo sapiens cDNA: FLJ22615 fis, clone HSI05118	16.5
	421335	X99977	Hs.103505	ARS component B	16.5
	427154	AL137262	Hs.288991	Homo sapiens cDNA: FLJ22523 fis, clone HRC12507	16.5
20	401010			predicted exon	16.5
	436678	BE512828	Hs.5273	NADH dehydrogenase (ubiquinone) Fe-S protein 3 (30k	16.5
	401589			predicted exon	16.5
	402538			predicted exon	16.5
	430478	NM_014349	Hs.241535	TNF-inducible protein CG12-1	16.5
25	437623	D63880	Hs.5719	chromosome condensation-related SMC-associated pro	16.5
	401244			predicted exon	16.5
	415167	AA160784	Hs.28410	ESTs	16.5
	438291	BE514605	Hs.289092	Homo sapiens cDNA: FLJ22380 fis, clone HRC07453,	16.5
	405183			predicted exon	16.5
30	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	16.5
	456691	AI023428	Hs.205696	ESTs	16.5
	418332	R34976	Hs.78293	ESTs	16.5
	446052	AA358760		gb:EST67699 Fetal lung II Homo sapiens cDNA 5' end	16.5
	444859	AW449137	Hs.157487	ESTs	16.5
35	437192	AW975786	Hs.76355	ubiquitin-conjugating enzyme E2N (homologous to yea	16.5
	400891			predicted exon	16.5
	448372	AW445166	Hs.170802	ESTs	16.5
	425798	AA364002		gb:EST74529 Pineal gland II Homo sapiens cDNA 5' en	16.5
	459253	AL157476	Hs.32913	Homo sapiens mRNA; cDNA DKFZp761C082 (from c	16.5
40	420746	AW195932	Hs.197488	ESTs	16.4
	414717	BE271039	Hs.77060	proteasome (prosome, macropain) subunit, beta type, 6	16.4
	400727			predicted exon	16.4
	422691	NM_003365	Hs.119251	ubiquinol-cytochrome c reductase core protein I	16.4
	405639			predicted exon	16.4
45	414444	BE298594		gb:601119754F1 NIH_MGC_17 Homo sapiens cDNA	16.4
	456146	AL034349	Hs.79005	protein tyrosine phosphatase, receptor type, K	16.4
	414610	BE388044		gb:601263747F1 NIH_MGC_44 Homo sapiens cDNA	16.4
	414267	AL078459	Hs.289109	dimethylarginine dimethylaminohydrolase 1	16.4
	401268			predicted exon	16.4
50	403613			predicted exon	16.4
	414203	BE262170		gb:601150419F1 NIH_MGC_19 Homo sapiens cDNA	16.4
	454315	AW373564	Hs.251928	nuclear pore complex interacting protein	16.4
	452114	N22687	Hs.8236	ESTs	16.4
	404638			predicted exon	16.4
	404600			predicted exon	16.3
55	448855	AF070574	Hs.22316	Homo sapiens clone 24819 mRNA sequence	16.3
	406629	AW277078	Hs.181165	eukaryotic translation elongation factor 1 alpha 1	16.3
	450957	BE515202	Hs.21497	Homo sapiens mRNA for FLJ00042 protein, partial cds	16.3
	449966	H60542	Hs.37848	ESTs	16.3
60	402585			predicted exon	16.3
	436008	AI078428	Hs.58785	ESTs	16.3
	401492			predicted exon	16.3
	412288	NM_003005	Hs.73800	selectin P (granule membrane protein 140kD, antigen C	16.3
	405088			predicted exon	16.3
65	437345	BE259522	Hs.5556	NADH dehydrogenase (ubiquinone) 1, alpha/beta subco	16.3
	432280	BE440142	Hs.2943	signal recognition particle 19kD	16.3
	419598	BE379320	Hs.91448	MKP-1 like protein tyrosine phosphatase	16.3
	428801	AW277121	Hs.254881	ESTs	16.3
	431394	AK000692	Hs.252351	HERV-H LTR-associating 2	16.3
70	452998	BE019681	Hs.6019	Homo sapiens cDNA: FLJ21288 fis, clone COL01927	16.3
	439938	AI147392	Hs.124607	ESTs	16.3
	418844	M62982	Hs.1200	arachidonate 12-lipoxygenase	16.3
	446081	AA972412	Hs.13755	I-box and WD-40 domain protein 2	16.3
	443534	AI076123		gb:xy92e04.x1 Soares_fetal_liver_spleen_1NFLS_S1 H	16.3
75	458910	AA076706		gb:7B01802 Chromosome 7 Fetal Brain cDNA Library	16.3
	450517	AI523755	Hs.59236	ESTs, Weakly similar to B35049 ankyrin 1, erythrocyte	16.3
	451938	AI354355	Hs.16697	down-regulator of transcription 1, TBP-binding (negativ	16.3
	454478	AW805749		gb:QV1-UM0105-180400-162-f10 UM0105 Homo sap	16.2
	407214	AA412048	Hs.279574	CGI-39 protein; cell death-regulatory protein GRIM19	16.2
80	406580			predicted exon	16.2
	409452	BE336714	Hs.289271	cytochrome c-1	16.2
	416841	N33878	Hs.249495	heterogeneous nuclear ribonucleoprotein A1	16.2
	458710	AV660856		gb:AV660856 GLC Homo sapiens cDNA clone GLCG	16.2
	450657	AK001579	Hs.25277	hypothetical protein FLJ21065	16.2
	404230			predicted exon	16.2

	439471	W69839	Hs.58033	ESTs	16.2
	400848			predicted exon	16.2
	428787	AA496205	Hs.193700	Homo sapiens mRNA: cDNA DKFZp586G0324 (from c	16.2
5	416272	AA178882		gb:zp38b09.r1 Stratagene muscle 537209 Homo sapiens	16.2
	444465	A1205592	Hs.143843	ESTs	16.2
	431257	AF039597		gb:Homo sapiens Ku86 autoantigen related protein 1 (K	16.2
	447775	BE179318		gb:RC1-HT0615-290300-021-g05 HT0615 Homo sapie	16.2
	403833			predicted exon	16.2
10	444140	AV648089	Hs.282383	ESTs	16.2
	446102	AW168067	Hs.252956	ESTs	16.2
	416475	T70298		gb:yd26g02.s1 Soares fetal liver spleen 1NFLS Homo s	16.2
	430783	AW971248	Hs.291289	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFA	16.2
	414070	AW963783		gb:EST375856 MAGE resequences, MAGH Homo sap	16.2
15	444283	A1138971	Hs.154636	ESTs	16.2
	405599	X92715	Hs.3057	zinc finger protein 74 (Cos52)	16.2
	409427	AW389668		gb:RC2-ST0168-071299-013-f06 ST0168 Homo sapien	16.2
	409417	AA156247	Hs.295908	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFA	16.2
	435380	AA679001	Hs.192221	ESTs	16.2
20	406762	A1285598	Hs.217493	annexin A2	16.2
	406096	F12200	Hs.5811	chromosome 21 open reading frame 59	16.2
	417551	A1816291	Hs.82273	hypothetical protein	16.2
	441252	AW360901	Hs.183047	ESTs, Weakly similar to unnamed protein product [H.s	16.2
	419608	AL037237	Hs.91586	transmembrane 9 superfamily member 1	16.1
25	438894	A1630819	Hs.330431	ESTs	16.1
	451287	AK002158	Hs.26194	hypothetical protein FLJ11296	16.1
	412499	AW856916	Hs.11238	KIAA0622 protein; Drosophila "multiple asters" (Mast	16.1
	433355	A1808235		gb:wf44e01.x1 Soares_NFL_T_GBC_S1 Homo sapien	16.1
	416818	A1866408	Hs.204766	ESTs, Weakly similar to B48013 proline-rich proteogly	16.1
30	438765	A1031888	Hs.132594	ESTs	16.1
	424470	BE244261	Hs.5815	nuclear RNA export factor 1	16.1
	418194	H27114	Hs.301212	ESTs	16.1
	446702	R44518	Hs.143496	ESTs	16.1
	414222	AL135173	Hs.878	sorbitol dehydrogenase	16.1
35	443122	A1806656	Hs.209022	ESTs, Weakly similar to Pro-Pol-dUTPase polypeptide	16.1
	448848	BE514345	Hs.159089	ESTs	16.1
	456394	W28506		gb:48f1 Human retina cDNA randomly primed sub libra	16.1
	445887	A1263105	Hs.145597	ESTs	16.1
	412332	AW937661	Hs.288324	Homo sapiens cDNA FLJ13283 fis, clone OVARC1001	16.1
40	403912			predicted exon	16.1
	441446	R66269	Hs.28714	ESTs	16.1
	403153			predicted exon	16.0
	444907	AW772596	Hs.148586	ESTs	16.0
	421946	R99629	Hs.109773	hypothetical protein FLJ20625	16.0
45	437513	AW410681	Hs.5648	proteasome (prosome, macropain) 26S subunit, non-AT	16.0
	407752	AA573581	Hs.13328	ESTs	16.0
	447953	A1804218	Hs.209614	Homo sapiens cDNA: FLJ22343 fis, clone HRC06043	16.0
	425708	AK001342	Hs.14570	Homo sapiens cDNA: FLJ22530 fis, clone HRC12866	16.0
	421449	AA713491	Hs.291501	ESTs	16.0
50	418323	NM_002118	Hs.1162	major histocompatibility complex, class II, DM beta	16.0
	447787	BE620108		gb:601483015F1 NIH_MGC_69 Homo sapiens cDNA	16.0
	422716	A1702835	Hs.124475	ESTs	16.0
	443958	BE241880	Hs.10029	cathepsin C	16.0
	417908	AA207221		gb:zq55h04.s1 Stratagene neuroepithelium (937231) Ho	16.0
55	438542	AA810131	Hs.123317	ESTs	16.0
	402088	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor, alpha polypeptid	16.0
	456825	H57220	Hs.146406	nitrilase 1	16.0
	431360	NM_000427	Hs.251680	loricrin	16.0
	414268	BE267834		gb:601124428F1 NIH_MGC_8 Homo sapiens cDNA c	16.0
60	440571	AA904461	Hs.130798	ESTs	16.0
	426075	AW513691	Hs.270149	ESTs	16.0
	413488	BE144017	Hs.184693	transcription elongation factor B (SII), polypeptide 1 (I	16.0
	448767	A1380107	Hs.158954	ESTs	16.0
	418008	W56044	Hs.211556	Homo sapiens cDNA: FLJ23378 fis, clone HEP16248	16.0
65	404239			predicted exon	16.0
	458401	AW236939	Hs.172154	ESTs	16.0
	412855	BE241849	Hs.75082	ras homolog gene family, member G (rho G)	15.9
	423072	A1792948	Hs.123116	solute carrier family 12 (sodium/potassium/chloride tran	15.9
	444954	AW247076	Hs.12163	eukaryotic translation initiation factor 2, subunit 2 (beta	15.9
70	449023	A1823261	Hs.248875	ESTs	15.9
	435729	BE048886	Hs.275017	EST	15.9
	438575	BE304709	Hs.146550	myosin, heavy polypeptide 9, non-muscle	15.9
	413047	H02209		gb:yf36c09.r1 Soares placenta Nb2HP Homo sapiens cD	15.9
	425997	AK000086	Hs.165948	hypothetical protein FLJ20079	15.9
75	446863	AW614370	Hs.254620	ESTs	15.9
	448564	AL044962	Hs.21453	Homo sapiens mRNA for inositol 1,4,5-bisphosphate 3	15.9
	455640	BE064059		gb:QV3-BT0296-010300-111-e04 BT0296 Homo sapie	15.9
	404345	AA730407	Hs.159156	protocadherin 11	15.9
	418512	AW498974	Hs.89981	diacylglycerol kinase, zeta (104kD)	15.9
80	411551	AW851309		gb:IL3-CT0220-170200-067-C11 CT0220 Homo sapien	15.9
	446726	AW300144	Hs.209209	Homo sapiens cDNA FLJ11629 fis, clone HEMBA100	15.9
	410748	BE383816	Hs.136005	ESTs, Highly similar to bG115G20.2 [H.sapiens]	15.9
	449618	A1076459	Hs.14366	Homo sapiens cDNA FLJ12819 fis, clone NT2RP2002	15.9
	429697	AW296451	Hs.24605	ESTs	15.9
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homology to p53	15.9

	403151		predicted exon	15.8	
	452363	AI582743	Hs.94953	ESTs, Highly similar to C1QC_HUMAN COMPLEME	15.8
	425971	AF135024	Hs.165296	kallikrein 13	15.8
	432826	X75383	Hs.250770	kallikrein 15	15.8
5	431972	AI805145	Hs.191711	ESTs	15.8
	400269		predicted exon	15.8	
	404703	AI904493	Hs.99890	polymerase (DNA directed), delta 1, catalytic subunit (1	15.8
	449335	AW150717	Hs.296176	STAT induced STAT inhibitor 3	15.8
10	418443	NM_005239	Hs.85146	v-ets avian erythroblastosis virus E26 oncogene homolo	15.8
	445773	H73456	Hs.13299	Homo sapiens mRNA; cDNA DKFZp761M0111 (from	15.8
	433782	AF090945		gb:Homo sapiens clone HQ0670	15.8
	406473		predicted exon	15.8	
	420831	AA280824	Hs.190035	ESTs	15.8
	402939		predicted exon	15.8	
15	405196		predicted exon	15.8	
	452947	AW130413		gb:cd50f04.x1 NCI_CGAP_Gas4 Homo sapiens cDNA	15.8
	414170	AA335996	Hs.3743	matrix metalloproteinase 24 (membrane-inserted)	15.8
	437133	AB018319	Hs.5460	KIAA0776 protein	15.8
20	458356	AI024855	Hs.131575	ESTs	15.8
	407857	AI928445	Hs.92254	hypothetical protein FLJ20163	15.8
	405687		predicted exon	15.8	
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molecule (CD31 antig	15.8
	408662	AW247699	Hs.105897	ESTs	15.7
25	448338	AI492857		gb:th72h08.x1 Soares_NhHMPu_S1 Homo sapiens cDN	15.7
	402694		predicted exon	15.7	
	430224	AW675175	Hs.235975	hypothetical protein DKFZp434D0412	15.7
	458782	N56666		gb:yrw75e02.r1 Soares_placenta_8to9weeks_2NbHP8to	15.7
	402944		predicted exon	15.7	
30	422675	BE018517	Hs.119140	eukaryotic translation initiation factor 5A	15.7
	408661	AW247625		gb:2820094.Sprime NIH_MGC_7 Homo sapiens cDNA	15.7
	423238	AA323569	Hs.280482	ESTs	15.7
	421517	AB018352	Hs.105399	KIAA0809 protein	15.7
	428865	AB023217	Hs.225968	KIAA1000 protein	15.7
35	440815	AW071945	Hs.7436	putative acyltransferase	15.7
	400634		predicted exon	15.7	
	451034	AL050341	Hs.25846	zinc metalloproteinase, STE24 (yeast, homolog)	15.7
	457571	AJ375726	Hs.279918	hypothetical protein	15.7
	450105	BE281124	Hs.288013	similar to yeast BET3 (S. cerevisiae)	15.7
40	407464	AJ276396		gb:Homo sapiens mRNA for matrix extracellular phosph	15.7
	439465	AF086285		gb:Homo sapiens full length insert cDNA clone ZD478	15.7
	451837	T82157	Hs.16970	ESTs	15.7
	435313	AJ769400	Hs.189729	ESTs	15.7
	402738		predicted exon	15.7	
45	432966	AA650114		gb:ns92h09.s1 NCI_CGAP_Pr3 Homo sapiens cDNA c	15.7
	457666	AW470302	Hs.129663	ESTs	15.7
	401269		predicted exon	15.7	
	427509	M62505	Hs.2161	complement component 5 receptor 1 (C5a ligand)	15.7
	418846	AI821602	Hs.115127	ESTs	15.6
50	448891	AJ587332	Hs.209115	ESTs	15.6
	445930	AF055009	Hs.13456	Homo sapiens clone 24747 mRNA sequence	15.6
	421254	AK001724	Hs.102950	coat protein gamma-cop	15.6
	447073	AW204821	Hs.157726	ESTs	15.6
	445438	AB014578	Hs.12707	KIAA0678 protein	15.6
55	432128	AA865239	Hs.55144	ESTs	15.6
	424091	AF235097	Hs.139263	calcium channel, voltage-dependent, alpha 1F subunit	15.6
	440832	AJ057548	Hs.128224	ESTs	15.6
	449228	AJ403107	Hs.148590	ESTs, Weakly similar to AF208846 1 BM-004 [H.sapie	15.6
	434253	AJ393345	Hs.116215	ESTs	15.6
60	459270	AL039604		gb:DKFZp434E2211_r1 434 (synonym: hias3) Homo s	15.6
	454425	AW300927	Hs.27192	hypothetical protein dJ1057820.2	15.6
	412055	AA099907	Hs.271806	ESTs	15.6
	400837		predicted exon	15.6	
	458866	BE616694	Hs.286042	Homo sapiens cDNA FLJ14299 fis, clone PLACE1010	15.6
65	417124	BE122762	Hs.25338	ESTs	15.6
	414376	BE393856	Hs.66915	ESTs, Weakly similar to 16.7Kd protein [H.sapiens]	15.6
	418636	AW749855		gb:QV4-BT0534-281299-053-c05 BT0534 Homo sapie	15.6
	454128	AL031259	Hs.41639	programmed cell death 2	15.6
	441074	AW500001	Hs.4783	Homo sapiens cDNA: FLJ22035 fis, clone HEP08838	15.6
70	451742	T77609	Hs.117970	ankyrin 2, neuronal	15.6
	403687		predicted exon	15.6	
	431838	AI097229	Hs.217484	ESTs	15.6
	402855		predicted exon	15.6	
	449835	AJ989942	Hs.232150	ESTs	15.6
75	434392	AW983709	Hs.268051	ESTs	15.6
	444301	AK000136	Hs.10760	hypothetical protein FLJ20129	15.6
	414973	C19089		gb:C19089 Human placenta cDNA (TFujiiwara) Homo	15.5
	428374	AW405156	Hs.183994	protein phosphatase 1, catalytic subunit, alpha isoform	15.5
	415745	AJ301107	Hs.150790	ESTs	15.5
80	432532	AW058459	Hs.162246	ESTs	15.5
	417112	AA193439		gb:cz41b09.s1 Soares_NhHMPu_S1 Homo sapiens cDN	15.5
	418101	AL047476	Hs.98485	gap junction protein, beta 4 (connexin 30.3)	15.5
	453110	AW384928	Hs.225160	Homo sapiens cDNA FLJ13102 fis, clone NT2RP3002	15.5
	458608	AJ239397		gb:AJ239397 Uni-ZAP XR retinal pigment epithelium H	15.5
	436989	AA741028	Hs.256155	ESTs	15.5

	407395	AF011757		gb:Homo sapiens RAGE binding protein (P12) mRNA,	15.5
	449584	AI659166	Hs.207144	ESTs	15.5
	454666	AW812994		gb:RC3-ST0186-230300-019-g02 ST0186 Homo sapien	15.5
5	430492	U15197	Hs.300803	Human histo-blood group ABO protein mRNA, partial	15.5
	439460	AA836220	Hs.13774	ESTs	15.5
	449231	BE410360		gb:601302340F1 NIH_MGC_21 Homo sapiens cDNA	15.5
	453060	AW294092	Hs.21594	ESTs	15.5
	416961	BE391476	Hs.80617	ribosomal protein S16	15.5
10	439988	AA860119	Hs.255976	ESTs	15.5
	400917			predicted exon	15.5
	424585	AA464840		gb:zx43h111.r1 Soares_total_fetus_Nb2HF8_9w Homo	15.5
	431029	BE392725	Hs.248571	Homo sapiens PAC clone RP5-1163J12 from 7q21.2-q3	15.5
	441680	AW444598	Hs.7940	RAP1, GTP-GDP dissociation stimulator 1	15.5
15	437830	AB020658	Hs.5867	KIAA0851 protein	15.5
	409479	BE163800	Hs.136912	ESTs	15.5
	409885	AW503068		gb:U1-HF-8P0p-aje-g-10-0-ULr1 NIH_MGC_51 Homo	15.4
	459080	AA443323	Hs.107812	ESTs, Weakly similar to SPOP [H.sapiens]	15.4
	429324	AA488101	Hs.199245	Inactivation escape 1	15.4
	403766			predicted exon	15.4
20	413970	U59309	Hs.75653	umarate hydratase	15.4
	456674	BE266120	Hs.269358	ESTs	15.4
	417931	W95642	Hs.82961	trefol factor 3 (intestinal)	15.4
	430125	U46418	Hs.233950	serine protease inhibitor, Kunitz type 1	15.4
25	452154	AW953265	Hs.271277	hypothetical protein from EUROIMAGE 363668	15.4
	422884	W28614	Hs.75984	chorionic somatomammotropin hormone 2	15.4
	408649	BE242232	Hs.26045	protein tyrosine phosphatase, receptor type, A	15.4
	417497	AW402482	Hs.82212	CD53 antigen	15.4
	404666			predicted exon	15.4
30	456847	AI360456	Hs.37776	ESTs	15.4
	426995	AA400646	Hs.221988	ESTs	15.4
	445350	AF052112	Hs.12540	lysophospholipase I	15.4
	450214	BE439763	Hs.227571	regulator of G-protein signalling 4	15.4
	449733	R74546	Hs.29438	Homo sapiens cDNA FLJ12094 fis, clone HEMBB100	15.4
35	411660	AW855718		gb:RC1-CT0279-070100-021-a06 CT0279 Homo sapie	15.4
	442553	BE269247	Hs.170226	Homo sapiens clone 23579 mRNA sequence	15.4
	447552	AI394125	Hs.160413	ESTs	15.4
	448712	W01046	Hs.181634	Homo sapiens cDNA: FLJ23602 fis, clone LNG15735	15.4
	420180	AI004035	Hs.25191	ESTs	15.4
40	440099	AL080058	Hs.6909	DKFZP564G202 protein	15.4
	427550	BE242818	Hs.179606	nuclear RNA helicase, DECD variant of DEAD box fam	15.4
	432894	AW167668	Hs.279772	brain specific protein	15.3
	412113	AW181274	Hs.74427	p53-induced protein	15.3
	431614	AI189827		gb:xd19d07.x1 Soares_placenta_8to9weeks_2NbHP8to	15.3
45	445870	AW410053	Hs.13406	syntaxin 18	15.3
	424347	AA723883	Hs.145513	Homo sapiens mRNA; cDNA DKFZP434L0435 (from	15.3
	425132	AW250114		gb:2821134.5prime NIH_MGC_7 Homo sapiens cDNA	15.3
	439756	AL359651	Hs.283852	Homo sapiens mRNA full length insert cDNA clone EU	15.3
	432946	U60899	Hs.279854	mannosidase, alpha, class 2B, member 1	15.3
50	406130			predicted exon	15.3
	453359	AA448787	Hs.24872	ESTs, Weakly similar to aortic carboxypeptidase-like p	15.3
	405491			predicted exon	15.3
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-conjugating enzy	15.3
	446826	AK000626	Hs.16230	hypothetical protein FLJ20619	15.3
55	441211	AW946155	Hs.7750	hypothetical protein AL133206	15.3
	418711	AW247977	Hs.87595	translocase of inner mitochondrial membrane 22 (yeast)	15.3
	457301	AA469146		gb:nc67e03.s1 NCI_CGAP_Pr1 Homo sapiens cDNA c	15.3
	449999	AI679421	Hs.231098	ESTs, Highly similar to ALU4_HUMAN ALU SUBFA	15.3
	439090	H65724	Hs.271663	ESTs	15.3
60	416586	D44643	Hs.14144	secreted modular calcium-binding protein 1	15.3
	411940	AW876686		gb:CM4-PT0031-180200-507-e05 PT0031 Homo sapie	15.3
	407639	AW205369	Hs.252938	ESTs	15.3
	458012	AI424859	Hs.188211	ESTs	15.3
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	15.3
65	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	15.3
	437371	AK000868	Hs.5570	hypothetical protein FLJ10008	15.3
	437134	AA349944	Hs.42915	ARP2 (actin-related protein 2, yeast) homolog	15.3
	441890	AI809547	Hs.128075	ESTs	15.3
	409442	AA310162	Hs.169248	cytochrome c	15.3
70	407078	Z26256		gb:H.sapiens isoform 1 gene for L-type calcium channe	15.2
	436553	AW407157	Hs.181125	immunoglobulin lambda locus	15.2
	443177	BE268461	Hs.202	benzodiazepine receptor (peripheral)	15.2
	448771	BE315511	Hs.296244	SNARE protein	15.2
	436837	AI968248	Hs.187869	ESTs	15.2
75	423623	AB011117	Hs.129943	KIAA0545 protein	15.2
	422651	NM_015670	Hs.118926	DKFZP586K0919 protein	15.2
	403221	AL134878	Hs.119500	karyopherin alpha 4 (importin alpha 3)	15.2
	431620	AA126109	Hs.264981	2'-5'-oligoadenylate synthetase 2	15.2
	404794	NM_000078	Hs.89538	cholesteryl ester transfer protein, plasma	15.2
80	412944	AA384110	Hs.197143	ESTs	15.2
	450817	N71597	Hs.29698	ESTs	15.2
	418666	AF001434	Hs.155119	EH domain containing 1	15.2
	451636	AW173270	Hs.140444	ESTs	15.2
	426302	AA459085	Hs.275163	non-metastatic cells 2, protein (NM23B) expressed in	15.2
	454485	AW795322		gb:PM0-UM0018-120400-002-h01 UM0018 Homo sap	15.2

	440617	AA894880	Hs.181181	ESTs	15.2
	449718	AA459480	Hs.23956	hypothetical protein FLJ20502	15.2
	405227			predicted exon	15.2
5	431006	BE152871		gb:CM1-HT0333-101299-064-d12 HT0333 Homo sapi	15.2
	443476	AW068594	Hs.133878	ESTs, Weakly similar to AF151889 1 CGI-131 protein	15.2
	438828	AL134275	Hs.6434	hypothetical protein DKFZp761F2014	15.2
	407634	AW016569	Hs.301280	ESTs, Highly similar to AF241831 1 Intracellular hyalu	15.2
	436857	AA732647		gb:ncz89d01.s1 NCL CGAP_GCB1 Homo sapiens cDN	15.2
10	431526	Y10129	Hs.258742	myosin-binding protein C, cardiac	15.1
	447386	NM_006289	Hs.18420	KIAA1027 protein	15.1
	436573	AA723297	Hs.127138	ESTs	15.1
	432858	BE618609	Hs.279591	Homo sapiens clone 25056 mRNA sequence	15.1
	437352	AL353957	Hs.284181	hypothetical protein DKFZp434P0531	15.1
15	413209	AW083791	Hs.21263	Homo sapiens cDNA FLJ13152 fls, clone NT2RP3003	15.1
	407376	AA931138	Hs.142287	ESTs, Weakly similar to ALLUF_HUMAN !!! ALU CL	15.1
	430475	BE387420	Hs.241531	pellin	15.1
	446764	AW291276	Hs.285532	ESTs	15.1
	425868	AB017548	Hs.160100	Homo sapiens gene for Sepiapterin Reductase, partial c	15.1
20	453464	AB849111	Hs.32589	receptor (calcitonin) activity modifying protein 1	15.1
	447246	AW449032	Hs.170257	ESTs	15.1
	401780			predicted exon	15.1
	434063	AA018893	Hs.3727	unc-interacting protein	15.1
	416114	AI695549	Hs.183868	glucuronidase, beta	15.1
25	441018	AI809587	Hs.148782	ESTs	15.1
	425972	BE391563	Hs.165433	ESTs, Highly similar to T17342 hypothetical protein D	15.1
	426082	N57014	Hs.44013	ESTs	15.1
	451234	AI914901	Hs.24052	ESTs	15.1
	428565	AB020719	Hs.207802	KIAA0912 protein	15.1
30	418092	R45154	Hs.106604	ESTs	15.1
	424550	AI650541	Hs.115298	ESTs	15.1
	425023	AW956889	Hs.154210	endothelial differentiation, sphingolipid G-protein-cou	15.1
	445213	AW204314	Hs.170784	ESTs	15.1
	418102	R58958	Hs.26608	ESTs	15.0
35	450082	AI908894	Hs.245893	ESTs	15.0
	446749	NM_016069	Hs.16089	CGI-136 protein	15.0
	406124			predicted exon	15.0
	457408	AL137507	Hs.255348	Homo sapiens mRNA; cDNA DKFZp761P211 (from c	15.0
	410051	U25773	Hs.218182	ESTs, Weakly similar to dJ1042K10.2 [H.sapiens]	15.0
40	440965	AI523646	Hs.169859	ESTs	15.0
	440190	AW752597		gb:LL3-CT0214-161299-045-806 CT0214 Homo sapien	15.0
	417437	U52682	Hs.82132	interferon regulatory factor 4	15.0
	454249	AW249008		gb:2821048.Sprime NIH_MGC_7 Homo sapiens cDNA	15.0
	432276	AF163302	Hs.274255	somatostatin receptor-interacting protein	15.0
45	401116			predicted exon	15.0
	423960	AA164516	Hs.136309	CGI-61 protein	15.0
	451661	AB020650	Hs.26777	KIAA0843 protein	15.0
	450983	AA305384	Hs.25740	ERO1 [S. cerevisiae]-like	15.0
	446187	AK001241	Hs.14229	hypothetical protein FLJ10379	15.0
50	404122			predicted exon	15.0
	411299	BE409857	Hs.69499	hypothetical protein	15.0
	403077			predicted exon	15.0
	438000	AI825880	Hs.5985	non-kinase Cdc42 effector protein SPEC2	15.0
	447118	AB014599	Hs.17411	KIAA0699 protein	15.0
55	417878	U90916	Hs.82845	Human clone 23815 mRNA sequence	15.0
	444079	H09048	Hs.23606	ESTs	15.0
	458234	BE551408	Hs.127198	ESTs	15.0
	434208	T92641	Hs.127648	hypothetical protein PRO2176	15.0
	423136	AW375506	Hs.124147	ESTs	15.0
60	403177			predicted exon	15.0
	448699	AI857269	Hs.227351	ESTs	15.0
	425248	AW957442	Hs.252766	ESTs	15.0
	429430	AL381837	Hs.155335	ESTs	15.0

TABLE 3B:

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey	CAT Number	Accession
408310	1051011_1	AW179023 AW179010
408647	1071855_1	AW245831 AW273207
408661	1073036_1	AW247625 AW249214
408987	109306_1	H85615 H85300 H85263 H86282 AA059278 H86304
409427	1129667_1	AW389668 AW389657 AW609198 AW389649
409545	1138823_1	BE296182 AW629821
409828	1155571_1	AW501137 AW501295 AW501212
409865	1156518_1	AW502208 AW502366 AW502148
409885	1157385_1	AW503068 AW503789
410003	116761_1	AA079487 AA128547 AA128291 AA079587 AA079600
410186	1182096_1	AW602528 BE073859 Z38412
410626	1212621_1	BE407727
411004	1228975_1	AW813242 BE146089 AW813195 AW813173 AW813206 BE145953 BE146212 AW813196 AW854582 AW813241 BE061582
411014	1229091_1	AW816072 AW813375 AW813385 AW813372 AW813436 AW816148 AW813475 AW816107 AW813398 AW813479 AW814475 AW813317
411028	1229404_1	AW813703 AW813839

411236	1236374_1	AW833752 AW833633 AW833776 AW833719 AW833652 AW833749
411420	1245222_1	BE390652
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411551	1249196_1	AW851309 AW850688 AW851419 AW851412 AW851299
411651	1252835_1	AW855392 AW855559 AW855423
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411696	1254304_1	AW857404 AW857401 BE144856
411811	1259427_1	AW864370 AW864319 AW864504
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413154	1351077_1	BE067870 BE067866 BE165133 BE165334 BE165329 BE165332
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413442	1370508_1	BE140643 BE140645 BE140644 BE140657 BE140660 BE140659 BE140661
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413605	1379792_1	BE152644 BE152712 BE152668 BE152659 BE152810 BE152811 BE152816 BE152643 BE152706 BE152656 BE152660 BE152715 BE152662
		BE152669 BE152661 BE152672 BE152653 BE152716 BE152651 BE152767 BE152677 BE152652 BE152714 BE152708 BE152665 BE152679
		BE152771 BE152775 BE152666 BE152768 BE152813 BE152664 BE152676 BE152681 BE152709 BE152667 BE152814 BE152808 BE152711
		BE152707 BE152815 BE152678 BE152673 BE152782 BE152671 BE152682 BE152760 BE152809 BE152778 BE152780 BE152762 BE152776
		BE152781 BE152774 BE152763 BE152769
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		BE156789 BE156833 BE156844 BE156831 BE156849 BE156797 BE156784 BE156801 BE156843 BE156793 BE156852
413679	1382784_1	BE162391
413758	1386900_1	AW963783 F36521 F30687 AW753177 AW753195 AW853065 AA135150 AA375028
414070	141442_1	BE263293
414195	1424854_3	BE262170 BE382553 BE261026 BE273627
414203	1425510_2	BE267834 BE514180 BE514096
414266	1430984_1	BE297862
414276	1432115_1	BE274897 BE408199 BE274723
414333	1436492_1	BE298594
414444	1446827_1	BE379046 BE395459
414539	1460320_1	BE378050
414540	1460324_1	BE390440
414605	1465790_1	BE388044 BE391117 BE391530
414610	1466027_1	BE410589 BE390949 BE408297 BE389529
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414642	1469660_1	BE396326
414663	1472628_1	C19089 C18814 C16621
414973	1510755_1	T82802 D78670 R08505
415160	1525766_1	W70022 R35201 F12763 T74725 H63485 Z45782 H61126
415606	1540470_1	Z43912 H09194
415917	1561575_1	AA178882 AA179898 AA178897
416272	158407_1	T70298 H58072 R02750
416475	1596398_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
416913	1630001_1	AA193439 AA193537 AW814128
417112	165068_1	AW993983 AW994798 AW993990 AW993989 AW993989 AA204755
417611	168900_1	AA207221 BE538271
417908	170764_1	AW749855 AA225995 AW750208 AW750206
418636	177402_1	T60872 T60906
418874	1799516_1	AA528295 AW971284 AA247945
419618	186533_1	AA251600 AA279607
419889	188798_1	AA742277 AW976493 AA281585
420902	197525_1	AW582898 AA305114
422160	212412_1	AL138411 AL138412 AA315860
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423050	224288_1	AA322029 BE315237
423103	225019_1	H38340 H39081 AA324112
423287	226793_1	BE002904 H64880 AA328679
423621	230314_1	AA464840 AA343628
424585	241151_1	Z45023 AA349514
424895	245794_1	AW250114 Z43124 AA431421 A1879054 AA351616 AA351035 AL048999
425132	247059_1	BE004257 AW811190 AA360576 BE172402 BE181703
425612	253969_1	AA364002 AI522307
425798	256586_1	N32049 R34821 R78237
426065	260276_1	BE536838 AA376153
426356	265381_1	BE537380 BE255215
426383	266126_1	AA422028 W79191
428151	287658_1	BE152871 BE152870 AA490552
431006	326833_1	AF039597 BE243938
431257	33049_1	AI189827 AW860554 AW860552 AA508543
431614	335668_1	AA516049 AW004922
431822	338082_1	AA650114 AW974148 AA572946
432966	356839_1	AA582307 BE273018
433300	362452_1	AI808235 AI024295 AA584528
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433459	366899_1	F12741 T75155 AA594014
433469	367263_1	AF080945 AW996754 AI064870
433782	37414_1	AA625499 AA625269 AA625184
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5	436857	428068_1	AA732647 BE008970 BE009028
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	439848	477806_1	AW979249 D63277 AA846968
	440190	488021_1	AW752597 AW848781 AW849062 AW848490 AW752699 AW752604 AW752700
	440669	499861_1	AI206964 AI350890 AA902772 AJ768881
	441552	520138_1	AA937975 F11215 BE005635
	442257	53699_1	AW503831 AW503317 BE565665
10	443198	562555_1	AI039813 AI684642 Z40121 AI951414 BE501049
	443534	572957_1	AI076123 AI244834 AI695239
	446052	65988_1	AA358760 AA158850 AW062737 AW062738 AV656291
	446598	68463_1	AW250546 BE257108 BE251006 BE255957 BE250926 BE513012 AV659318
	447224	71279_1	BE617125
15	447252	714160_1	R90918 AL120023 R18429 Z42095 AI369730 R90824
	447383	71990_1	N24231 BE617964 N36313
	447775	73665_1	BE179318 BE620044
	447787	73719_1	BE620108 BE312062 AW896316 BE262546
	448218	75525_1	AI188489 BE622201
20	448338	758968_1	AI492857 AW070478 AI885157
	448838	78409_4	BE614761 AA263136 W00335 W00327
	449231	80303_1	BE410360 AA442408 AA315540
	450594	83962_1	N31036 N42915 F07753 AA010329
	451400	868459_1	BE160479 BE160478 BE069211 AW861059 AI793147
25	452544	921487_1	AW851888 AW851889 AW852147
	452947	939810_1	AW130413 AI932362
	453758	980026_1	U83527 AL120938 U83522
	454163	1048369_1	AW175997 AW176000 AW175999 AW175994 AW176004 AW175989
	454178	1049458_1	AW177274 AW177249 AW177223 AW177216 AW177233
30	454181	1049567_1	AW177377 AW177357 AW177359 AW177385 AW177358 AW177395 AW177394 AW177396 AW177383 AW177333 AW177384 AW177382
	454209	1051071_1	AW177360 AW177355
	454249	1073933_1	AW179083 AW179085 AW179087 AW179081 AW179084 AW179085 AW179082 AW801493 AW801658 AW801714
	454377	114761_1	AW249008 BE295653 BE296765
35	454478	1214744_1	AA076811 AW814764
	454485	1215381_1	AW805749 AW805872 AW794466 AW798102 AW796921 AW794538 AW794380
	454505	1219564_1	AW785322 AW795308 AW795311 AW795310 AW795314 AW795321
	454574	1225636_1	AW801365 AW801435 AW801372
	454610	1226543_1	AW809109 AW809112 AW809122 AW809126 AW809128 AW809133 AW809131 AW809113 AW809111 AW809132
40	454633	1227504_1	AW810224 AW810337 AW810295 AW810333 AW810335 AW810296 AW816053
	454666	1228600_1	AW811380 AW811385
	454803	1235520_1	AW812994 AW812723 AW812930
	454961	1246745_1	AW860148 AW862380 AW821887 AW821863 AW821870 AW821894 AW862351 AW862378
	455132	1254686_1	AW847807 AW847935 AW847636
45	455426	1289303_1	AW857955 AW861636 AW857967 AW857958 AW857943 AW857945 AW857963 AW857968 AW857959 AW857961 AW857956 BE072135
	455640	1348141_1	AW857972 BE072137 AW857952 AW857935 AW857940 AW857944 AW857947 AW857934
	455694	1350650_1	AW937792 BE072250 BE072251 BE072264
	455910	1382504_1	BE064059 BE063903 BE063838 BE063863 BE064056 BE063974 BE063904 BE063898 BE063896 BE063906 BE063960
50	455993	1396665_1	BE067300 BE067293 BE067279
	456054	1452761_1	Z43712 BE156729 BE156538 BE156731 BE156673 BE156539 BE156674 BE156430 BE156672 BE156675 BE156432 BE156541
	456329	1789807_1	BE179085 BE179084 BE179086 BE179264
	456394	1843275_2	BE313241 BE383148
55	457301	314434_1	T41418 T41320 T41379
	458025	46409_1	W28506
	458608	65568_1	AA469146 AA469396 AA469218 AA469395
	458640	670076_1	AI275406 L23208
	458710	69727_1	AJ239397 AV655764
	458792	748294_1	AI284935 AW409822 BE408182
60	459170	920846_1	AV660856 BE167375
	459270	969232_1	N56668 AI460076
			AI905518 AI905516 AI905457 AI905515 AW176013 AW176037
			AL039604 AL039497

TABLE 3C:

Pkey: Unique number corresponding to an Eos probe set

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495

Strand: Indicates DNA strand from which exons were predicted

Nt_position: Indicates nucleotide positions of predicted exons

70	Pkey	Ref	Strand	Nt_position
	400449	9887692	Minus	50889-51188
	400613	9864507	Plus	92278-92472
	400634	8567750	Minus	101102-101223,101886-102018
	400642	8117693	Plus	10475-10845
	400661	8118474	Plus	84912-85187
75	400684	8118768	Plus	58189-58323
	400685	8118768	Minus	72959-73050,73713-73800
	400727	6705887	Plus	106175-107016
	400749	7331445	Minus	9162-9293
	400807	8567878	Plus	69375-70295
80	400837	9188531	Plus	144778-144838,145582-145670,146656-146751,147255-147419,147682-147807
	400842	1927148	Plus	90462-90673
	400848	1927148	Plus	107149-107339,110873-111171
	400891	9958279	Minus	140073-140427
	400917	7283186	Minus	173258-173631

	400931	7651921	Minus	142145-142353,144311-144721
	400964	7139719	Minus	155282-155403
	400965	7770576	Minus	173043-173564
5	400970	7960452	Minus	92744-92895
	400982	8078794	Minus	119245-119471
	401010	8117391	Minus	83967-84160
	401072	3687273	Plus	64370-64524
	401088	8492704	Plus	194659-195179
10	401116	9966559	Plus	123579-124447
	401117	8570083	Minus	28948-29204
	401167	9438381	Plus	18944-19176
	401204	9743388	Minus	33694-33872
	401220	9929324	Minus	48079-48279
	401244	4827300	Minus	55359-56376
15	401245	4827300	Minus	59373-59531
	401268	9797154	Plus	152272-152483,157312-157418,158025-158205,158838-158974,160716-160952
	401269	8954206	Plus	2259-2591
	401283	9800093	Minus	47256-47456
20	401373	7248205	Minus	84211-84336
	401405	7768126	Minus	69276-69452,69548-69958
	401465	6682292	Plus	25676-25800
	401492	7341778	Plus	171020-171282,171858-172241
	401521	7705251	Plus	9127-9234
25	401566	8469090	Minus	96277-96420,96979-97160
	401575	7229804	Minus	76253-76364
	401589	9966292	Plus	135969-136263
	401628	8575954	Minus	210617-210796
	401657	9100664	Minus	7312-8183
30	401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
	401757	7239630	Plus	88641-88751
	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29587,29705-29787,30224-30573
	401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,85290-86814
35	401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
	401789	7249213	Minus	70399-70629,70941-71055
	401809	7342191	Minus	107548-108298
	401847	7139731	Plus	85447-85593
	401887	7229981	Plus	93973-94120
40	401913	9369520	Minus	33753-33904
	401962	3176728	Minus	71433-71648,76711-76833,78677-78845,79585-79763,82349-82485
	401991	4156128	Plus	2398-2513
	401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45189-45281,46337-46732
	402023	7528158	Minus	132872-133040
45	402066	6649269	Plus	135543-136031
	402071	8117361	Plus	85924-86039
	402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
	402131	7704961	Minus	33114-33209,33496-33678
	402144	7242326	Plus	115425-115977
50	402203	8576119	Minus	8124-8285
	402277	2894631	Plus	16980-17152,17933-18018,18170-18306
	402292	2447220	Plus	33880-34029,34176-34336,34953-35103
	402297	6558824	Plus	35279-35405,35573-35659
	402407	3962498	Minus	115812-116187
55	402421	9796341	Minus	46609-46662,46758-46811,86293-86346,89776-89829,90048-90101,102817-102924
	402427	9796372	Plus	16266-16431
	402430	9796372	Minus	62382-62552
	402520	7596899	Minus	171761-171996
	402538	9801137	Minus	96314-96539
60	402543	9838066	Minus	89684-90893
	402570	9884747	Minus	12649-12866
	402585	9908890	Minus	174893-175050,183210-183435
	402639	9958129	Minus	20167-22383
	402694	8569867	Plus	2218-2440
65	402699	8570304	Minus	182773-182883,184551-184732
	402738	7331557	Minus	8725-8859
	402855	9662953	Minus	59763-59909
	402869	6434643	Minus	138639-139335
	402939	9187334	Minus	18329-18535
70	402944	9368423	Plus	110411-110716,111173-111640
	402948	9368458	Minus	143456-143626,143808-143935
	402958	9368493	Plus	13324-13507
	403010	3132346	Plus	78385-79052
	403036	3132360	Plus	66545-66712
75	403051	4827080	Minus	5269-5411
	403065	8954197	Minus	71615-71773,73930-74144
	403077	8954241	Plus	146923-147222,147326-147628
	403093	8954241	Plus	177083-177373,177464-177751
	403151	7407965	Minus	14055-14264
80	403153	9799871	Minus	42232-43389
	403177	9838213	Minus	142560-142726
	403223	7630969	Plus	81529-81692
	403234	7637801	Plus	180641-180822
	403273	8018055	Plus	133809-134099
	403286	8080320	Plus	118369-118872

	403287	8080320	Minus	126097-126411
	403348	7239527	Plus	13809-13968
	403359	8570207	Minus	108939-109229
5	403362	8571772	Plus	64099-64260
	403447	9837821	Minus	159072-159387
	403508	7630896	Plus	5570-5719
	403582	8101186	Plus	18308-18458
	403613	8493504	Plus	81290-81465
10	403642	8699671	Plus	7062-7311
	403662	5823349	Plus	58627-59062,59222-59548
	403674	7321642	Plus	104988-105623,107394-107590
	403687	7387384	Plus	9009-9534
	403695	3046276	Plus	168272-168514
15	403703	4968380	Plus	83681-84042
	403741	7630932	Minus	2833-3468
	403747	7658395	Minus	20493-20621
	403766	7229888	Plus	136283-136830
	403786	8083636	Minus	73028-73217
20	403796	8099896	Minus	75073-77664
	403833	887461	Plus	13522-13664
	403852	7708872	Minus	124007-124202
	403861	7708966	Plus	58363-58649
	403912	7710730	Minus	72000-72290,72431-72700,72929-73199
25	403924	7711688	Minus	89369-89592
	403964	7596976	Plus	178174-178300
	404034	8567760	Minus	44635-47010
	404067	3282162	Plus	1415-2071
	404097	7770701	Plus	55512-55781
30	404122	9796270	Plus	90540-92677
	404230	7981448	Minus	92934-93093
	404239	5002624	Plus	94841-95095
	404240	5002624	Minus	116132-116407,116653-116922
	404270	9828129	Minus	3649-3750,4161-4306,5962-6049,6849-6965
35	404356	7630858	Minus	126433-126623
	404600	8705107	Plus	118354-118444,118649-118792
	404601	8705107	Plus	128449-128693,129085-129249,130525-130733
	404638	9796751	Minus	99433-99528,100035-100161
	404666	7272179	Minus	18677-18993
40	404675	9797204	Minus	48532-48645,49808-49975,51088-51369,54944-55063
	404727	8081050	Plus	115534-115747
	404750	7596836	Plus	181879-182188
	404763	7882612	Plus	50981-51392
	404767	7882627	Minus	23244-23769
45	404828	6580415	Minus	26291-27253
	404850	5420148	Minus	35145-35413,40635-41062
	404881	5931510	Minus	36360-36608
	404890	7329390	Plus	101280-101408
50	404971	3212939	Minus	74585-75532
	405022	7330304	Plus	217163-217439
	405028	7533974	Minus	110588-110847,110933-111115
	405071	7708797	Minus	11115-11552
	405088	8072518	Minus	115690-117621
	405133	8516055	Minus	28127-28288
55	405138	8576241	Plus	90303-90516
	405183	7209940	Plus	12335-12653
	405194	7230072	Plus	190465-190645,193346-193610
	405196	7230083	Minus	135716-135851
	405208	7230142	Plus	8068-8214
60	405226	7248966	Plus	53547-54128
	405227	6731245	Minus	22550-22802
	405256	7329310	Plus	26070-26309
	405277	3980473	Plus	23471-23572
	405307	3638954	Plus	39195-39429
65	405311	3638954	Plus	46313-46496
	405333	3165399	Plus	149905-150215
	405411	3451356	Minus	17503-17778,18021-18290
	405423	4753276	Plus	6162-6983
	405491	5801645	Plus	81857-82045
70	405501	9211311	Minus	49085-49400,49565-49679,50117-50262
	405515	9454624	Plus	37329-37469
	405545	1054740	Plus	118677-118807,119091-119296,121626-121823
	405580	4512267	Plus	169232-169647
	405586	5002511	Plus	38810-39017
75	405600	5923640	Plus	26662-27225
	405610	5757553	Minus	71907-72080
	405639	5091650	Plus	211184-211350
	405687	6249668	Minus	54787-54891,55844-55917
	405699	4165331	Plus	100727-100859
80	405783	5738434	Minus	27238-27885
	405867	6758731	Minus	74553-75173
	405886	7107817	Plus	9418-9573
	406124	9149714	Minus	1331-1774
	406130	9161404	Minus	32394-32498
	406140	9168231	Minus	49887-50219

406160	7144945	Plus	55498-56268
406207	5923650	Minus	162607-162800
406215	7342161	Plus	310-432
406268	6682695	Minus	6605-7072
406277	5686030	Minus	4759-5490
406326	9212385	Plus	84508-84655
406388	9256205	Plus	85153-85277
406457	9755793	Plus	44966-45406
406473	9795566	Minus	109669-109931
406537	7711478	Plus	32904-33017
406571	7711622	Minus	65634-65912,66116-66596
406580	7711838	Minus	96654-97640

TABLE 4A lists about 131 genes up-regulated in ovarian cancer compared to normal ovaries that are likely to be extracellular or cell-surface proteins. These were selected as for Table 3A, except that the ratio was greater than or equal to 10, and the predicted protein contained a PFAM domain that is indicative of extracellular localization.

TABLE 4A: ABOUT 131 UP-REGULATED GENES ENCODING EXTRACELLULAR/CELL SURFACE PROTEINS, OVARIAN CANCER VERSUS NORMAL OVARY

Key: Primekey

Ex. Accn: Exemplar Accession

UG ID: UniGene ID

Title: Unigene Title

PFAM domains

ratio: tumor vs. normal ovary

Key	Ex. Accn	UG ID	Title	PFAM	ratio
403077			predicted exon	fn3	15.0
426535	AU077012	Hs.288582	ESTs, Weakly similar to ubiquitous TP	Kunitz_BPTI	14.9
403089			predicted exon	fn3	14.9
457148	AF091035	Hs.184627	KIAA0118 protein	artras	14.8
431176	AI026984	Hs.293662	ESTs	laminin_EGF_laminin_B;	14.8
434293	NM_004445	Hs.3796	EphB6	fn3;pktnase;EPH_lbd	14.8
408482	NM_000676	Hs.45743	adenosine A2b receptor	7tm_1	14.6
428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	7tm_1	14.5
426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) ho	EGF	14.4
423732	AF058055	Hs.132183	solute carrier family 16 (monocarboxy	sugar_tr;MCT	14.3
422125	NM_003459	Hs.111967	solute carrier family 30 (zinc transport	Cation_efflux	14.2
407483	NM_012368		(NONE)	7tm_1	14.2
446689	AW594695	Hs.167046	ESTs	7tm_1	14.1
410184	AW503667	Hs.59545	ring finger protein 15	zf-C3HC4;SPRY;zf-B_box	14.0
423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermol	fn3;vwa	14.0
405448	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp5	trypsin;sushi;CUB	14.0
450684	AA872605	Hs.25333	Interleukin 1 receptor, type II	lg	14.0
406692	L36607		gbc:Homo sapiens (clone 22) pregnancy	lg	13.9
425549	U64863	Hs.158297	programmed cell death 1	lg	13.8
452755	AW138937	Hs.213436	ESTs	cystatin	13.8
427637	AK000816	Hs.179986	flotillin 1	Band_7	13.7
424591	R55704	Hs.150968	hypocretin (orexin) receptor 1	7tm_1	13.7
405024			predicted exon	TGF-beta;TGFB_propeptide	13.7
405285			predicted exon	A2M;A2M_N	13.7
412116	AW402166	Hs.784	Epstein-Barr virus induced gene 2 (lym	7tm_1	13.7
420258	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascu	cadherin;Cadherin_C_tern	13.6
420511	AF052692	Hs.98485	gap junction protein, beta 4 (connexin 3	connexin	13.5
448638	R17122	Hs.21639	nuclear protein, marker for differentiat	lg	13.4
431117	AF003522	Hs.250500	delta (Drosophila)-like 1	EGF;DSL	13.4
439285	AL133916	Hs.298998	ESTs	lg;pktnase;LRRNT;LRRCT	13.4
424283	AA338246	Hs.301678	ESTs	E1-E2_ATPase;Hydrolase	13.3
436233	AI742878	Hs.124116	ESTs	lg	13.3
443859	NM_013409	Hs.9914	folistatin	kazal	13.2
410016	AA297977	Hs.57907	small inducible cytokine subfamily A (IL8	13.2
414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologo	IL8	13.2
400242			predicted exon	Ephrin	13.0
429057	AF156557	Hs.194816	stromatin-like protein 1	Band_7;SCP2	12.9
438294	AI693753	Hs.143004	ESTs	E1-E2_ATPase;Hydrolase	12.9
458493	AV649408	Hs.282418	ESTs	RYDR_ITPR	12.8
444181	AB033063	Hs.10491	KAA1237 protein	fn3;lg;PH;RhoGEF	12.8
422357	AF016272	Hs.115418	cadherin 16, KSP-cadherin	cadherin	12.7
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	serpin	12.7
407000	U12139		gbc:Human alpha1(X) collagen (COL1	TSPN;Collagen;COLF1	12.6
417064	W02903	Hs.15440	ESTs	lectin_c	12.6
439389	AA318940	Hs.56004	ESTs	hemopexin;Peptidase_M10	12.6
407786	AA687538	Hs.38972	tetraspan 1	transmembrane4	12.5
410498	AA355749		gbc:EST64459 Jurkat T-cells VI Homo	ea_pemeases	12.5
422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	vwd	12.5
422330	D30783	Hs.115263	epiregulin	EGF	12.5
402425			predicted exon	ion_trans	12.4
414875	H42679	Hs.77522	major histocompatibility complex, clas	lg	12.2
424239	M67439	Hs.143526	dopamine receptor D5	7tm_1	12.2
442622	NM_000435	Hs.8546	Notch (Drosophila) homolog 3	EGF;ank;notch	12.2
405368			predicted exon	7tm_1	12.2
402406			predicted exon	Gal-bind_lectin	12.1
426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteoge	TGF-beta;TGFB_propeptide	12.1
406811	U82979	Hs.67846	leukocyte immunoglobulin-like recepto	lg	12.0
416441	BE407197		gbc:60130155ZF1 NIH_MGC_21 Homo	SDF	12.0

5	433221	AB040917	Hs.87860	KIAA1484 protein	fn3jg;LRRCT	11.9
	442915	AA852875	Hs.8850	a disintegrin and metalloproteinase dom	disintegrin;Reprolysin;	11.9
	423613	AF036035	Hs.129910	hyaluronoglucosaminidase 3	lg;Sema;Acetyltransf	11.9
	411213	AA676939	Hs.69285	neuropilin 1	CUB;MAM;F5_F8_type_C	11.9
	425483	AF231022	Hs.301273	Homo sapiens protocadherin Fat2 (FA	EGF;cadherin;aminin_G	11.8
	421258	AA286731		gb:zs53d08.1 NCL_CGAP_GCB1 Hom	7m_3	11.8
	423795	AW849759		gb:IL3-CT0216-240200-077-C04 CT0	arf;ras	11.7
	422424	AI186431	Hs.116577	prostate differentiation factor	TGF-beta	11.7
10	443296	AI765286		gb:wi73b05.x1 NCL_CGAP_Kid12 Ho	lg	11.7
	448999	AF179274	Hs.22791	transmembrane protein with EGF-like	kazal	11.7
	414878	AA341040	Hs.77541	ADP-ribosylation factor 5	arf;ras	11.5
	429344	R94038	Hs.199538	inhibin, beta C	TGF-beta	11.5
	402114			predicted exon	laminin_EGF;laminin_G	11.5
15	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (IL8	11.5
	430263	D12614	Hs.36	lypotoxin alpha (TNF superfamily, m	TNF	11.4
	400464			predicted exon	Peptidase_S9	11.4
	456841	AA875863	Hs.152345	poxvirus receptor-related 1 (herpesvir	lg	11.4
	409420	Z15008	Hs.54451	laminin, gamma 2 (niclin (100kD), kal	laminin_EGF;laminin_B	11.4
20	418043	AW377752	Hs.83341	H.sapiens mRNA for tyrosine kinase re	fn3jg;pkase	11.3
	426523	S68616	Hs.170222	solute carrier family 9 (sodium/hydrog	Na_H_Exchange	11.3
	446051	BE048061	Hs.153315	ESTs	Reprolysin;disintegrin	11.3
	439710	AF086543		gb:Homo sapiens full length insert cDN	Xlink	11.3
	416602	NM_006159	Hs.79389	nel (chicken)-like 2	vw;TSPN	11.3
	418299	AA279530	Hs.83968	Integrin, beta 2 (antigen CD18 (p95), ly	Integrin_B	11.3
25	425721	AC002115	Hs.159309	uropod 1A,	transmembrane4;COX5B;Ets	11.2
	409757	NM_001898	Hs.123114	cystatin SN	cystatin	11.2
	430630	AW269920	Hs.2621	cystatin A (stefin A)	7m_3;ANF_receptor	11.2
	428630	M85289	Hs.211573	heparan sulfate proteoglycan 2 (perleca	laminin_EGF;lg;ldl_recept_a	11.1
30	427289	AI097346	Hs.174203	solute carrier family 1 (glutamate/neur	SDF	11.1
	401248	AB028989	Hs.88500	mitogen-activated protein kinase 8 inte	vw;vwd;TIL	11.1
	412627	BE391959	Hs.74276	chloride intracellular channel 1	G-patch;lg;MutS_C	11.1
	420104	U09825	Hs.1287	zinc finger protein 173	zf-C3HC4;SPRY;zf-B_box	11.1
	405276	AB028989	Hs.88500	mitogen-activated protein kinase 8 inte	vw;vwd;TIL	11.1
35	425864	U56420	Hs.159903	olfactory receptor, family 5, subfamily	7m_1	11.1
	446745	AW118189	Hs.156400	ESTs	vwa	11.1
	441834	AL138034	Hs.7979	KIAA0736 gene product	sugar_tr	11.0
	450986	BE241845	Hs.25744	Novel human gene mapping to chromo	Ph;RhoGAP;Gal-bind_lectin	11.0
40	416118	N52773	Hs.167721	ESTs	hemopexin;Peptidase_M10	11.0
	443071	AL080021	Hs.8988	complement component 1, q subcompo	C1q;Collagen	10.9
	431247	AL021578	Hs.278489	maltrin 4	EGF;vwa	10.9
	431449	M55994	Hs.256278	tumor necrosis factor receptor superfam	TNFR_c6	10.9
	457044	S73899	Hs.2131	arginine vasopressin receptor 1A	7m_1	10.9
	416319	AI815601	Hs.78197	CD83 antigen (activated B lymphocyte	lg	10.8
45	402172			predicted exon	lg	10.7
	424218	AF031824	Hs.143212	cystatin F (leukocystatin)	cystatin	10.6
	409208	Y00093	Hs.51077	integrin, alpha X (antigen CD11C (p15	vwa	10.6
	426330	M77235	Hs.169331	sodium channel, voltage-gated, type V,	ion_trans;Q	10.6
	439758	AA845235	Hs.124470	ESTs	transmembrane4	10.6
50	412429	AV650262	Hs.75765	GRO2 oncogene	IL8	10.6
	449987	AW079749	Hs.184719	ESTs, Weakly similar to AF116721 11	ABC_tran;ABC_membrane	10.6
	432408	N39127	Hs.76391	myxovirus (influenza) resistance 1, hom	ion_trans;K_tetra	10.6
	406672	M26041	Hs.198253	major histocompatibility complex, clas	lg;MHC_II_alpha	10.5
	419749	X73608	Hs.93029	sparc/osteonectin, cwcv and kazal-like	kazal;thyroglobulin_1	10.5
55	419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	fn3;wap	10.5
	425009	X58288	Hs.154161	protein tyrosine phosphatase, receptor t	fn3;lg;Y_phosphatase;MAM	10.5
	432869	BE409301	Hs.134012	C1q-related factor	GTP_EFTU;EFG_C	10.4
	430209	AF177841	Hs.235368	Pro-(alpha)3(V) collagen	Collagen;COLF;TSPN	10.4
	400834			predicted exon	IRK	10.4
60	442941	AU076728	Hs.8867	cysteine-rich, angiogenic inducer, 61	Oys_knot;isp_1;vw;IGFBP	10.4
	403691			predicted exon	isp_1;Reprolysin;	10.4
	430776	AJ011021	Hs.247905	potassium voltage-gated channel, subfa	ion_trans	10.3
	432342	AL036128	Hs.274404	plasminogen activator, tissue	EGF;fn1;kringle;trypsin	10.3
65	413731	BE243845	Hs.75511	connective tissue growth factor	Oys_knot;isp_1;vw	10.3
	423309	BE006775	Hs.126782	sushi-repeat protein	sushi;HYR	10.3
	431728	NM_007351	Hs.268107	multimerin	EGF;C1q	10.3
	450245	AA007538	Hs.271767	ESTs, Moderately similar to ALU1_HU	lg	10.2
	446983	AA157484	Hs.97199	complement component C1q receptor	EGF;Xlink	10.2
	414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	death;ank;ZU5	10.1
70	400253			predicted exon	7m_1	10.0
	406694	M94891	Hs.226932	pregnancy specific beta-1-glycoprotein	lg	10.0
	418793	AW362987	Hs.88474	prostaglandin-endoperoxide synthase 1	EGF	10.0
	410664	NM_006033	Hs.65370	lipase, endothelial	Ribosomal_L22	10.0
	427274	NM_005211	Hs.174142	colony stimulating factor 1 receptor, fo	pkase;lg	10.0

TABLE 4B:

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

80	Pkey	CAT Number	Accession
	410498	120611_1	AA355749 AA085520 AW956333 AA340319 BE170936
	416441	159480_1	BE407197 AA182474 AA180369 BE275628 BE276131
	421258	200725_1	AA286731 AA287621 AW188228 AW137774
	423795	232093_1	AW849759 AW849758 T89549 AA331069

439710 47550_1 AF086543 W96291 W96225
443296 56539_2 A1765286 AW297086 BE568658

TABLE 4C:

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495

Strand: Indicates DNA strand from which exons were predicted

NL_position: Indicates nucleotide positions of predicted exons

Pkey	Ref	Strand	NL_position
400464	9929670	Plus	22074-22214
400834	8705192	Plus	121963-122288
402114	8318588	Plus	71578-71715
402172	8575911	Minus	143378-143671
402406	3970929	Plus	10872-11123,12932-13048
402425	9786347	Minus	50224-50395
403077	8954241	Plus	146923-147222,147326-147628
403089	8954241	Plus	171864-172239
403691	7387384	Minus	88280-88463
405024	7107727	Plus	88500-88697
405285	6139075	Minus	55744-55903,57080-57170,61478-61560
405368	2104517	Plus	46055-47188

TABLE 6A lists about 685 genes down-regulated in ovarian cancer compared to normal ovaries. These were selected as for Table 3A, except that the numerator and denominator were switched, and the ratio was greater than or equal to 3.0 (i.e. 3-fold down-regulated in tumor vs. normal ovary).

TABLE 6A: 685 DOWN-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY

Pkey: Primekey

Ex. Accn: Exemplar Accession

UG ID: UniGene ID

Title: UniGene Title

ratio: ratio normal ovary vs tumor

Pkey	Ex. Accn	UG ID	Title	ratio
421013	M62397	Hs.1345	mutated in colorectal cancers	14.8
439360	AA448488	Hs.56346	ESTs, Weakly similar to Z141_HUMAN ZINC FINGER	12.8
407644	D16815	Hs.37288	nuclear receptor subfamily 1, group D, member 2	12.6
424851	AA676441	Hs.119059	ESTs	11.6
455056	AW853057		gb:RC1-CT0249-170200-025-h04 CT0249 Homo sapie	11.5
420727	H75701	Hs.99886	complement component 4-binding protein, beta	11.3
451617	C01056	Hs.168000	ESTs	10.0
401308			predicted exon	9.9
440987	AA911705	Hs.130229	ESTs	9.7
409725	T40760	Hs.90455	EST	9.7
415752	BE314524	Hs.78776	putative transmembrane protein	9.7
437690	AA804362	Hs.180544	ESTs	9.6
437787	AJ908263	Hs.291625	ESTs	9.5
458054	AW798466	Hs.82396	2',5'-oligoadenylate synthetase 1	9.2
435330	R16769	Hs.185689	ESTs	9.2
436642	AA724430	Hs.127960	ESTs	9.1
453752	AL120800		gb:DKFZp762E152.r1 762 (synonym: hmal2) Homo sa	9.1
451683	AJ808964	Hs.207673	ESTs	9.1
401464	AF039241	Hs.9028	histone deacetylase 5	9.0
435812	AW298067		gb:U1H-BW0-ajp-g-09-0-ULs1 NCL_CGAP_Sub6 Hom	8.7
410758	BE535988		gb:601052418F1 NIH_MGC_10 Homo sapiens cDNA	8.7
412637	AA115097	Hs.261313	ESTs	8.4
419166	AA234638	Hs.293584	ESTs	8.3
423739	AA398155	Hs.97600	ESTs	8.1
413813	M96956	Hs.75561	teratocarcinoma-derived growth factor 1	8.1
416211	R14625		gb:yg45c03.r1 Soares Infant brain 1NIB Homo sapiens	8.0
443131	AJ033833	Hs.132689	ESTs	7.9
415866	T10115	Hs.92423	KIAA1566 protein	7.9
410130	AJ912097	Hs.163208	ESTs	7.9
439426	AJ131502	Hs.143135	ESTs, Weakly similar to FAFY_HUMAN PROBABLE	7.8
408141	U69205	Hs.45152	ESTs, Moderately similar to neurogenic basic-helix-loop	7.7
419015	T79262	Hs.14463	ESTs	7.6
441573	BE563966	Hs.6529	ESTs	7.5
419386	AA236867	Hs.143968	ESTs	7.5
430562	D78260	Hs.285097	ESTs	7.5
434738	AA836265		gb:cd17e02.s1 NCL_CGAP_GCB1 Homo sapiens cDNA	7.4
403283			predicted exon	7.4
415861	Z43123	Hs.144513	ESTs	7.4
412732	AW993300		gb:RC2-BN0033-180200-015-g06 BN0033 Homo sapie	7.4
441247	AW118681	Hs.128051	ESTs	7.4
442865	N57659	Hs.114541	ESTs, Weakly similar to neuronal thread protein AD7c-	7.3
409699	BE154650		gb:PM3-HT0344-071299-003-c08 HT0344 Homo sapie	7.3
420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens cDNA	7.3
421418	AA806639		gb:xb88g05.s1 NCL_CGAP_GCB1 Homo sapiens cDN	7.2
413597	AW302885	Hs.117183	ESTs	7.2
454102	AW752363		gb:RC0-CT0201-270999-011-03 CT0201 Homo sapien	7.1
445487	AJ806287	Hs.201217	ESTs	7.1
457604	AJ004397	Hs.130558	ESTs, Weakly similar to similar to O-sialoglycoprotein	7.1

	400942		predicted exon	6.9
	407596	R86913	gb:q30r05.r1 Soares fetal liver spleen 1NFLS Homo sa	6.9
	422046	AU638562	gb:ts50a10.x1 NCL_CGAP_U11 Homo sapiens cDNA c	6.9
5	441284	AA927876	ESTs	6.9
	446224	AW450551	ESTs	6.9
	424943	AU077260	death-associated protein kinase 1	6.9
	453967	AW009077	ESTs	6.9
	448683	AA167642	ESTs	6.8
10	431877	AA521204	ESTs	6.8
	411337	AW837349	gb:QV2-LT0038-270300-108-d12 LT0038 Homo sapie	6.8
	410596	AA374186	gb:EST86290 HSC172 cells 1 Homo sapiens cDNA 5' e	6.8
	417762	AA205976	gb:zq48a10.r1 Stratagene hNT neuron (937233) Homo	6.7
	406364		predicted exon	6.7
15	452238	F01811	ESTs, Moderately similar to S22703 voltage-gated pota	6.7
	415288	R15794	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFA	6.7
	407437	AF220264	gb:Homo sapiens MOST-1 mRNA, complete cds.	6.7
	439126	AF085984	gb:Homo sapiens full length insert cDNA clone YT99F	6.6
	452453	AI92519	gb:QV-BT009-101198-051 BT009 Homo sapiens cDNA	6.6
20	431800	AW452768	ESTs	6.5
	426380	AJ291267	ESTs, Weakly similar to unnamed protein product [H.s	6.5
	449529	AI90559	ESTs	6.4
	437755	AW204256	ESTs	6.4
	448307	AJ480289	ESTs	6.4
	439588	AA922936	ESTs	6.4
25	420061	N35696	ESTs	6.4
	425806	AI522299	ESTs	6.4
	433923	AJ823453	ESTs	6.4
	408159	H63977	ESTs	6.3
30	434844	AF157118	hypothetical protein LOC56757	6.3
	430197	AA468888	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFA	6.3
	440332	AJ218517	ESTs	6.3
	450061	AJ797034	ESTs	6.3
	454894	AW850178	gb:IL3-CT0219-271099-022-H04 CT0219 Homo saplen	6.3
35	402105		predicted exon	6.3
	409090	W56057	ESTs	6.2
	405752		predicted exon	6.2
	408074	R20723	ESTs	6.2
40	459200	Y09308	homeodomain-interacting protein kinase 3	6.1
	416310	T81421	ESTs	6.1
	421978	AL139443	mRNA for FLJ00023 protein	6.1
	429755	NM_001364	discs, large (Drosophila) homolog 2 (chapsyn-110)	6.0
	448732	BE614063	gb:601503993F1 NIH_MGC_71 Homo sapiens cDNA	6.0
	453909	AW004045	ESTs	6.0
45	431178	AA493884	Homo sapiens cDNA: FLJ21440 fis, clone COLD4389	6.0
	449671	AW959755	Homo sapiens cDNA FLJ12977 fis, clone NT2RP20062	6.0
	421349	W01715	ESTs, Weakly similar to Lpg6p [S.cerevisiae]	6.0
	453282	AK000043	hypothetical protein FLJ20036	5.9
	420618	AA278781	ESTs	5.9
50	412480	BE142364	gb:CMO-HT0143-270999-062-d12 HT0143 Homo sapi	5.9
	449658	AW205979	ESTs	5.9
	429884	AL049925	DKFZP547G0910 protein	5.9
	416453	H56968	ESTs	5.9
	459497	AA825742	ESTs	5.9
55	433773	AA759293	ESTs	5.9
	458942	AA009647	a disintegrin and metalloproteinase domain 12 (meltrin a	5.9
	436054	AJ076262	ESTs	5.9
	410495	N95428	gb:zb80d09.s1 Soares_senescent_fibroblasts_NbHSF H	5.8
	403277		predicted exon	5.8
60	444302	AI140115	ESTs	5.8
	439834	AJ754576	ESTs	5.8
	404020		predicted exon	5.8
	454338	AW381251	pleckstrin homology, Sec7 and coiled-coil domains 1(cy	5.7
	430922	AW373747	ESTs	5.7
	420289	N55394	8-oxoguanine DNA glycosylase	5.7
65	428498	AA429575	ESTs	5.7
	445597	H65649	gb:yr72d10.r1 Soares fetal liver spleen 1NFLS Homo sa	5.7
	411543	AW851248	gb:IL3-CT0220-160200-066-F01 CT0220 Homo saplen	5.7
	408354	AJ382803	ESTs	5.7
70	444431	AW513324	ESTs	5.7
	406605		predicted exon	5.7
	405541	AF039241	histone deacetylase 5	5.6
	458090	AI282149	ESTs, Highly similar to FXD3_HUMAN FORKHEAD	5.6
	454529	Z45439	ESTs	5.6
75	445832	AI261545	gb:zq30a07.x1 NCL_CGAP_Kid11 Homo sapiens cDNA	5.6
	441223	AI475087	ESTs	5.6
	432552	AI537170	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFA	5.6
	443650	AI698330	ESTs	5.6
	403714		predicted exon	5.6
80	444165	AL137443	hypothetical protein FLJ11236	5.6
	458914	BE327696	ESTs	5.6
	420620	AA278807	ESTs	5.5
	458228	AA934995	ESTs, Weakly similar to R28830 1 [H.sapiens]	5.5
	448067	R68568	src homology 3 domain-containing protein HIP-55	5.5
	427000	AI187420	ESTs	5.5

452351	AA025647		gbze85d01.r1 Soares_fetal_heart_NbHH19W Homo sa	5.5
453359	N99545		gbza40a05.r1 Soares fetal liver spleen 1NFLS Homo sa	5.5
408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.5
450938	AW753734	Hs.277215	ESTs	5.5
431888	H99557	Hs.2864	early endosome antigen 1, 162kD	5.4
459418	W96550	Hs.26418	ESTs	5.4
416718	R83017	Hs.204828	ESTs	5.4
413236	H16442	Hs.127376	KIAA0266 gene product	5.4
439063	AF085922	Hs.113968	ESTs	5.4
446361	AI291234	Hs.282241	ESTs	5.4
458253	AW296952	Hs.196802	ESTs	5.4
433682	AA642418	Hs.17381	ESTs	5.4
455790	BE090690		gb:RC1-BT0720-280300-011-g02 BT0720 Homo sapie	5.4
457555	AW294870	Hs.223672	ESTs	5.3
436513	AJ278110	Hs.125507	DEAD-box protein	5.3
416671	N94087	Hs.26073	ESTs, Moderately similar to HG14_HUMAN NONHIS	5.3
440231	AW015420	Hs.163323	ESTs	5.3
429866	AA460104	Hs.99540	ESTs	5.3
437779	AA345232	Hs.21227	ESTs	5.3
424029	AB014594	Hs.137579	KIAA0694 gene product	5.3
425614	AI334963	Hs.156258	ESTs	5.3
430653	AW902062	Hs.30280	ESTs	5.2
408855	T83061	Hs.279604	desmin	5.2
410454	AW749041		gb:RC3-BT0319-100100-012-c05 BT0319 Homo sapie	5.2
438116	AJ904105	Hs.122018	ESTs	5.2
409138	W73159	Hs.58290	ESTs	5.2
423047	NM_005323	Hs.123064	H1 histone family, member T (testis-specific)	5.2
440212	AW300959	Hs.126216	ESTs, Weakly similar to good similarity to E. coli hypo	5.2
404108			predicted exon	5.2
456253	T12198		gb:A588F Heart Homo sapiens cDNA clone A588, mRN	5.2
409365	AA702376	Hs.228440	Homo sapiens clone 24881 mRNA sequence	5.1
444013	T08531	Hs.44404	hypothetical protein PRO1488	5.1
454071	AJ041793	Hs.42502	ESTs	5.1
419761	M17373	Hs.93177	interferon, beta 1, fibroblast	5.1
451250	AA491275	Hs.236940	Homo sapiens cDNA FLJ12542 fis, clone NT2RM4000	5.1
405290			predicted exon	5.1
454487	AW796342		gb:PM2-UM0027-230200-002-h02 UM0027 Homo sap	5.1
444131	AJ806600	Hs.207119	EST, Weakly similar to intrinsic factor-B12 receptor pr	5.1
441679	BE502267	Hs.65996	ESTs	5.1
450077	AA523752	Hs.120855	ESTs	5.1
421209	AJ010230	Hs.102576	ret finger protein-like 1 antisense	5.1
445140	AJ650599	Hs.197913	ESTs	5.1
421126	M74587	Hs.102122	insulin-like growth factor binding protein 1	5.1
447037	AJ357568	Hs.157612	ESTs	5.1
407188	R45175		gb:yg40R1.s1 Soares infant brain 1NIB Homo sapiens	5.0
436196	AK001084		gb:Homo sapiens cDNA FLJ10222 fis, clone HEMBB1	5.0
442772	AW503680	Hs.300513	ESTs, Weakly similar to T1587.2 [C.elegans]	5.0
444138	AJ701572	Hs.151153	ESTs	5.0
458589	AV654623	Hs.288141	Homo sapiens cDNA FLJ13016 fis, clone NT2RP30006	5.0
451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on chromos	5.0
441318	AJ078234	Hs.176130	ESTs	5.0
407490	S79281		gb:pancreatic ribonuclease [human, mRNA Recombinan	4.9
438224	AA933999		gb:091R04.s1 Soares_NFL_T_GBC_S1 Homo sapiens	4.9
451638	AW798466	Hs.82396	Z,S'-oligoadenylate synthetase 1	4.9
457356	AA489621	Hs.191670	ESTs	4.9
430679	R44428	Hs.22801	ESTs	4.9
445747	AJ820863	Hs.145328	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFA	4.9
409036	T88693	Hs.226410	ESTs	4.9
433382	T64293	Hs.291453	ESTs	4.9
401287			predicted exon	4.9
424188	AW954552	Hs.142634	zinc finger protein	4.9
404868			predicted exon	4.9
410152	AW593104	Hs.23681	ESTs	4.9
444997	AJ204451	Hs.146196	ESTs	4.9
431075	BE267477		gb:601189542F2 NIH_MGC_7 Homo sapiens cDNA cl	4.8
429033	NM_007374	Hs.194756	sine oculis homeobox (Drosophila) homolog 6	4.8
414337	BE386608		gb:601273980F1 NIH_MGC_20 Homo sapiens cDNA	4.8
410336	BE391510	Hs.18498	Homo sapiens cDNA FLJ12277 fis, clone MAMMA10	4.8
445283	AW515763	Hs.246872	ESTs	4.8
434792	AA649253	Hs.132458	ESTs	4.8
433403	AF040247		gb:Homo sapiens erythroid differentiation-related factor	4.8
454940	AW846202		gb:QV0-CT0179-011299-061-f10 CT0179 Homo sapie	4.8
455534	AW991925		gb:PM3-BN0011-130100-002-b07 BN0011 Homo sapi	4.8
416437	N48990	Hs.37204	ESTs	4.8
433767	AA609245		gb:af13a11.s1 Soares_testis_NHT Homo sapiens cDNA	4.8
434977	AJ734233	Hs.226142	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFA	4.8
416192	NM_005038	Hs.998	peroxisome proliferative activated receptor, alpha	4.8
459218	AA812633	Hs.10845	ESTs	4.8
402109			predicted exon	4.8
444490	AJ151080	Hs.146830	ESTs	4.8
432632	AW973801	Hs.134656	ESTs	4.8
438683	AA813982	Hs.291842	ESTs	4.8
404044			predicted exon	4.8
449862	AI672277	Hs.199475	ESTs	4.8

	419002	T78625	Hs.268594	ESTs	4.7
	425582	AL157686	Hs.293737	ESTs	4.7
	416086	H18252	Hs.227263	ESTs	4.7
5	441133	AA918191	Hs.194457	ESTs	4.7
	446323	AI288274	Hs.149868	ESTs	4.7
	440347	AI125590	Hs.142884	ESTs	4.7
	439481	AF086294	Hs.125844	ESTs	4.6
	456388	W28557		gb:48d8 Human retina cDNA randomly primed sublibrary	4.6
10	441884	R34177	Hs.181315	ESTs, Moderately similar to ALU4_HUMAN ALU SU	4.6
	445910	R93483	Hs.260273	ESTs	4.6
	403531			predicted exon	4.6
	429773	AI332482	Hs.218791	proteoglycan 4, (megakaryocyte stimulating factor, artc	4.6
	422563	BE299342	Hs.19348	Homo sapiens cDNA FLJ13119 fs, clone NT2RP30026	4.6
	422890	Z43784	Hs.78713	solute carrier family 25 (mitochondrial carrier; phospho	4.6
15	453663	AL048807	Hs.180714	cytochrome c oxidase subunit VIa polypeptide 1	4.6
	447839	N72050	Hs.164144	ESTs	4.5
	415612	F12893	Hs.13301	ESTs	4.5
	433371	T25451		gb:PTH188 HTCDL1 Homo sapiens cDNA 5/3' simila	4.5
20	410667	AW936099		gb:QV0-DT0020-210100-095-d04 DT0020 Homo sapie	4.5
	410890	AW809575		gb:MR4-ST0121-060200-002-a12 ST0121 Homo sapie	4.5
	404451			predicted exon	4.5
	441705	AI087052	Hs.55993	ESTs	4.5
	439597	W79578	Hs.58552	ESTs	4.5
25	407825	NM_006152	Hs.40202	lymphoid-restricted membrane protein	4.5
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Drosophila) ho	4.5
	455278	BE300369	Hs.42643	ESTs, Weakly similar to KIAA1016 protein [H.sapiens	4.5
	424719	H90452		gb:yy01c03.r1 Soares fetal liver spleen 1NFLS Homo sa	4.5
	439542	AW297571	Hs.17646	ESTs	4.5
30	444433	AV649844	Hs.282436	ESTs	4.5
	438831	BE263273	Hs.301128	ESTs	4.5
	410065	AW812744		gb:RC3-ST0186-181099-012-c09 ST0186 Homo sapien	4.5
	453895	AA039843	Hs.61948	ESTs	4.5
	458250	AI807339	Hs.152174	ESTs, Weakly similar to Z140_HUMAN ZINC FINGER	4.5
35	423403	AA325483		gb:EST28475 Cerebellum II Homo sapiens cDNA 5' en	4.5
	454679	AW813110		gb:CM4-ST0189-051099-021-05 ST0189 Homo sapien	4.5
	445368	AI221631	Hs.166788	ESTs	4.5
	401004			predicted exon	4.5
	425837	AF007567	Hs.159609	insulin receptor substrate 4	4.5
40	420497	AW206285	Hs.253548	ESTs	4.5
	449438	AA927317	Hs.176719	ESTs	4.5
	429409	AI694817	Hs.155980	ESTs	4.5
	447859	AI452784	Hs.270270	ESTs	4.4
	407340	AA810168	Hs.232119	ESTs	4.4
45	424326	NM_014479	Hs.145296	disintegrin protease	4.4
	443479	AF027219	Hs.9443	zinc finger protein 202	4.4
	443246	T75157	Hs.285516	ESTs, Weakly similar to hypothetical protein [H.sapien	4.4
	414475	BE302955	Hs.119598	ribosomal protein L3	4.4
	432075	AW972934		gb:EST385030 MAGE resequences, MAGM Homo sap	4.4
50	417905	R24769	Hs.23725	ESTs	4.4
	406518	W28077	Hs.79389	nel (chicken)-like 2	4.4
	441460	AI962478	Hs.225804	ESTs, Moderately similar to ALUC_HUMAN III ALU	4.4
	450549	T49427	Hs.181244	major histocompatibility complex, class I, A	4.4
	426528	AA380828		gb:EST93827 Activated T-cells VII Homo sapiens cDN	4.4
55	430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo sapi	4.4
	408479	BE047329	Hs.144483	ESTs	4.3
	448636	AI557139	Hs.129179	Homo sapiens cDNA FLJ13581 fs, clone PLACE10090	4.3
	411280	N50817		gb:yy89h02.r1 Soares_multiple_sclerosis_2NbHMSF H	4.3
	440780	AW593050	Hs.128580	ESTs	4.3
60	458301	AF003834		gb:AF003834 Clontech H11149x Homo sapiens cDNA	4.3
	442277	AW448914	Hs.202391	ESTs	4.3
	449463	AI657038	Hs.196109	ESTs	4.3
	433426	H69125	Hs.133525	ESTs	4.3
	410782	AW504860	Hs.288836	Homo sapiens cDNA FLJ12673 fs, clone NT2RM4002	4.3
65	423040	AA320749	Hs.209464	KIAA1604 protein	4.3
	432430	AW079984	Hs.262480	ESTs	4.3
	432072	N62937	Hs.269109	ESTs	4.3
	452213	AL110237	Hs.28425	Homo sapiens mRNA; cDNA DKFZp566D224 (from c	4.3
	403635			predicted exon	4.3
70	441919	AI553802	Hs.128121	ESTs	4.3
	416717	H79559	Hs.297726	ESTs	4.3
	430995	NM_005092	Hs.248197	tumor necrosis factor (ligand) superfamily, member 18	4.2
	429269	AA449013	Hs.99203	ESTs	4.2
	415840	R15955	Hs.21758	ESTs	4.2
75	451300	AA017066	Hs.237686	EST	4.2
	445366	AI221511	Hs.298662	ESTs	4.2
	424194	BE245833	Hs.169854	hypothetical protein SP192	4.2
	459105	NM_014517	Hs.28423	upstream binding protein 1 (LBP-1a)	4.2
	455387	BE069037		gb:QV3-BT0379-161299-040-e12 BT0379 Homo sapie	4.2
80	410507	AA355288	Hs.271408	ESTs	4.2
	453823	AL137967		gb:DKFZp761D2315_r1 761 (synonym: hamy2) Homo	4.2
	450966	AA017245	Hs.32794	ESTs	4.2
	432694	AW991585	Hs.276755	ESTs, Weakly similar to F53B1.2 [C.elegans]	4.2
	455108	AW856866		gb:RC0-CT0299-291199-031-G02 CT0299 Homo sapie	4.2
	443609	AV650231	Hs.282941	ESTs	4.2

	427469	AA403084	Hs.269347	ESTs	4.2
	417178	N51636		gb:yy67b01.s1 Soares_multiple_sclerosis_2NbHMSP H	4.2
	439751	AA196090	Hs.50794	Homo sapiens mRNA full length insert cDNA clone EU	4.2
5	431982	AW419296	Hs.105754	ESTs	4.1
	442641	AI890955	Hs.262983	ESTs	4.1
	422128	AW881145		gb:QV0-OT0033-010400-182-a07 OT0033 Homo sapie	4.1
	449158	AF103907	Hs.171353	prostate cancer antigen 3	4.1
	419668	AI033098	Hs.132777	ESTs	4.1
10	418236	AW994005	Hs.172572	hypothetical protein FLJ20093	4.1
	432663	AI584317	Hs.122589	ESTs	4.1
	448313	BE622486	Hs.121688	Homo sapiens cDNA FLJ13463 fis, clone PLACE10034	4.1
	411279	AW884776		gb:QV4-OT0067-010300-121-d01 OT0067 Homo sapie	4.1
	440852	AI216751	Hs.143977	ESTs	4.1
	416608	R11499	Hs.189716	ESTs	4.1
15	420405	AA743396	Hs.189023	ESTs	4.1
	405717			predicted exon	4.1
	435267	N23797	Hs.110114	ESTs	4.1
	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr virus) recepto	4.1
20	403560	AI929721	Hs.5120	dynein, cytoplasmic, light polypeptide	4.1
	449162	AI632740	Hs.10476	ESTs	4.1
	459157	AI504385		gb:CM-BT054-080399-054 BT054 Homo sapiens cDN	4.1
	432474	AA584042		gb:nf65e09.s1 NCI_CGAP_Lar1 Homo sapiens cDNA	4.1
	455388	AW936234		gb:QV0-DT0020-090200-106-g05 DT0020 Homo sapie	4.0
25	426458	AA580748	Hs.130658	ESTs	4.0
	438597	AA811662	Hs.171497	ESTs	4.0
	437934	AW880871	Hs.77496	small nuclear ribonucleoprotein polypeptide G	4.0
	459385	BE380047		gb:601159362F2 NIH_MGC_53 Homo sapiens cDNA	4.0
	436404	AW968556	Hs.137240	Homo sapiens mRNA for partial 3'UTR, sequence 2	4.0
	457740	AW500458		gb:U1-HF-BN0-akb-4-07-0-ULr1 NIH_MGC_50 Homo	4.0
30	437385	AA757055	Hs.164060	ESTs	4.0
	444530	AV650124	Hs.282435	ESTs	4.0
	408066	AA046914		gb:z47h10.r1 Soares retina N2b4HR Homo sapiens cD	4.0
	411256	AW834039		gb:QV0-TT0010-091199-053-c09 TT0010 Homo sapie	4.0
35	433582	BE548749	Hs.148016	ESTs	4.0
	438837	BE500941	Hs.126730	ESTs, Weakly similar to KIAA1214 protein [Hsapiens	4.0
	414571	BE410746	Hs.22868	protein tyrosine phosphatase, non-receptor type 11	4.0
	446190	AI279299	Hs.256584	ESTs	4.0
	443542	AI927065	Hs.146040	ESTs	4.0
40	430444	AW296421	Hs.121035	ESTs	4.0
	454573	BE146471		gb:QV0-HT0216-011199-043-c09 HT0216 Homo sapie	4.0
	409946	AW501748		gb:U1-HF-BR0p-ajm-b-12-0-ULr1 NIH_MGC_52 Hom	4.0
	456141	AI751357	Hs.288741	Homo sapiens cDNA: FLJ22256 fis, clone HRC02860	4.0
	456140	AA169515	Hs.6006	ESTs	4.0
45	441685	AI459261	Hs.144481	ESTs	4.0
	416677	T83470		gb:y046g06.r1 Soares fetal liver spleen 1NFLS Homo s	4.0
	401740			predicted exon	4.0
	420122	AA255714	Hs.284153	Fanconi anemia, complementation group A	4.0
	442594	AW272467	Hs.254655	Unfilled	3.9
50	426294	AA374185		gb:EST86289 HSC172 cells I Homo sapiens cDNA 5' e	3.9
	411922	AW876260		gb:PM4-PT0019-131299-006-E04 PT0019 Homo sapie	3.9
	452320	AA042873	Hs.160412	ESTs	3.9
	431644	AW972822	Hs.169248	cytochrome c	3.9
	409892	AW956113		gb:EST368183 MAGE resequences, MAGD Homo sap	3.9
55	418132	T92670	Hs.117421	ESTs	3.9
	414372	AA143654		gb:z065a02.r1 Stratagene pancreas (937208) Homo sap	3.9
	400196			predicted exon	3.9
	416900	M59964	Hs.1048	KIT ligand	3.9
	445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled-coil domains, bind	3.9
60	435957	N39015	Hs.190368	ESTs	3.9
	442299	AW467791	Hs.155561	ESTs	3.9
	419499	AA808136	Hs.177698	ESTs	3.9
	438403	AA806607	Hs.292206	ESTs	3.9
	449386	AA001308	Hs.193213	ESTs	3.9
65	443283	BE568610		gb:601342622F1 NIH_MGC_53 Homo sapiens cDNA	3.9
	406481			predicted exon	3.9
	453530	AW021633		gb:xd26c02.y1 Morton Fetal Cochlea Homo sapiens cDN	3.9
	415558	AA885143	Hs.125719	ESTs	3.9
	416874	H98752	Hs.42558	ESTs	3.9
70	454885	AW836922		gb:QV1-LT0036-150200-074-h06 LT0036 Homo sapie	3.9
	419896	Z99362		gb:HS299362 DKFZphar11 Homo sapiens cDNA clon	3.9
	440962	AI989961	Hs.233477	ESTs, Moderately similar to A Chain A, Sczypa Compl	3.9
	419401	AW804663		gb:QV4-UM0094-160300-135-d06 UM0094 Homo sap	3.9
	406562			predicted exon	3.8
75	405690	BE409855	Hs.808	heterogeneous nuclear ribonucleoprotein F	3.8
	435282	AA677428	Hs.189731	ESTs	3.8
	402451			predicted exon	3.8
	451577	N69101	Hs.32703	ESTs	3.8
	457141	AA521410	Hs.41371	ESTs	3.8
80	407817	H92553	Hs.40400	ESTs	3.8
	412613	AA653507	Hs.285711	Homo sapiens cDNA FLJ13089 fis, clone NT2RP30021	3.8
	418355	L42563	Hs.1165	ATPase, H+/K+ transporting, nongastric, alpha polypep	3.8
	446357	AW161533	Hs.300866	ESTs	3.8
	407448	AJ001865		gb:Homo Sapiens mRNA, partial cDNA sequence for h	3.8
	456383	AI148037		gb:xgg61e01.r1 Soares_testis_NHT Homo sapiens cDNA	3.8

	444651	W58469	Hs.103120	ESTs	3.8
	455067	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo sapie	3.8
	442657	BE502631	Hs.130645	ESTs	3.8
5	429142	AA835639	Hs.104972	ESTs	3.8
	428274	AJ379772	Hs.98206	ESTs	3.8
	437774	AW978199	Hs.291648	ESTs	3.8
	427737	AA435988	Hs.178066	ESTs, Weakly similar to AF068289 5 HDOME31P [H.s	3.8
	405671			predicted exon	3.8
10	413627	BE182082	Hs.246973	ESTs	3.8
	438858	R37529	Hs.269924	ESTs	3.8
	416612	H70565		gb:yr97c04.r1 Soares fetal liver spleen 1NFLS Homo sa	3.8
	423045	AW967472	Hs.301511	ESTs, Highly similar to KPT2_HUMAN SERINE/THR	3.8
	453361	AA035197	Hs.107375	ESTs	3.7
15	437243	AA747549	Hs.259122	ESTs	3.7
	437987	AW450202	Hs.122963	ESTs	3.7
	409781	BE148621	Hs.254602	ESTs	3.7
	455895	BE154837		gb:PM1-HT0345-121199-001-c08 HT0345 Homo sapie	3.7
	413492	AW612343		gb:hg97c10.x1 NCL_CGAP_Kid111 Homo sapiens cDN	3.7
20	413247	AW963969		gb:EST376042 MAGE resequences, MAGH Homo sap	3.7
	422866	NM_002410	Hs.121502	mannosyl (alpha-1,6)-glycoprotein beta-1,6-N-acetyl-g	3.7
	431828	AA572994		gb:nm33f12.s1 NCL_CGAP_Lip2 Homo sapiens cDNA	3.7
	438872	R64197	Hs.23589	ESTs	3.7
	438673	AJ824717	Hs.123443	ESTs	3.7
25	416624	H69044		gb:yr77h05.s1 Soares fetal liver spleen 1NFLS Homo sa	3.7
	401963			predicted exon	3.7
	402867			predicted exon	3.7
	408315	AW179148		gb:MR4-ST0067-200899-002-B07 ST0067 Homo sapie	3.7
30	418320	D86981	Hs.84084	amyloid beta precursor protein (cytoplasmic tail)-bindin	3.7
	447199	AJ939421	Hs.160900	ESTs	3.7
	422590	AA312758	Hs.193945	Homo sapiens cDNA FLJ13962 fis, clone Y79AA10012	3.7
	451996	AW514021	Hs.245510	ESTs	3.7
	412463	AW953444	Hs.78672	laminin, alpha 4	3.7
35	440928	AL046575	Hs.130198	ESTs	3.7
	441951	W31002	Hs.128195	ESTs	3.7
	440705	AA904244	Hs.153205	ESTs	3.7
	434231	AF119901	Hs.250568	hypothetical protein PRO2831	3.7
	411039	AL135674	Hs.163348	ESTs	3.7
	413137	BE066915		gb:PM0-BT0340-231199-001-b07 BT0340 Homo sapie	3.7
40	417970	AA309234	Hs.57760	Homo sapiens cDNA: FLJ23119 fis, clone LNG07978	3.7
	439786	AV652707	Hs.33755	Homo sapiens mRNA full length insert cDNA clone EU	3.7
	459595	AL040421		gb:DKFZp434B0714_r1 434 (synonym: htes3) Homo s	3.7
	443601	AJ078554	Hs.15682	ESTs	3.7
	404041			predicted exon	3.6
45	408122			predicted exon	3.6
	404582			predicted exon	3.6
	455786	BE090077		gb:RC6-BT0710-300300-021-F02 BT0710 Homo sapie	3.6
	411899	AA370573		gb:EST82238 Prostate gland I Homo sapiens cDNA 5' e	3.6
50	426758	AL038430	Hs.197772	ESTs	3.6
	421776	AW301994	Hs.108183	candidate tumor suppressor p33 ING1 homolog	3.6
	430169	AA488531	Hs.189047	ESTs	3.6
	407695	AJ808007	Hs.66450	ESTs	3.6
	454584	AW807573		gb:MR1-ST0088-021299-004-g01 ST0088 Homo sapie	3.6
55	425802	X52509	Hs.161640	tyrosine aminotransferase	3.6
	439328	W07411	Hs.118212	ESTs, Moderately similar to ALU3_HUMAN ALU SU	3.6
	428066	AA868555	Hs.178222	ESTs	3.6
	426690	AJ948490	Hs.98765	ESTs	3.6
	437302	AA837146	Hs.180275	ESTs	3.6
	443973	AJ580083	Hs.176154	ESTs	3.6
60	453993	AW615224	Hs.252839	ESTs	3.6
	413623	AA825721	Hs.246973	ESTs	3.6
	409196	NM_001874	Hs.169765	carboxypeptidase M	3.6
	424916	AW867440	Hs.23096	ESTs	3.6
	424769	H06469	Hs.142653	ret finger protein	3.6
	400080			predicted exon	3.6
65	421521	AJ638760	Hs.161795	ESTs	3.6
	405549			predicted exon	3.6
	446114	AJ275715	Hs.145926	ESTs	3.6
	441392	AW451831	Hs.222119	ESTs, Weakly similar to K1CQ_HUMAN KERATIN, T	3.6
70	424025	AJ701852	Hs.301296	ESTs	3.5
	448527	AJ525606		gb:PT1.3_03_G05.r tumor1 Homo sapiens cDNA 5', mR	3.5
	437063	AA351109	Hs.5437	Tax1 (human T-cell leukemia virus type I) binding prot	3.5
	449880	AJ673006	Hs.231948	ESTs, Weakly similar to ALUB_HUMAN !!! ALU CL	3.5
	449311	AJ657014		gb:tt49a12.x1 NCL_CGAP_GC6 Homo sapiens cDNA c	3.5
75	442999	AW662889	Hs.132395	ESTs	3.5
	416238	W90448		gb:zh78c08.s1 Soares fetal liver spleen 1NFLS, S1 H	3.5
	423209	BE278528	Hs.105823	H.sapiens gene from PAC 42616, similar to syntaxin 7	3.5
	409854	AW501833		gb:UL-HF-BR0p-ajp-d-01-0-UL.r1 NIH_MGC_52 Hom	3.5
	414941	C14865	Hs.182159	ESTs	3.5
80	456337	AW751681	Hs.65919	ESTs	3.5
	415298	F05088		gb:HSCD1A011 normalized infant brain cDNA Homo s	3.5
	423338	AB007961	Hs.127338	KAAD492 protein	3.5
	415618	F12954		gb:HSC3GG091 normalized infant brain cDNA Homo s	3.5
	405583			predicted exon	3.5
	435601	AF217509	Hs.283077	centrosomal P4.1-associated protein; uncharacterized bo	3.5

5	450867	AA011454	Hs.245122	ESTs	3.5
	431339	AA506294	Hs.257268	ESTs	3.5
	441969	A1733388	Hs.129194	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFA	3.5
	431343	AW970603	Hs.300941	Homo sapiens cDNA FLJ11661 fis, clone HEMBA100	3.5
	434317	A1674095	Hs.116323	ESTs	3.5
	414741	R51321	Hs.25780	Homo sapiens cDNA FLJ12252 fis, clone MAMMA10	3.5
	439707	AW297702	Hs.102915	ESTs	3.5
	443178	A1631241	Hs.47312	ESTs	3.5
10	400397	AJ270770	Hs.154485	transcription factor 7-like 2 (T-cell specific, HMG-box)	3.5
	455887	BE154173		gb:PM1-HT0340-201299-004-F12 HT0340 Homo sapie	3.5
	434362	W27081	Hs.295446	ESTs	3.5
	409211	AA078835		gb:zmm94h04.s1 Stratagene colon HT29 (937221) Homo	3.5
	414390	BE281040		gb:601156234F1 NIH_MGC_21 Homo sapiens cDNA	3.5
15	457142	A1924353	Hs.290969	EST	3.5
	423006	U29700	Hs.123014	anti-Mullerian hormone receptor, type II	3.5
	453363	A1989776	Hs.232623	ESTs	3.5
	418913	BE046745		gb:hn35b06.x1 NCI_CGAP_RDF2 Homo sapiens cDN	3.4
	440016	AW118114	Hs.137057	ESTs	3.4
20	405096			predicted exon	3.4
	435072	AW592176	Hs.116932	ESTs	3.4
	438535	L09078		gb:Homo sapiens mRNA fragment	3.4
	424001	W67883	Hs.137476	KIAA1051 protein	3.4
	428361	NM_015905	Hs.183858	transcriptional intermediary factor 1	3.4
25	410587	AA370706	Hs.11252	ESTs, Weakly similar to Weak similarity with the Ysy6	3.4
	454543	AW806895		gb:QV4-ST0023-160400-172-c06 ST0023 Homo sapien	3.4
	419515	S81944	Hs.90791	gamma-aminobutyric acid (GABA) A receptor, alpha 6	3.4
	410280	AA083558	Hs.261286	ESTs	3.4
	425714	AW963278		gb:EST375351 MAGE resequences, MAGH Homo sap	3.4
30	416895	AW961600		gb:EST373672 MAGE resequences, MAGG Homo sap	3.4
	427935	AW503587	Hs.119424	ESTs, Weakly similar to unnamed protein product [Hsa	3.4
	411673	BE064863		gb:RC1-BT0313-110300-015-f06 BT0313 Homo sapien	3.4
	453339	AW992599	Hs.252797	ESTs	3.4
	424898	BE439547	Hs.151903	Homo sapiens clone 24706 mRNA sequence	3.4
35	436242	AK002187		gb:Homo sapiens cDNA FLJ11325 fis, clone PLACE10	3.4
	442837	AJ022082	Hs.50492	ESTs	3.4
	452807	AA028933	Hs.162434	ESTs	3.4
	418110	R43523	Hs.217754	Homo sapiens cDNA: FLJ22202 fis, clone HRC01333	3.4
	433936	AJ208072	Hs.123459	ESTs	3.4
40	458177	AJ744995	Hs.267072	ESTs, Moderately similar to ALU4_HUMAN ALU SU	3.4
	401898			predicted exon	3.4
	406237			predicted exon	3.4
	457688	AL110157	Hs.3843	Homo sapiens mRNA; cDNA DKFZp586F2224 (from	3.4
	456914	AW363582	Hs.75323	prohibitin	3.4
45	421916	R34441	Hs.101007	Homo sapiens cDNA: FLJ23546 fis, clone LNG08361	3.4
	419321	N48146	Hs.269069	ESTs	3.4
	447876	AV654978	Hs.19904	cystathionase (cystathionine gamma-lyase)	3.4
	406197			predicted exon	3.4
	443005	AJ027184	Hs.200918	ESTs	3.4
50	450078	AJ681743		gb:tx38g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA	3.4
	431301	AA502384	Hs.151529	ESTs	3.4
	430202	T85775		gb:yd50g02.r1 Soares fetal liver spleen 1NFLS Homo s	3.4
	428659	H24338	Hs.27041	ESTs	3.4
	455731	BE072188		gb:QV4-BT0536-211299-055-b09 BT0536 Homo sapie	3.4
55	420735	AW297440	Hs.88653	ESTs	3.4
	430881	NM_000809	Hs.248112	gamma-aminobutyric acid (GABA) A receptor, alpha 4	3.3
	405836			predicted exon	3.3
	449178	AJ633748	Hs.197597	ESTs	3.3
	453265	U61232	Hs.32675	tubulin-specific chaperone c	3.3
60	430700	AA768902	Hs.247812	H2A histone family, member K, pseudogene	3.3
	424498	A1733451	Hs.129212	ESTs	3.3
	446963	A1862668	Hs.176333	ESTs	3.3
	422879	AJ241409	Hs.188092	ESTs	3.3
	419831	AW448930	Hs.5415	ESTs	3.3
65	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_1NFLS_S1 H	3.3
	406255			predicted exon	3.3
	412319	AW936903		gb:RC1-DT0029-030200-012-d02 DT0029 Homo sapie	3.3
	401350			predicted exon	3.3
	439098	AF085955		gb:Homo sapiens full length insert cDNA clone YR86G	3.3
70	450589	AJ701505	Hs.202526	ESTs	3.3
	430749	AJ242958	Hs.25960	v-myc avian myelocytomatosis viral related oncogene, n	3.3
	430689	A1695595	Hs.293219	ESTs	3.3
	454753	AW818212		gb:CM1-ST0283-071299-061-c07 ST0283 Homo sapie	3.3
	444479	AA194980	Hs.30818	Homo sapiens cDNA FLJ13681 fis, clone PLACE20000	3.3
75	413516	BE145907		gb:MRO-HT0208-221299-204-e12 HT0208 Homo sapie	3.3
	425541	AA359119		gb:EST68172 Fetal lung II Homo sapiens cDNA 5' end,	3.3
	457107	AA418246	Hs.185796	ESTs, Weakly similar to b3418.1 [H.sapiens]	3.3
	421480	NM_016158	Hs.104671	erythrocyte transmembrane protein	3.3
	444289	BE267060	Hs.76391	myxovirus (influenza) resistance 1, homolog of murine	3.3
80	417725	R25257	Hs.21503	ESTs	3.3
	453631	AL046418		gb:DKFZp434N247_r1 434 (synonym: htes3) Homo sa	3.3
	450692	H50603	Hs.94037	hypothetical protein FLJ23053	3.3
	413357	W47611		gb:z35e06.r1 Soares_senescent_fibroblasts_NbHSF H	3.3
	415327	H22769	Hs.1861	membrane protein, palmitoylated 1 (55kD)	3.3
	457569	AW970021	Hs.291120	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFA	3.3

	448601	R61666	Hs.293690	ESTs	3.3
	436526	AW993633	Hs.287681	Homo sapiens cDNA: FLJ21685 fis, clone COL09372	3.3
	440589	BE397763	Hs.194478	Homo sapiens mRNA; cDNA DKFZp434O1572 (from	3.3
	418768	T39310	Hs.1139	cold shock domain protein A	3.3
5	426768	AW303337	Hs.270411	ESTs	3.3
	400394	AF040257	Hs.283818	Homo sapiens TNF receptor homolog mRNA, partial cd	3.3
	433565	AA599763	Hs.112520	ESTs	3.3
	424093	AA335025		gb:EST39621 Eplididymus Homo sapiens cDNA 5' end,	3.3
	449552	AA001742	Hs.83722	ESTs	3.3
10	431892	AA521315	Hs.194424	ESTs	3.3
	405512			predicted exon	3.3
	446990	AJ354717	Hs.223908	ESTs	3.3
	457729	AJ821863	Hs.293467	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFA	3.2
	417333	AL157645	Hs.42179	bromodomain and PHD finger containing, 3	3.2
15	456420	AW401361	Hs.91773	protein phosphatase 2 (formerly 2A), catalytic subunit,	3.2
	403497			predicted exon	3.2
	427145	R52635	Hs.25935	ESTs	3.2
	406454			predicted exon	3.2
20	441033	BE562555		gb:601335867F1 NIH_MGC_44 Homo sapiens cDNA	3.2
	408444	AW661839	Hs.253204	ESTs	3.2
	434739	AA804487	Hs.144130	ESTs	3.2
	437060	AA745591	Hs.292063	ESTs	3.2
	423092	BE274837	Hs.123637	putative homeodomain transcription factor	3.2
	424695	U58331	Hs.151899	sarcoglycan, delta (35kD dystrophin-associated glycopr	3.2
25	443362	AJ053464	Hs.166505	ESTs	3.2
	437500	AL390150		gb:Homo sapiens mRNA; cDNA DKFZp547L156 (from	3.2
	425458	H89317	Hs.182889	ESTs	3.2
	439171	AA831133	Hs.294128	ESTs	3.2
30	407647	AW860158		gb:RC0-CT0379-290100-032-b04 CT0379 Homo sapie	3.2
	435608	AW183971	Hs.250896	ESTs	3.2
	426743	AA383833	Hs.245022	ESTs	3.2
	457525	AW973800		gb:EST385901 IMAGE resequences, MAGM Homo sap	3.2
	413800	AJ129238	Hs.192235	ESTs	3.2
35	414193	BE260069		gb:601150954F1 NIH_MGC_19 Homo sapiens cDNA	3.2
	455565	BE000537		gb:RC3-BN0072-240200-011-d07 BN0072 Homo sapie	3.2
	410061	T91029	Hs.15069	ESTs	3.2
	450666	T99968	Hs.18799	ESTs	3.2
	458529	AV652120	Hs.213232	ESTs	3.2
40	424751	AA769482	Hs.296320	ESTs	3.2
	442225	AJ306597	Hs.129192	ESTs	3.2
	410990	AW812929		gb:RC3-ST0186-250200-018-c05 ST0186 Homo sapien	3.2
	435644	AA700867	Hs.269659	ESTs	3.2
	405347			predicted exon	3.2
45	441202	AI632143	Hs.135853	ESTs	3.2
	446694	AV659942	Hs.258132	ESTs	3.2
	454652	AW812088		gb:RC4-ST0173-191099-032-a07 ST0173 Homo sapien	3.2
	418985	AJ042330	Hs.87128	ESTs, Weakly similar to similar to YBS4 YEAST [C.cl	3.2
	430118	AJ377255	Hs.183287	ESTs	3.2
50	430691	C14187	Hs.103538	ESTs	3.2
	416313	H47208	Hs.194109	ESTs, Weakly similar to ALUB_HUMAN IIII ALU CL	3.2
	446122	AJ362790	Hs.181801	ESTs	3.2
	453725	W28543		gb:48c5 Human retina cDNA randomly primed sublibra	3.2
	453954	AW118336	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding protein 1	3.2
55	428168	AA423849	Hs.79530	MS-14 protein	3.2
	447506	R78778	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone CAS05917	3.2
	401871			predicted exon	3.2
	442160	AI337127	Hs.156325	ESTs	3.2
	404708			predicted exon	3.1
60	412588	AW993055	Hs.44024	ESTs	3.1
	431976	AA719001	Hs.291065	ESTs	3.1
	408884	AW891024	Hs.281172	ESTs	3.1
	433811	AW975015	Hs.123138	ESTs	3.1
	431691	AI208511	Hs.292510	ESTs	3.1
65	418719	AW975590	Hs.161707	ESTs	3.1
	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721 67 PRO1777 [H	3.1
	435699	AI911488	Hs.213724	ESTs	3.1
	459344	AW499533	Hs.257976	ESTs	3.1
	431729	AW004714	Hs.162033	ESTs	3.1
70	436771	AW975587	Hs.292979	ESTs	3.1
	434480	AW956268	Hs.59395	Homo sapiens clone IMAGE:112574 mRNA sequence	3.1
	459547	AI400579	Hs.225186	EST	3.1
	427962	AA946582	Hs.133546	Homo sapiens cDNA: FLJ21120 fis, clone CAS05691	3.1
	403743			predicted exon	3.1
75	413560	BE148411		gb:MRD-HT0241-131299-002-F04 HT0241 Homo sapie	3.1
	454372	H96643	Hs.283565	FOS-like antigen-1	3.1
	450018	AA421642	Hs.24309	hypothetical protein FLJ111106	3.1
	428839	AI767756	Hs.82302	ESTs	3.1
	407110	AA018042	Hs.95078	ESTs	3.1
80	436133	T77531	Hs.191124	ESTs	3.1
	418872	R94785	Hs.270263	ESTs	3.1
	404418			predicted exon	3.1
	446877	AI559472	Hs.270720	ESTs	3.1
	429053	AA443967	Hs.194114	ESTs	3.1
	425189	H16622		gb:ym26c07.r1 Soares infant brain 1N18 Homo sapiens	3.1

	404134			predicted exon	3.1
	441404	AI638880	Hs.126895	ESTs	3.1
	400078			predicted exon	3.1
5	411876	AW961336	Hs.69705	ESTs, Weakly similar to KIAA0443 [Hsapiens]	3.1
	451048	AA013349	Hs.60602	ESTs	3.1
	447021	AI356564	Hs.161406	ESTs	3.1
	404083			predicted exon	3.0
	415833	H05175	Hs.107510	ESTs	3.0
10	402142			predicted exon	3.0
	415820	R53720	Hs.189745	ESTs	3.0
	441140	AW016534	Hs.226994	ESTs	3.0
	449376	AA001278	Hs.59905	ESTs	3.0
	457593	AI738815	Hs.117323	ESTs	3.0
15	411542	AW850767		gb:IL3-CT0220-031199-025-A05 CT0220 Homo sapien	3.0
	403375			predicted exon	3.0
	449561	AI022240	Hs.17924	ESTs	3.0
	406241			predicted exon	3.0
	420306	AA258318	Hs.219228	ESTs	3.0
20	413161	BE068130		gb:CM2-BT0368-171299-056-a01 BT0368 Homo sapie	3.0
	448221	BE522615		gb:601440775T1 NIH_MGC_72 Homo sapiens cDNA	3.0
	415920	Z45684		gb:HSC2RD121 normalized infant brain cDNA Homo	3.0
	459135	AI902802		gb:RC-BT015-311298-026 BT015 Homo sapiens cDNA	3.0
	425357	AA355842		gb:EST64303 Jurkat T-cells VI Homo sapiens cDNA 5'	3.0
25	454724	AA091228		gb:ccnh2152.seq.F Human fetal heart, Lambda ZAP Ex	3.0
	428395	AK002071	Hs.201624	hypothetical protein FLJ11209	3.0
	427607	AA406119	Hs.270479	ESTs	3.0
	443598	AW499970	Hs.14822	ESTs	3.0
	437948	AA772920		gb:ca73c09.s1 Stratagene schizo brain S11 Homo sapien	3.0
30	418105	AW937488	Hs.178000	ESTs	3.0
	426763	AL042262	Hs.172101	Human DNA sequence from clone RP1-202121 on chro	3.0
	403473			predicted exon	3.0
	427501	AI369280	Hs.131743	ESTs	3.0
	453246	NM_000933	Hs.32539	KIAA1264 protein	3.0
35	404587	M99587	Hs.104134	homeo box (H6 family) 1	3.0
	433964	AW241987	Hs.197025	ESTs	3.0
	453472	AL037925		gb:DKFZp564M037_r1 564 (synonym: hibr2) Homo sa	3.0
	433183	AF231338	Hs.222024	transcription factor BMAL2	3.0
	435899	W89093	Hs.189914	ESTs	3.0
40	425626	AI537538	Hs.173519	ESTs	3.0
	428931	AA994979	Hs.98967	ATPase, H(+)-transporting, lysosomal, noncatalytic acc	3.0
	426593	AW958560		gb:EST370630 MAGE resequences, MAGE Homo sapl	3.0
	431899	AA521381	Hs.187726	ESTs	3.0
	422405	AF025441	Hs.116206	Opa-interacting protein 5	3.0
45	448178	AI479482	Hs.170789	ESTs	3.0
	404227			predicted exon	3.0
	440575	AA889870	Hs.126006	ESTs	3.0
	431198	AL047634	Hs.231913	ESTs	3.0
	434221	AF119885	Hs.283040	hypothetical protein PRO2543	3.0
50	459459	AA460445		gb:z66h11.1 Soares_t0tal_tetus_Nb2HFB_9w Homo	3.0

TABLE 5B:

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

55	Pkey	CAT Number	Accession
	407596	1003489_1	R86913 R86901 H25352 R01370 H43764 AW044451 W21298
	407647	1007366_1	AW850158 AW862385 AW860159 AW862386 AW862341 AW821869 AW821893 AW062660 AW062656
60	408068	103649_1	AA046914 AA057231 H38371
	408315	1051132_1	AW179148 AW179150
	409211	110906_1	AA078835 AA079319 AA078816 AA079025 AA122167 AA111933 AA068989 AA084691 AA068999 AA069038 AA069225 AA650522
	409699	1149033_1	BE154650 BE154785 AW468343 BE154816 BE154667
	409846	1156150_1	AW501748 AW502972 AW502513
65	409854	1156229_1	AW501833 AW502145 AW502581
	409892	1157859_1	AW956113 AW503580
	410065	1174258_1	AW812744 AW581974 AW812725
	410454	1204164_1	AW749041 BE068025 H85202
	410495	1205826_1	N95428 W24040 AW751366 H81987
70	410596	121053_1	AA374186 AW963684 AA086107 AI491986
	410687	1214679_1	AW936099 AW936243 AW936097 BE162104 BE162109 AW794263
	410758	1219899_1	BE535988 AW801777
	410890	1226008_1	AW809575 BE090626 BE090617 AW936551 AW936552 AW936530 AW936550 AW936481
	410990	1226649_1	AW812929 AW812779 AW813088
75	411256	1236790_1	AW834039 AW834040 AW834047 AW845410 BE003128 AW852479
	411279	1237516_1	AW884776 AW935737 AW835261 AW835247 AW835263 AW835240 AW835258
	411280	1237585_1	N50617 N47321 R54159 AW860545 AW835317
	411337	1239217_1	AW837349 AW837355 AW882717
	411542	1249055_1	AW850767 AW851180 AW851359 AW851223 AW851360 AW851222 AW851108
80	411543	1249127_1	AW851248 AW851425 AW850805 AW851021 AW850905
	411673	1253737_1	BE064863 BE153698 AW856751 BE153820 BE064737 BE153674 BE064730 BE065062 BE153536 AW856622 BE155079 BE064651
			BE153665 BE064650 BE064691
	411899	126497_1	AA370573 BE160501 BE160500 BE160498 BE160502 BE160497 N72424 AA096462
	411922	1265825_1	AW876260 AW876269 AW876340 AW876146 AW876323 AW876320 AW876171 AW876421 AW876227 AW876243
	412319	1288602_1	AW936903 AW936907 AW936908 AW936914

412480	129929_1	BE142364 BE142341 AA112025
412732	1323951_1	AW993300 N23107 R22345
413137	1350383_1	BE066915 BE066942
413181	1351262_1	BE068130 BE068135 BE068134 BE068183 BE068184 BE068094
413247	135544_1	AW963969 AW963971 AA127651 AA376726
413357	1364165_1	W47611 BE087851
413516	1374595_1	BE145907 BE145796 BE145803 BE145851 BE145923 BE145812 BE145809 BE145852 BE145856
413560	1376621_1	BE148411 BE148415 H59098
414183	1424706_2	BE260069
414337	1436706_1	BE386606 BE275195 BE274984
414372	143909_1	AA143654 AW753140 AA213770 AW970865 AA569075 AA492132
414390	1441570_1	BE281040
415296	1533528_1	F05086 F05091 R17158
415618	1540651_1	F12854 H10624 R11948 R56523 T75190
415920	1561733_1	Z45684 H09361 R53285
416211	1576993_1	R14625 R17952 H29120 R14650
416238	1580451_1	W90448 H30749
416612	1603885_1	H70565 N77403 H67949
416624	1604694_1	H69044 T47567 H75691 T50292
416677	1608621_1	T83470 T84283 H74054
416895	162874_1	AW961600 AA190217 AA321260
417178	1655565_1	N51636 T51874 T51829
417762	169750_1	AA205976 AA205930
418913	180520_1	BE046745 A1074878 A1817476 AW572513 AA447586 H28330 AA232486 AA365704 BE271167
419401	184454_1	AW804663 AW805017 AA236969
419886	1886662_1	Z99362 Z99363
420352	192979_1	BE258835 AW968316 AA258918 AW843305 R14744 A1580388 BE071923 R36280
421418	202288_1	AA806639 AA291008 AA836274 AW978806
422046	210744_1	A1638562 T16929 H13401 F07773 R55836
422128	211994_1	AW881145 AA490718 M85637 AA304575 T06067 AA331991
423403	227942_1	AA325483 AW962169 AW962660
424093	235233_1	AA335025 AA335496 AW966145
424719	242889_1	H90452 AA345767 AW964302 H90399
425189	247825_1	H16622 R17322 AA351959
425357	250578_1	AA355842
425541	252945_1	AA359119 AW963014 D79884
425714	255333_1	AW963278 AA362266 AA362267
426294	263994_1	AA374185 AW956180 H38344
426528	268722_1	AA380828 AW963760 AA380805 AA380830
426593	269748_1	AW958560 AA382199 AW444933
430202	314322_1	T85775 AW968345 AA468998
430535	319643_1	AW968485 AW968670 AA480922 BE350425
431075	327638_1	BE267477 AA491488 AW836723
431492	333930_1	AW612343 AA922558 AA505925 AA927038 AW972537 A1693564
431828	338201_1	AA572994 AA516249 AA702595
432075	341066_1	AW972934 AA525260 AA525266 AA835021 BE000149 BE000148
432474	348197_1	AA584042 AW973273 AA548798
433371	364430_1	T25451 AA585296 AA585305
433403	36534_1	AF040247
433767	374014_1	AA609245 AA724581 AW241989 A377274 T47300
434738	392582_1	AA836265 AA648266 AW974440
436198	41562_1	AK001084 AA078092 AA829049
436242	41641_1	AK002187 R66351
436812	427323_1	AW298067 AA731845 AA810101 AW194180 A1690673 AW978773
437500	43772_1	AL390150 AW959182 AA358923
437948	445966_1	AA772920 D59870 D61151 A1591331
438224	452656_1	AA933999 AA781181
438535	45946_1	L09078 L03145 L09094 L09098 L03165 L09102
439098	46859_1	AF085955 H69158 H69081
439126	46887_1	AF085984 H95905 H95906
441033	50807_1	BE562555
443283	56492_1	BE568610
445597	644513_1	H65649 AW753545 A1244270
445832	651825_1	A1261545 N59134 AW875371 AW875247
448221	75534_1	BE622615
448527	766707_1	A1525606 BE549857
448732	77773_1	BE814063
449311	804513_1	A1657014 AW594035 A1657036 A1638390
449570	81018_1	AA001793 AA001871
450078	823882_1	A1681743 AW897287 AW897205 AW897284
452351	91233_1	AA025647 R45716 AW753785
452453	918300_1	A1902519 A1902518 A1902516
453472	968371_1	AL037925 AL037931 AL037957
453530	97021_1	AW021633 AA036730 A1866854
453831	975024_1	AL046418 N52738 R33840
453725	978760_1	W28543 AL119531
453752	979899_1	AL120800 BE378580
453823	982526_1	AL137967 BE064160 BE064186
454102	1011603_1	AW752363 BE147120 N22640
454487	1216101_1	AW796342 AW796356 BE161430
454543	1223775_1	AW806895 AW865476 AW866465 AW866535 AW866623
454564	1224407_1	AW807573 AW807566 AW807572
454573	1225624_1	BE146471 AW833743 AW833609 AW821469 AW821488 AW821541 AW821531 AW821513 AW821549 AW821384 AW821625 AW821577
		AW821547 AW834577

5	454652	1228071_1	AW812088 AW812105 AW812082
	454679	1228929_1	AW813110 AW813113
	454724	123128_1	AA091228 H71860 H71073
	454753	1233576_1	AW819212 AW819170 BE158474 AW819172 AW819213 AW819200 AW819256 AW819254 AW819178 AW819214 AW819215 AW819233
			AW819171
	454885	1238874_1	AW836922 AW876719 AW876688 AW836919 AW836997 AW836908 AW836912 AW836993
	454940	1245640_1	AW846202 AW846174 AW846532 AW846181 AW846458 AW846206 AW846432 AW846553 AW846533 AW846197 AW846198 AW846189
			AW846469 AW846530 AW846560 AW846536 AW846472 AW846470 AW846466 AW846192 AW846479 AW846260 AW846204 AW846139
			AW846187 AW846353 AW846462 AW846151 AW846549 AW846538 AW846527 AW846567 AW846531
10	454994	1248637_1	AW850176 AW850513 AW850412 AW850451
	455056	1250934_1	AW853057 AW853039 AW853042 AW853050 AW853114 AW853105 AW853102 AW853111 AW853121 AW853109 AW853126
	455087	1252050_1	AW854538 AW854418 AW854412
	455108	1253916_1	AW856866 AW856858 AW856856
	455387	1287871_1	BE069037 AW936025 BE069178 AW936034
15	455388	1287804_1	AW936234 AW936074 AW936181 AW936179 AW936217 AW936077 AW936227 AW936191
	455534	1322942_1	AW931925 AW991919
	455565	1329591_1	BE000537 BE180584 BE180540 BE180542 BE180546
	455731	1353872_1	BE072188 BE072299 BE072269 BE072317 BE072238
	455786	1365510_1	BE090077 BE090079
20	455790	1365950_1	BE090690 BE090688 BE090681 BE090693 BE090675
	455887	1380836_1	BE154173 BE154098 BE154098
	455895	1381386_1	BE154837 BE154879 BE154850 BE154877 BE154835 BE154849 BE154902 BE154905 BE154867 BE154901 BE154904 BE154899
	456253	1699178_1	T12188 T19584 T11583 R15526 R15585 R45876 R15562
25	456383	184252_1	A1148037 AA287178 AA236756
	456388	1842839_1	W28557
	457525	351732_1	AW973800 AA557589 AA559888
	457740	39528_1	AW500458 AW160900 AF161382 AF150327 AW576393 AW360921 AW360920 AW360902 AW360890 AW732529
	458301	543058_1	AF003834 W36292
30	459135	918516_1	A1902802 A1902783 A1902800
	459157	919804_2	A1904385 A1904382

TABLE 5C:

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495

Strand: Indicates DNA strand from which exons were predicted

NL_position: Indicates nucleotide positions of predicted exons

40	Pkey	Ref	Strand	NL_position
	400942	7656749	Minus	91593-91757,92720-92843,93962-94079,94824-94997
	401004	7229982	Plus	62580-62772
	401287	9801612	Minus	42287-42431
	401308	9212516	Plus	169019-169649
45	401350	9931226	Plus	14471-14623
	401740	2982169	Plus	148357-148484,148591-148690
	401871	8079355	Minus	58158-59585
	401896	8569194	Plus	115129-115294
	401963	3126783	Plus	51382-51521
50	402105	8131588	Minus	22856-24055
	402109	8131678	Minus	171722-171859,173197-173303
	402142	7704985	Minus	29932-30698
	402451	9796677	Minus	48137-48343
	402867	6596716	Plus	52806-53108,53500-53818
55	403277	8072597	Minus	27494-27642
	403283	8076905	Minus	71124-71996
	403375	9255944	Minus	92554-92795
	403473	9945095	Minus	54241-54437
	403497	6067111	Plus	7221-7441
60	403531	8076842	Minus	75903-76134
	403635	6862664	Minus	157028-157145,161725-161900
	403714	7210030	Minus	145556-145873
	403743	7652003	Minus	136463-136646
	404020	8655966	Minus	174449-174663
65	404041	8886967	Minus	1334-1503,2483-2585,5230-5337,19656-19804
	404044	9558573	Minus	225757-225939
	404083	9944029	Minus	16650-17082
	404108	8247074	Minus	63603-64942
	404134	6981900	Minus	40633-40911
70	404227	7838233	Minus	93110-93259
	404418	7382420	Minus	153339-153481,155099-155294
	404451	7638438	Minus	105191-105622
	404582	9739220	Plus	53230-53424
	404708	9800828	Plus	77522-77658
	404868	9454593	Plus	39954-40430
75	405096	8072599	Plus	140844-140897,148510-148581
	405290	3900849	Minus	79582-79765
	405347	2979602	Minus	977-1116
	405512	9454624	Plus	17802-17966,18573-18697
80	405549	1552494	Plus	10878-11048
	405583	4512287	Plus	56211-56353
	405671	2565031	Plus	25805-26923
	405717	9588573	Plus	11275-11973
	405752	9212305	Plus	91392-91528
	405836	5686282	Minus	5031-5217

5	406122	9144087	Minus	30940-31386
	406197	7289992	Minus	47520-47961
	406237	7417725	Plus	30032-30501
	406241	7417725	Minus	34951-35752
	406255	7417729	Plus	2959-3200
	406364	9256114	Minus	50715-50833
	406454	9583380	Minus	91746-91958
	406481	9864741	Minus	91439-91579
10	406562	7711584	Plus	37316-37426
	406605	8272666	Minus	23275-23493,23723-23903

TABLE 6A lists about 68 genes highly down-regulated in ovarian cancer compared to normal ovaries. These were selected as for Table 5A, except the "average" ovarian cancer level was set to the maximum value amongst various ovarian cancers and the "average" normal ovary level was set to the minimum value from various non-malignant ovary specimens, and the ratio was greater than or equal to 2.5 (i.e. 2.5-fold down-regulated in the highest tumor vs. the lowest normal ovary). This has the overall effect of increasing stringency, and reducing the number of false-positives.

TABLE 6A: ABOUT 68 HIGHLY DOWN-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY

Key: Primekey

Ex. Acct. Exemplar Accession

UG ID: UniGene ID

Title: UniGene Title

ratio: ratio of normal ovary vs. tumor

	Key	Ex. Acct.	UG ID	Title	ratio
	424851	AA576441	Hs.119059	ESTs	7.9
	437690	AA804362	Hs.180544	ESTs	4.7
	433682	AA642418	Hs.17381	ESTs	4.1
	407437	AF220284		gb:Homo sapiens MOST-1 mRNA, complete cds.	4.1
30	437787	AI908263	Hs.291625	ESTs	4.0
	453282	AK000043	Hs.32922	hypothetical protein FLJ20036	4.0
	440987	AA911705	Hs.130229	ESTs	3.8
	443131	AI033833	Hs.132689	ESTs	3.8
	431075	BE267477		gb:601189542F2 NIH_MGC_7 Homo sapiens cDNA clo	3.6
35	412637	AA115097	Hs.261313	ESTs	3.6
	408141	U69205	Hs.45152	ESTs, Moderately similar to neurogenic basic-helix-loop	3.5
	420122	AA255714	Hs.284153	Fanconi anemia, complementation group A	3.5
	430653	AW902062	Hs.30280	ESTs	3.4
	401308			predicted exon	3.4
40	410758	BE535988		gb:601062418F1 NIH_MGC_10 Homo sapiens cDNA c	3.4
	421418	AA806639		gb:cb88g05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA	3.4
	450061	AI797034	Hs.201115	ESTs	3.3
	409725	T40760	Hs.90459	EST	3.3
	434738	AA836265		gb:6017e02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA	3.3
45	431644	AW972822	Hs.169248	cytochrome c	3.3
	450938	AW753734	Hs.277215	ESTs	3.2
	420497	AW206285	Hs.253548	ESTs	3.2
	439428	AI131502	Hs.143135	ESTs, Weakly similar to FAFY_HUMAN PROBABLE C	3.2
	407596	R86913		gb:cy30f05.r1 Soares fetal liver spleen 1NLS Homo sap	3.2
50	448683	AA167642	Hs.14632	ESTs	3.2
	431982	AW419296	Hs.105754	ESTs	3.1
	452320	AA042873	Hs.160412	ESTs	3.1
	419401	AW804663		gb:QV4-UM0094-160300-135-d06 UM0094 Homo sapien	3.1
	402105			predicted exon	3.1
55	444997	AI204451	Hs.146196	ESTs	3.1
	403283			predicted exon	3.0
	455388	AW936234		gb:QV0-DT0020-090200-106-g05 DT0020 Homo sapie	3.0
	428559	H24338	Hs.27041	ESTs	2.9
60	419002	T78625	Hs.268594	ESTs	2.9
	404868			predicted exon	2.9
	409090	W56067	Hs.103105	ESTs	2.9
	406605			predicted exon	2.9
	441202	AI632143	Hs.135853	ESTs	2.8
65	422046	AI638562		gb:ts50a10.x1 NCI_CGAP_Ut1 Homo sapiens cDNA cl	2.8
	442865	N57659	Hs.114541	ESTs, Weakly similar to neuronal thread protein AD7c-N	2.8
	444431	AW513324	Hs.42280	ESTs	2.8
	426294	AA374185		gb:EST86289.HSC172 cells 1 Homo sapiens cDNA 5' en	2.8
	412480	BE142364		gb:CMO-HT0143-270999-062-d12 HT0143 Homo sapie	2.8
70	449858	AW205979	Hs.196065	ESTs	2.8
	401464	AF039241	Hs.9028	histone deacetylase 5	2.7
	439126	AF085984		gb:Homo sapiens full length insert cDNA clone YT99F0	2.7
	403277			predicted exon	2.7
	450078	AI681743		gb:cb38g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA	2.7
75	458090	AI282149	Hs.56213	ESTs, Highly similar to FXD3_HUMAN FORKHEAD D	2.7
	420620	AA278807	Hs.173343	ESTs	2.7
	459054	AW798466	Hs.82396	2,5-oligoadenylate synthetase 1	2.6
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cys-X-Cys), mem	2.6
	454338	AW381251	Hs.1050	pleckstrin homology, Sec7 and coiled-coil domains 1(cyt	2.6
	454529	Z45439	Hs.270425	ESTs	2.6
80	446877	AI559472	Hs.270720	ESTs	2.6
	412588	AW993055	Hs.44024	ESTs	2.6
	449862	AI672277	Hs.199475	ESTs	2.6
	446694	AV659942	Hs.258132	ESTs	2.6
	424029	AB014594	Hs.137579	KIAA0694 gene product	2.6

454102	AW752363		gb:RC0-CT0201-270999-011-f03 CT0201 Homo sapien	2.6
430922	AW373747	Hs.183337	ESTs	2.6
420289	N55394	Hs.96398	8-oxoguanine DNA glycosylase	2.6
410495	N95428		gb:zb80d09.s1 Soares_senescent_fibroblasts_NbHSF Ho	2.5
412319	AW936903		gb:RC1-DT0029-030200-012-d02 DT0029 Homo sapien	2.5
409699	BE154650		gb:PM3-HT0344-071299-003-c08 HT0344 Homo sapien	2.5
445832	AI261545		gb:xq230s07.x1 NCL_CGAP_K0d11 Homo sapiens cDNA	2.5
429755	NM_001364	Hs.215839	discs, large (Drosophila) homolog 2 (chapsyn-110)	2.5
445755	AW294870	Hs.223672	ESTs	2.5

TABLE 6B:

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey	CAT Number	Accession
407596	1003489_1	R86913 R86901 H25352 R01370 H43764 AW044451 W21298
409699	1149033_1	BE154650 BE154785 AW468343 BE154816 BE154657
410495	1205826_1	N95428 W24040 AW751366 H81987
410758	1219899_1	BE535988 AW801777
412319	1288602_1	AW936903 AW936907 AW936908 AW936914
412480	129929_1	BE142364 BE142341 AA112025
419401	184454_1	AW804663 AW805017 AA236969
421418	202288_1	AA806539 AA291008 AA836274 AW978806
422046	210744_1	AJ638562 T16929 H13401 F07773 R55836
426294	263994_1	AA374185 AW856180 H38344
431075	327638_1	BE267477 AA491488 AW836723
434738	392562_1	AA836265 AA648266 AW974440
439126	46887_1	AF085984 H95905 H95906
445832	651925_1	AJ261545 N59134 AW875371 AW875247
450078	823882_1	AI681743 AW897287 AW897205 AW897284
454102	1011603_1	AW752363 BE147120 N22640
455388	1287904_1	AW936234 AW936074 AW936181 AW936179 AW936217 AW936077 AW936227 AW936191

TABLE 6C:

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495

Strand: Indicates DNA strand from which exons were predicted

N1_position: Indicates nucleotide positions of predicted exons

401308	9212516	Plus	169019-169649
402105	8131588	Minus	22856-24055
403277	8072597	Minus	27494-27642
403283	8076905	Minus	71124-71996
404868	9454593	Plus	39954-40430
406605	8272666	Minus	23275-23493,23723-23903

Table 7A lists about 770 genes up-regulated in ovarian cancer compared to normal adult tissues. These were selected from 35403 probesets on the Affymetrix/Eos-Hu01 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" ovarian cancer level was set to the 2nd highest amongst various ovarian cancers. The "average" normal adult tissue level was set to the 7th highest amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 7A: ABOUT 770 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES

Pkey: Primekey

Ex. Accn: Exemplar Accession

UG ID: UniGene ID

Title: UniGene Title

ratio: ratio tumor vs. normal tissues

Pkey	Ex. Accn	UG ID	Title	ratio
109680	F09255	Hs.4993	ESTs	23.2
119743	W70242	Hs.58086	ESTs	22.0
132528	AA283006	Hs.50758	chromosome-associated polypeptide C	22.0
129571	XS1630	Hs.1145	Wilms tumor 1	20.0
102151	U17280	Hs.3132	steroidogenic acute regulatory protein	19.6
130941	D49394	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3A	17.5
132624	AA164819	Hs.53631	ESTs	15.9
102610	U65011	Hs.30743	preferentially expressed antigen in melanoma	15.4
101249	L33881	Hs.1904	protein kinase C, iota	14.5
122802	AA460530	Hs.256579	ESTs	14.5
135242	M74093	Hs.9700	cyclin E1	13.8
101804	M86699	Hs.169840	TTK protein kinase	12.2
123005	AA479726	Hs.105577	ESTs	12.0
114965	AA250737	Hs.72472	ESTs	11.5
115536	AA347193	Hs.62180	ESTs	11.4
132191	AA449431	Hs.158688	KIAA0741 gene product	10.9
121853	AA425887	Hs.98502	ESTs	10.9
115881	AA435577	Hs.184942	G protein-coupled receptor 64	10.8
119780	W72867	Hs.191381	ESTs; Weakly similar to hypothetical protein	10.5
104301	D45332	Hs.6783	ESTs	10.3
132632	N59764	Hs.5398	guanine-monomophosphate synthetase	10.1

5	105298	AA233459	Hs.26369	ESTs	9.7
	108857	AA133250	Hs.62180	ESTs	9.1
	113168	T53592	Hs.161586	EST	9.0
	115892	AA435946	Hs.50831	ESTs	8.9
	125668	AA199856	Hs.118811	ESTs	8.9
	102200	U21551	Hs.157205	branched chain aminotransferase 1; cytosolic	8.8
	108055	AA043562	Hs.62637	ESTs	8.6
	132572	AA448287	Hs.237825	signal recognition particle 72kD	8.6
10	115909	AA436666	Hs.59761	ESTs	8.5
	109166	AA179845	Hs.73625	RAB6 Interacting; kinesin-like (rabkinesin6)	8.3
	121779	AA422036	Hs.98367	ESTs	8.3
	102915	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin 2)	8.0
	105317	AA233928	Hs.23635	ESTs	7.8
	125250	W87465	Hs.222926	ESTs; Weakly similar to D2092.2 [C.elegans]	7.8
15	126960	AA317900	Hs.161756	ESTs	7.8
	122969	AA478539	Hs.104336	ESTs	7.7
	130376	R40873	Hs.155174	KIAA0432 gene product	7.7
	123339	AA504253	Hs.101515	ESTs	7.7
20	134972	M19720	Hs.169252	Human L-myc protein gene; complete cds	7.6
	111234	N69287	Hs.21943	ESTs; Weakly similar to ORF YGL221c [S.cerevi]	7.5
	123689	AA609556	Hs.256562	ESTs	7.5
	123494	AA599786	Hs.112110	ESTs	7.4
	131985	AA434329	Hs.36563	ESTs	7.4
25	108738	AA470145	Hs.25130	ESTs	7.4
	108768	AA127741	Hs.61345	ESTs	7.3
	106474	AA450212	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (from cl	7.2
	123308	AA496211	Hs.103638	ESTs	7.2
	106124	AA423987	Hs.7567	ESTs	7.2
30	111345	N89820	Hs.14559	ESTs	7.1
	105200	AA195399	Hs.24641	ESTs	7.1
	116416	AA609219	Hs.39982	ESTs	7.1
	118846	N80567	Hs.50895	ESTs	7.1
	133434	AA278852	Hs.250786	ESTs	7.1
35	120472	AA251875	Hs.104472	ESTs; Weakly similar to Gag-Pol polyprotein [6.9
	115291	AA279943	Hs.122579	ESTs	6.9
	111185	N67551	Hs.12844	EGF-like-domain; multiple 6	6.9
	108778	AA128548	Hs.90847	general transcription factor IIIc; polypeptid	6.9
	132939	U76189	Hs.61152	exostoses (multiple)-like 2	6.9
40	134520	N21407	Hs.257325	ESTs	6.9
	114724	AA131701	Hs.256287	ESTs; Highly similar to SPERM SURFACE PROTEIN	6.8
	116296	AA489033	Hs.62601	Homo sapiens mRNA; cDNA DKFZp586K1318 (from c	6.8
	102136	U15552	Hs.85769	acidic 82 kDa protein mRNA	6.7
	132725	L41887	Hs.184167	splicing factor; arginine/serine-rich 7 (35kD	6.6
45	109648	F04600	Hs.7154	ESTs	6.4
	116401	AA599963	Hs.59698	ESTs	6.4
	127563	AJ367707	Hs.150587	ESTs	6.4
	104252	AF002246	Hs.210863	cell adhesion molecule with homology to L1CAM	6.4
	120438	AA243441	Hs.99488	ESTs; Weakly similar to ORF YKR074w [S.cerevi]	6.2
50	131978	D80008	Hs.36232	KIAA0186 gene product	6.2
	134621	L02547	Hs.172865	cleavage stimulation factor; 3' pre-RNA; subu	6.2
	120571	AA280738	Hs.128679	ESTs	6.2
	102627	U66561	Hs.158174	zinc finger protein 184 (Kruppel-like)	6.1
	100681	HG2874-HT3018		Ribosomal Protein L39 Homolog	6.1
55	118204	N59859	Hs.48443	ESTs	6.0
	131386	AA096412	Hs.173135	dual-specificity tyrosine-(Y)-phosphorylation	6.0
	129097	S50223		HKR-T1=Kruppel-like zinc finger protein [huma	5.9
	131228	AA279157	Hs.24485	chondroitin sulfate proteoglycan 6 (barnacan)	5.9
	106369	AA443828	Hs.25324	ESTs	5.9
60	108255	AA063157	Hs.172608	ESTs	5.8
	125370	AA256743	Hs.151791	KIAA0092 gene product	5.8
	130010	N52966	Hs.142838	ESTs	5.8
	131945	M87339	Hs.35120	replication factor C (activator 1) 4 (37kD)	5.7
	116238	AA479362	Hs.47144	DKFZP586N0819 protein	5.7
65	102221	U24576		LIM domain only 4	5.6
	130757	R00641	Hs.18925	ESTs; Weakly similar to cDNA EST yk339a7.5 co	5.6
	131278	U81523	Hs.25185	endometrial bleeding associated factor (left-	5.6
	101383	M14113	Hs.79345	coagulation factor VIIIc; procoagulant compon	5.5
	131836	AA610086	Hs.32990	DKFZP566F084 protein	5.5
70	129628	U26727	Hs.1174	cyclin-dependent kinase inhibitor 2A (melanom	5.5
	106523	AA453441	Hs.31511	ESTs	5.5
	111772	R28287	Hs.237146	ESTs	5.5
	101255	L34600	Hs.149894	mitochondrial translational initiation factor	5.5
	106895	AA489665	Hs.25245	ESTs	5.5
75	104943	AA065217	Hs.169674	ESTs	5.5
	129229	AA211941	Hs.109543	polyadenylate binding protein-interacting pro	5.4
	102305	U33286	Hs.90073	chromosome segregation 1 (yeast homolog)-like	5.4
	106553	AA454967	Hs.5887	ESTs; Highly similar to RNA binding motif pro	5.4
	112305	R54822	Hs.26244	ESTs	5.3
80	123972	C14782	Hs.70337	immunoglobulin superfamily; member 4	5.3
	102676	U72514	Hs.12045	putative protein	5.3
	106459	AA449741	Hs.4029	glioma-amplified sequence-41	5.2
	107865	AA025104	Hs.61252	ESTs	5.2
	121121	AA399371	Hs.189095	ESTs; Weakly similar to zinc finger protein S	5.2
	127162	N76398	Hs.21187	ESTs	5.2

	131648	AA171895	Hs.30057	Homo sapiens clone 24749 and 24750 mRNA seque	5.2
	121770	AA421714	Hs.11469	KIAA0895 protein	5.2
	122512	AA449311	Hs.98658	budding uninhibited by benzimidazoles 1 (yeas	5.1
5	105870	AA399623	Hs.23505	ESTs	5.1
	100341	D63508	Hs.8813	syntaxin binding protein 3	5.1
	116848	H65187	Hs.39001	ESTs	5.1
	120821	AA347419	Hs.96870	Homo sapiens mRNA full length insert cDNA clo	5.1
	130690	AA084286	Hs.139033	paternally expressed gene 3	5.1
10	122661	AA454936	Hs.245541	ESTs	5.1
	123169	AA488892	Hs.104472	ESTs; Weakly similar to Gag-Pol polyprotein [5.1
	108810	AA130596	Hs.71331	ESTs; Weakly similar to POTENT HEAT-STABLE PR	5.0
	110799	N26101	Hs.7838	Human ring zinc-finger protein (ZNF127-Xp) ge	5.0
	120619	AA284372	Hs.111471	ESTs	5.0
15	122792	AA460225	Hs.99519	ESTs	5.0
	129912	AA047344	Hs.107213	ESTs; Highly similar to NY-REN-6 antigen [Hs	5.0
	102823	U90914	Hs.5057	carboxypeptidase D	4.9
	129890	M13699	Hs.111461	ceruloplasmin (ferroxidase)	4.9
	101084	L05425		Homo sapiens autoantigen mRNA; complete cds	4.9
20	134859	D87716	Hs.90315	KIAA0007 protein	4.9
	115955	AA446121	Hs.44198	Homo sapiens BAC clone RG054D04 from 7q31	4.9
	105518	AA257971	Hs.21214	ESTs	4.9
	114932	AA242751	Hs.16218	KIAA0903 protein	4.9
	106672	AA481300	Hs.30643	ESTs	4.8
25	106126	AA424006	Hs.22972	ESTs; Moderately similar to H5AR [M.musculus]	4.8
	110695	H93463	Hs.124777	ESTs	4.8
	102025	U03911	Hs.78934	mutS (E. coli) homolog 2 (colon cancer; nonpo	4.8
	133292	U52960	Hs.250855	SRB7 (suppressor of RNA polymerase II; yeast)	4.8
	119708	W67810	Hs.57904	mago-nashi (Drosophila) homolog; proliferatio	4.7
30	120695	AA291468		ESTs	4.7
	128651	AA446990	Hs.103135	ESTs	4.7
	103152	X66533	Hs.77890	guanylate cyclase 1; soluble; beta 3	4.7
	108699	AA121514	Hs.70832	ESTs	4.7
	115094	AA255921	Hs.88095	ESTs	4.7
35	121429	AA406293	Hs.193498	ESTs	4.7
	123203	AA489671	Hs.89709	glutamate-cysteine ligase (gamma-glutamylcyst	4.7
	126802	AA947601	Hs.97056	ESTs	4.7
	130527	C17384	Hs.184227	F-box protein 21	4.7
40	134470	X54942	Hs.83758	CDC28 protein kinase 2	4.7
	100449	D87470	Hs.75400	KIAA0280 protein	4.7
	110970	N51374	Hs.96870	Homo sapiens mRNA full length insert cDNA clo	4.7
	115901	AA436403	Hs.86909	ESTs; Moderately similar to Frizzled-6 [H.sap	4.7
	109799	F10770	Hs.180378	Homo sapiens clone 669 unknown mRNA; complete	4.6
	116195	AA465148	Hs.72402	ESTs	4.6
45	132122	U65092	Hs.40403	Chp/p300-interacting transactivator; with Glu	4.6
	108990	AA152296	Hs.72045	ESTs	4.6
	109055	AA160529	Hs.48524	ESTs	4.6
	115937	AA443269	Hs.30991	KIAA0957 protein	4.6
	133520	X74331	Hs.74519	primase; polypeptide 2A (58kD)	4.6
50	131200	AA609427	Hs.210708	ESTs; Moderately similar to III ALU SUBFAMIL	4.6
	121369	AA405657	Hs.128791	Human DNA sequence from clone 967N21 on chrom	4.5
	132880	AA444369	Hs.177537	ESTs	4.5
	127386	AA457411	Hs.106728	ESTs	4.5
	120067	W93592	Hs.47343	ESTs	4.5
55	122986	AA479063	Hs.102947	ESTs	4.5
	135288	AA401269	Hs.97849	ESTs	4.5
	130155	L33404	Hs.151254	kalikrein 7 (chymotryptic; stratum comeum)	4.5
	106103	AA421104	Hs.12094	ESTs	4.5
	102654	U68494	Hs.24385	Human hbc647 mRNA sequence	4.4
60	107876	AA025315	Hs.61184	Novel human gene mapping to chromosome X	4.4
	109454	AA232255	Hs.46912	ESTs	4.4
	125960	D63307	Hs.145968	ESTs	4.4
	126892	AI160190	Hs.76127	hecl (homologous to the E6-AP (UBE3A) carboxy	4.4
	100269	D38550	Hs.1189	E2F transcription factor 3	4.4
65	134161	U97188	Hs.79440	IGF-II mRNA-binding protein 3	4.3
	100502	HG1496-HT1496		Adrenal-Specific Protein Pg2	4.3
	105542	AA261858	Hs.8241	ESTs; Weakly similar to heat shock protein hs	4.3
	109787	F10610	Hs.34853	inhibitor of DNA binding 4; dominant negative	4.3
	110759	N21671	Hs.19025	ESTs	4.3
70	129970	AA478975	Hs.200434	ESTs	4.3
	134666	AA482319	Hs.8752	putative type II membrane protein	4.3
	117693	N40939	Hs.44162	ESTs; Weakly similar to cDNA EST yk342h12.5 c	4.3
	111008	N53388	Hs.7222	ESTs	4.3
	120977	AA398155	Hs.97600	ESTs	4.2
75	105808	AA393808	Hs.21490	KIAA0438 gene product	4.2
	121381	AA405747	Hs.97865	ESTs; Weakly similar to WASP-family protein [4.2
	100893	HG4557-HT4962		Small Nuclear Ribonucleoprotein U1, 1snrp	4.2
	107176	AA621762	Hs.7576	ESTs	4.2
	118976	N93629	Hs.93391	ESTs	4.2
80	130703	N63295	Hs.18103	ESTs	4.2
	106540	AA454607	Hs.38114	ESTs; Weakly similar to coded for by C. elega	4.2
	119367	T78324	Hs.90905	ESTs	4.2
	133633	D21262	Hs.75337	nucleolar phosphoprotein p130	4.2
	105520	AA258068	Hs.33085	WD repeat domain 3	4.2
	114264	Z40074	Hs.27695	ESTs	4.1

5	131046	X02530	Hs.2248	IP10; 'small inducible cytokine subfamily B (4.1
	105220	AA210695	Hs.17212	ESTs	4.1
	103111	X53187	Hs.2719	epididymis-specific; whey-acidic protein type	4.1
	125640	R37700	Hs.208261	ESTs	4.1
	110581	H59617	Hs.5199	ESTs; Weakly similar to UBIQUITIN-CONJUGATING	4.1
	118092	N54915	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (from c	4.1
	134891	F03517	Hs.90787	ESTs	4.1
	112364	R59312	Hs.197642	ESTs; Weakly similar to DNA-DIRECTED RNA POLY	4.1
10	120699	AA291716	Hs.97258	ESTs	4.1
	106272	AA432074	Hs.32538	ESTs	4.1
	112041	R43300	Hs.22929	ESTs	4.1
	131689	AA599553	Hs.30698	transcription factor-like 5 (basic helix-loop	4.1
	116134	AA460246	Hs.50441	ESTs; Highly similar to CGI-04 protein [H.sapiens]	4.1
15	107638	AA009528	Hs.42743	ESTs; Weakly similar to predicted using Genef	4.0
	131941	D62657	Hs.35086	ubiquitin-specific protease 1	4.0
	106154	AA425304	Hs.6994	ESTs	4.0
	105546	AA262032	Hs.26089	ESTs; Weakly similar to 6ZD9.a [D.melanogaster]	4.0
	105319	AA436606	Hs.7392	ESTs; Weakly similar to Gu protein [H.sapiens]	4.0
20	121816	AA424814	Hs.187509	ESTs	4.0
	122851	AA463627	Hs.99598	ESTs	4.0
	123337	AA504163	Hs.132797	ESTs; Weakly similar to ORF YGL050w [S.cerevi]	4.0
	128643	N40212	Hs.102958	ESTs	4.0
	129011	S72869	Hs.107932	DNA segment; single copy; probe pH4 (transfor	4.0
25	130895	AA609828	Hs.21015	ESTs; Highly similar to tetracycline transpor	4.0
	132323	AA436102	Hs.256559	ESTs	4.0
	134255	J05032	Hs.80758	aspartyl-tRNA synthetase	4.0
	102827	U91327	Hs.6456	chaperonin containing TCP1; subunit 2 (beta)	4.0
	102123	U14518	Hs.1594	centromere protein A (17kD)	4.0
30	102813	U90651	Hs.151461	embryonic ectoderm development protein	3.9
	113970	W86748	Hs.8109	ESTs	3.9
	107145	AA621108	Hs.173001	ESTs	3.9
	114212	Z39338	Hs.21201	DKFZP566B0846 protein	3.9
35	106614	AA458934	Hs.179912	ESTs	3.9
	132742	AA490862	Hs.55901	ESTs; Weakly similar to C43H8.1 [C.elegans]	3.9
	120948	AA397822	Hs.104650	ESTs; Highly similar to similar to mago nashi	3.9
	129337	R63542	Hs.110488	KIAA0990 protein	3.9
	103835	AA172215	Hs.93748	ESTs; Moderately similar to TRANSCRIPTION FAC	3.9
	133330	U42360	Hs.71119	Putative prostate cancer tumor suppressor	3.9
40	133928	N34096	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homologou	3.9
	133640	D83004	Hs.75355	ubiquitin-conjugating enzyme E2N (homologous	3.9
	133350	AA135468	Hs.71573	ESTs	3.9
	115623	AA401475	Hs.39733	postsynaptic protein CRIP1	3.9
	101973	S82597	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polypeptid	3.9
45	102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	3.9
	134248	AA292677	Hs.80624	ESTs	3.9
	102380	U40434	Hs.155981	mesothelin	3.9
	116157	AA461063	Hs.44298	ESTs; Highly similar to HSPC011 [H.sapiens]	3.8
	106691	AA463453	Hs.23259	ESTs; Weakly similar to ACTIN; CYTOPLASMIC 2	3.8
50	115844	AA430124	Hs.234607	ESTs	3.8
	107159	AA621340	Hs.10600	ESTs; Weakly similar to ORF YKR081c [S.cerevi]	3.8
	106498	AA452141	Hs.7171	ESTs	3.8
	134405	J04177	Hs.82772	collagen; type XI; alpha 1	3.8
	106260	AA431448	Hs.5250	ESTs; Weakly similar to BACR37P7.g [D.melanog	3.8
55	109864	H02554	Hs.30323	ESTs	3.8
	124648	N91948	Hs.125034	ESTs	3.8
	134719	L07515	Hs.89232	chromobox homolog 5 (Drosophila HP1 alpha)	3.8
	113702	T97307	Hs.161720	ESTs; Moderately similar to !!! ALU SUBFAMIL	3.8
	128839	N91246	Hs.102897	ESTs	3.8
60	111299	N73808	Hs.24936	ESTs	3.7
	129351	AA167268	Hs.62349	Human ras inhibitor mRNA; 3' end	3.7
	119741	W70205	Hs.43670	kinesin family member 3A	3.7
	105012	AA116036	Hs.9329	chromosome 20 open reading frame 1	3.7
	128734	AA343629	Hs.104570	kallikrein 8 (neurosinovasin)	3.7
65	130567	L07493	Hs.1608	replication protein A3 (14kD)	3.7
	114253	Z39909	Hs.14831	ESTs	3.7
	103169	X68560	Hs.44450	Sp3 transcription factor	3.7
	111269	N70711	Hs.18885	ESTs; Highly similar to CGI-116 protein [H.sapiens]	3.7
	112876	T03488	Hs.4842	ESTs	3.7
70	118261	N62780	Hs.94122	ESTs	3.7
	130385	AA126474	Hs.155223	stannocalcin 2	3.7
	129300	C20976	Hs.110165	ESTs; Highly similar to ribosomal protein L26	3.7
	134388	M15841	Hs.82575	small nuclear ribonucleoprotein polypeptide B	3.7
	106968	AA504631	Hs.26813	ESTs; Weakly similar to hypothetical 43.2 kDa	3.7
75	100906	HG4716-HT5158		Guanosine 5'-Monophosphate Synthase	3.7
	100418	D86978	Hs.84790	KIAA0225 protein	3.7
	101484	M24594	Hs.20315	interferon-induced protein 56	3.7
	102547	U57911	Hs.46638	chromosome 11 open reading frame 8	3.7
	103587	Z29083	Hs.82128	5T4 oncofetal trophoblast glycoprotein	3.7
80	130600	AA478601	Hs.258737	ESTs	3.7
	128733	AA328993	Hs.104558	ESTs	3.7
	134375	AA412720	Hs.82389	ESTs; Highly similar to CGI-118 protein [H.sapiens]	3.7
	134098	X06323	Hs.79086	ribosomal protein; mitochondria; L3	3.6
	101188	L20320	Hs.184298	cyclin-dependent kinase 7 (homolog of Xenopus	3.6
	132149	T10822	Hs.4095	ESTs	3.6

5	116200	AA465358	Hs.118793	ESTs; Highly similar to p621 [H.sapiens]	3.6
	121920	AA428300	Hs.161841	ESTs	3.6
	128609	AA234365	Hs.102456	survival of motor neuron protein interacting	3.6
	101078	LD4510	Hs.792	ADP-ribosylation factor domain protein 1; 64k	3.6
	108693	AA121289	Hs.49597	ESTs; Highly similar to retinolic acid-induced	3.6
10	109139	AA176121	Hs.59757	zinc finger protein 281	3.6
	111870	R37778	Hs.18685	ESTs; Weakly similar to hypothetical protein	3.6
	113848	W60080	Hs.27099	DKFZP564J0863 protein	3.6
	127947	AI432475	Hs.146327	ESTs	3.6
	128056	AI379480	Hs.125449	ESTs; Weakly similar to MaxiK channel beta 2	3.6
15	129914	U22377	Hs.13321	rearranged L-myc fusion sequence	3.6
	132148	AA283988	Hs.4094	ESTs	3.6
	134644	S83308	Hs.87224	SRY (sex-determining region Y)-box 5	3.6
	115047	AA252627	Hs.22554	homeo box B5	3.6
	102398	U42359		Human N33 protein form 1 (N33) gene, exon 1 a	3.6
20	127479	AA513722	Hs.179729	collagen; type X; alpha 1 (Schmid metaphyseal	3.6
	105545	AA262030	Hs.5152	ESTs; Weakly similar to katanin p80 subunit [3.6
	101483	M24486	Hs.76768	procollagen-proline; 2-oxoglutarate 4-dioxyge	3.6
	105709	AA291268	Hs.26761	DKFZP586L0724 protein	3.6
	122836	AA454103	Hs.110031	ESTs	3.6
25	124792	R44357	Hs.132784	ESTs; Weakly similar to cDNA EST EMBL: T01421	3.6
	103621	Z47727	Hs.150675	polymerase (RNA) II (DNA directed) polypeptid	3.5
	105427	AA251330	Hs.28248	ESTs	3.5
	121553	AA412488	Hs.48820	ESTs	3.5
	115167	AA258421	Hs.43728	hypothetical protein	3.5
30	134570	U66615	Hs.172280	SWI/SNF related; matrix associated; actin dep	3.5
	110787	N24716	Hs.12244	ESTs; Weakly similar to C44B9.1 [C.elegans]	3.5
	131621	U77665	Hs.139120	ribonuclease P (30kD)	3.5
	132813	N72116	Hs.57435	solute carrier family 11 (proton-coupled diva	3.5
	116370	AA521256	Hs.236204	ESTs; Moderately similar to NUCLEAR PORE COMP	3.5
35	131965	W90146	Hs.35962	ESTs	3.5
	115221	AA262942	Hs.79741	ESTs	3.5
	116093	AA456020	Hs.50848	ESTs; Weakly similar to KIAA0882 protein [Hs	3.5
	123507	AA600176	Hs.112345	ESTs	3.5
	129801	F11087	Hs.239666	ESTs	3.5
40	115084	AA255556	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (from d	3.5
	123442	AA598803	Hs.111496	ESTs	3.5
	115061	AA253217	Hs.41271	ESTs	3.5
	100146	D13645	Hs.2471	KIAA0020 gene product	3.5
	115140	AA258030	Hs.55356	ESTs; Weakly similar to supported by GENSCAN	3.5
45	115360	AA281950	Hs.5057	carboxypeptidase D	3.5
	130261	D63767	Hs.153678	reproduction 8	3.4
	100824	HG4058-HT4328		Oncogene Aml1-Evl-1, Fusion Activated	3.4
	102287	U31814	Hs.3352	histone deacetylase 2	3.4
	102788	U86602	Hs.74407	nucleolar protein p40	3.4
50	118836	N79820	Hs.50854	ESTs	3.4
	102423	U44754	Hs.179312	small nuclear RNA activating complex; polypep	3.4
	106300	AA435840	Hs.19114	high-mobility group (nonhistone chromosomal)	3.4
	108156	AA425354	Hs.4210	ESTs	3.4
	106483	AA451676	Hs.30299	IGF-II mRNA-binding protein 2	3.4
55	107868	AA025234	Hs.61260	ESTs	3.4
	108187	AA056538	Hs.27842	ESTs; Weakly similar to similar to 1-acyl-gly	3.4
	116123	AA459282	Hs.43756	ESTs	3.4
	119501	W37721	Hs.151363	ESTs	3.4
	129121	AA127459	Hs.108788	ESTs; Weakly similar to zesle [D.melanogaster	3.4
60	131638	D87120	Hs.29882	predicted osteoblast protein	3.4
	132962	N34893	Hs.8153	ESTs; Highly similar to CGI-48 protein [H.sap	3.4
	133767	D63875	Hs.173288	KIAA0155 gene product	3.4
	111823	R35253	Hs.24944	ESTs	3.4
	134372	D63877	Hs.82324	KIAA0157 protein	3.4
65	130938	AA013250	Hs.21398	ESTs; Moderately similar to PUTATIVE GLUCOSAM	3.4
	115169	AA258427	Hs.58427	ESTs	3.4
	123978	C20653	Hs.170278	ESTs	3.4
	108807	AA129968	Hs.49376	ESTs; Weakly similar to PROTEIN PHOSPHATASE P	3.4
	132581	R42266	Hs.52256	ESTs; Weakly similar to beta-TrCP protein E3R	3.4
70	134654	W23625	Hs.8739	ESTs; Weakly similar to ORF YGR200c [S.cerev	3.4
	105730	AA292701	Hs.5364	DKFZP564I052 protein	3.4
	111295	N73275	Hs.21275	ESTs; Weakly similar to ubiquitin-conjugating	3.3
	102009	U02680	Hs.82643	protein tyrosine kinase 9	3.3
	114161	Z38904	Hs.22385	ESTs; Weakly similar to KIAA0970 protein [Hs	3.3
75	130604	X03635	Hs.1657	estrogen receptor 1	3.3
	100103	AF007875	Hs.5085	dolichyl-phosphate mannosyltransferase polype	3.3
	121748	AA421171	Hs.234545	ESTs	3.3
	106698	AA463745	Hs.29403	ESTs; Weakly similar to PROBABLE ATP-DEPENDEN	3.3
	134353	S77154	Hs.82120	nuclear receptor subfamily 4; group A; member	3.3
80	134154	AA211320	Hs.79404	neuron-specific protein	3.3
	133142	F03321	Hs.65874	ESTs	3.3
	124461	N50641	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (from c	3.3
	104903	AA055534	Hs.124134	ESTs	3.3
	106772	AA478106	Hs.12692	ESTs; Weakly similar to protein phosphatase-1	3.3
	109704	F09687	Hs.12876	ESTs	3.3
	111131	N64267	Hs.10177	ESTs	3.3
	115019	AA251906	Hs.48473	ESTs	3.3
	116019	AA450312	Hs.237480	Homo sapiens mRNA; cDNA DKFZp434E102 (from d	3.3

	118528	N57889	Hs.49397	ESTs	3.3
	124027	F03625	Hs.107537	ESTs	3.3
	131699	R58657	Hs.90421	ESTs; Moderately similar to III ALU SUBFAMIL	3.3
5	111044	N55443	Hs.23625	ESTs	3.3
	103768	AA099997	Hs.180320	ESTs; Weakly similar to GOLGI 4-TRANSMEMBRANE	3.3
	131882	N49091	Hs.3385	ESTs; Highly similar to CGI-134 protein [Hsa	3.3
	123673	AA609471	Hs.112712	ESTs	3.3
	132936	AB002305	Hs.6111	KIAA0307 gene product	3.3
10	103023	X53793	Hs.117950	multifunctional polypeptide similar to SAICAR	3.3
	120572	AA280794	Hs.258787	ESTs	3.3
	132384	AA479333	Hs.46967	Human DNA sequence from clone 167A19 on chrom	3.3
	105658	AA282914	Hs.10176	ESTs	3.2
	105085	AA147719	Hs.169441	ESTs	3.2
15	118695	N71781	Hs.50081	Homo sapiens mRNA full length insert cDNA clo	3.2
	112082	R44538	Hs.140889	ESTs	3.2
	125154	W38419	Hs.24936	ESTs	3.2
	108040	AA041551	Hs.48644	ESTs	3.2
	133453	M58941	Hs.73826	protein tyrosine phosphatase; non-receptor ty	3.2
20	124006	D60302	Hs.108977	ESTs	3.2
	116083	AA456553	Hs.44581	ESTs; Weakly similar to HEAT SHOCK 70 KD PROT	3.2
	106753	AA476944	Hs.7331	ESTs	3.2
	102821	U68075	Hs.50924	GATA-binding protein 6	3.2
	103330	X85373	Hs.77496	small nuclear ribonucleoprotein polypeptide G	3.2
25	128926	AA481403	Hs.107213	ESTs; Highly similar to NY-REN-6 antigen [Hs	3.2
	101167	L15309	Hs.193677	zinc finger protein 141 (clone pHZ-44)	3.2
	104055	AA393755	Hs.117211	ESTs; Highly similar to CGI-62 protein [Hsap	3.2
	112917	T10198	Hs.4263	ESTs; Weakly similar to /prediction	3.2
	120358	AA213459	Hs.100932	transcription factor 17	3.2
	121857	AA426017	Hs.62694	ESTs; Highly similar to DNA-REPAIR PROTEIN CO	3.2
30	122124	AA434257	Hs.186679	ESTs; Moderately similar to III ALU SUBFAMIL	3.2
	132231	H99131	Hs.42635	ESTs	3.2
	134272	X76040	Hs.223014	protease; serine; 15	3.2
	115860	AA431719	Hs.61809	ESTs	3.2
35	115278	AA278757	Hs.67486	ESTs; Weakly similar to BACN32G11.d [D.melano	3.2
	134125	R38102	Hs.50421	KIAA0203 gene product	3.2
	129160	AA131252	Hs.109007	ESTs	3.2
	121710	AA419011	Hs.96744	DKFZP586D0823 protein	3.2
	102242	U27185	Hs.32943	retinoic acid receptor responder (lazarotene	3.2
40	104956	AA074880	Hs.120975	ESTs; Weakly similar to hypothetical protein	3.2
	113047	T25867	Hs.7549	ESTs	3.2
	115017	AA251880	Hs.179982	tumor protein p53-binding protein	3.2
	133780	M14219	Hs.76152	decorin	3.1
	129453	AA421213	Hs.111632	Lsm3 protein	3.1
45	130353	X86018	Hs.172210	MUF1 protein	3.1
	106036	AA412505	Hs.10653	ESTs	3.1
	102234	U26312	Hs.8123	chromobox homolog 3 (Drosophila HP1 gamma)	3.1
	106133	AA424346	Hs.107573	slatyltransferase	3.1
	116803	H47357		ESTs; Moderately similar to weak similarity I	3.1
50	106721	AA465194	Hs.6670	ESTs	3.1
	107115	AA610108	Hs.27693	ESTs; Highly similar to CGI-124 protein [Hsa	3.1
	133228	N90029	Hs.6831	Homo sapiens clone 1400 unknown protein mRNA;	3.1
	104733	AA019498	Hs.23071	ESTs	3.1
	103879	AA228148	Hs.50252	ESTs; Weakly similar to putative [C.elegans]	3.1
55	103038	X54941	Hs.77650	CDC28 protein kinase 1	3.1
	135154	AA126433	Hs.173242	sorting nexin 4	3.1
	114860	AA235112	Hs.106227	ESTs; Moderately similar to similar to murine	3.1
	102437	U46569	Hs.221986	aquaporin 5	3.1
	100352	D84159		Homo sapiens mRNA for 3-7 gene product, part	3.1
60	103631	Z48570		H.sapiens Sp17 gene	3.1
	104238	AB002364	Hs.27916	a disintegrin-like and metalloprotease (repro	3.1
	108613	AA100967	Hs.69165	ESTs	3.1
	115915	AA436884	Hs.48926	ESTs	3.1
	120640	AA286945	Hs.163933	ESTs	3.1
65	124068	H03099	Hs.101619	ESTs	3.1
	130376	U91931	Hs.155172	adaptor-related protein complex 3; beta 1 sub	3.1
	131632	AA443671	Hs.29826	ESTs	3.1
	131523	H88801	Hs.201676	M phase phosphoprotein 10 (U3 small nucleolar	3.1
	115827	AA427890	Hs.44426	ESTs; Weakly similar to PHOSPHOLIPID HYDROPER	3.1
70	108828	AA131584	Hs.71435	DKFZP564O0463 protein	3.1
	112198	R49483	Hs.22159	ESTs; Weakly similar to ZINC FINGER PROTEIN H	3.1
	123960	AA621785	Hs.170008	methylmalonate-semialdehyde dehydrogenase	3.1
	131538	Z29331	Hs.28505	ubiquitin-conjugating enzyme E2H (homologous	3.1
	105616	AA280670	Hs.24968	ESTs	3.1
75	101228	L27706	Hs.82916	chaperonin containing TCP1; subunit 6A (zeta	3.1
	100280	D42085	Hs.155314	KIAA0095 gene product	3.1
	132744	X54326	Hs.55921	glutaryl-prolyl-lysine synthetase	3.1
	103105	X61970	Hs.76913	proteasome (prosome; macropain) subunit; alph	3.1
	106984	AA521201	Hs.7129	ESTs	3.1
80	105127	AA158132	Hs.11817	ESTs; Weakly similar to contains similarity I	3.1
	102302	U33052	Hs.69171	protein kinase C-like 2	3.1
	117708	N45114	Hs.46476	ESTs	3.1
	111314	N74574	Hs.33922	H.sapiens novel gene from PAC 117P20; chromos	3.0
	132902	AA480969	Hs.168147	ESTs	3.0
	130356	X84373	Hs.155017	nuclear receptor interacting protein 1	3.0

	128420	AI088155	Hs.14146	ESTs; Weakly similar to unknown [H.sapiens]	3.0
	108746	AA126974	Hs.43388	ESTs	3.0
	127236	AI341818	Hs.98658	budding uninhibited by benzimidazoles 1 (yeas	3.0
	114208	Z39301	Hs.7859	ESTs	3.0
5	107071	AA609053	Hs.35198	ESTs	3.0
	104957	AA074919	Hs.10026	ESTs; Weakly similar to ORF YJL063c [S.cerevi	3.0
	124073	H05394	Hs.127376	KIAA0266 gene product	3.0
	130869	AA128100	Hs.2057	uridine monophosphate synthetase (protate pho	3.0
	101232	L28997	Hs.242894	ADP-ribosylation factor-like 1	3.0
10	104276	C02193	Hs.85222	ESTs; Weakly similar to R27090_2 [H.sapiens]	3.0
	126160	N90960	Hs.247277	ESTs; Weakly similar to transformation-relate	3.0
	128584	M11433	Hs.101850	retinol-binding protein 1; cellular	3.0
	100405	D68425	Hs.82733	nidogen 2	3.0
	101335	L49054		Homo sapiens t(3;5)(q25.1;p34) fusion gene NP	3.0
15	108761	AA127514	Hs.81603	ESTs	3.0
	111346	N89829	Hs.13259	ESTs	3.0
	114988	AA251089	Hs.94576	ESTs; Weakly similar to phosphocin; retinal [H	3.0
	116008	AA449338	Hs.48589	ESTs; Weakly similar to finger protein HZF6;	3.0
	116545	D20313	Hs.74899	ESTs	3.0
20	117873	M99967	Hs.46624	ESTs	3.0
	121463	AA411745	Hs.239681	ESTs; Weakly similar to KIAA0554 protein [Hs	3.0
	128625	AA242816	Hs.102652	ESTs; Weakly similar to KIAA0437 [H.sapiens]	3.0
	131185	M25753	Hs.23960	cyclin B1	3.0
	134380	D38073	Hs.179565	minichromosome maintenance deficient (S. cere	3.0
25	105740	AA293206	Hs.10852	ESTs	3.0
	130919	AA291710	Hs.21276	collagen; type IV; alpha 3 (Goodpasture antig	3.0
	134423	W96151	Hs.83006	ESTs; Highly similar to CG-139 protein [H.s	3.0
	104886	AA054228	Hs.23165	ESTs	3.0
	134407	X72964	Hs.82794	caltractin (20kD calcium-binding protein)	3.0
30	106378	AA445994	Hs.21331	ESTs	3.0
	112283	R53545	Hs.20952	Homo sapiens clone 24411 mRNA sequence	3.0
	108018	AA156960	Hs.114992	ESTs	3.0
	114239	Z39742	Hs.222478	ESTs	3.0
	114969	AA250775	Hs.87747	ESTs	3.0
35	116408	AA608752	Hs.71969	Homo sapiens mRNA; cDNA DKFZp564P0823 (from c	3.0
	115286	AA279803	Hs.82204	ESTs	2.9
	105809	AA393827	Hs.20104	ESTs	2.9
	113811	W44928	Hs.4878	ESTs	2.9
	107248	D58894	Hs.34782	ESTs	2.9
40	134489	U09284	Hs.112378	LIM and senescent cell antigen-like domains 1	2.9
	134084	D87685	Hs.78893	KIAA0244 protein	2.9
	127370	AI024352	Hs.70337	immunoglobulin superfamily; member 4	2.9
	113277	T65797	Hs.11774	protein (peptidyl-prolyl cis/trans isomerase)	2.9
45	132783	N74897	Hs.5683	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide	2.9
	109010	AA156460	Hs.44229	dual specificity phosphatase 12	2.9
	130095	F01831	Hs.14838	ESTs	2.9
	106618	AA459249	Hs.8715	ESTs; Weakly similar to Similarity with snail	2.9
	103427	X97303		H.sapiens mRNA for Ptg-12 protein	2.9
50	133980	D00760	Hs.181309	proteasome (prosome; macropain) subunit; alph	2.9
	111353	N90430	Hs.6616	ESTs	2.9
	105344	AA235303	Hs.8645	ESTs	2.9
	134498	M63180	Hs.84131	threonyl-tRNA synthetase	2.9
	117910	N50828	Hs.12940	zinc-fingers and homeoboxes 1	2.9
55	118903	N90774	Hs.132207	ESTs; Moderately similar to III ALU SUBFAMIL	2.9
	121713	AA419188	Hs.105577	ESTs	2.9
	129080	H19307	Hs.108507	ESTs	2.9
	129404	AA172056	Hs.111128	ESTs	2.9
	129457	X55330	Hs.207776	aspartylglucosaminidase	2.9
60	130352	D87450	Hs.154978	KIAA0261 protein	2.9
	133415	X69699	Hs.73149	paired box gene 8	2.9
	120649	AA287115	Hs.99697	ESTs	2.9
	131257	AA256042	Hs.24908	ESTs	2.9
	134480	AA024664	Hs.83916	NADH dehydrogenase (ubiquinone) 1 alpha subco	2.9
65	116734	F13789	Hs.93796	DKFZP586D2223 protein	2.9
	105028	AA126719	Hs.25282	ESTs	2.9
	114986	AA251010	Hs.87807	ESTs	2.9
	105651	AA282481	Hs.18439	ESTs	2.9
	101714	M68874		Human phosphatidylcholine 2-acylhydrolase (cP	2.9
70	123398	AA521265	Hs.105514	ESTs	2.9
	106007	AA411462	Hs.11042	ESTs; Weakly similar to vef1 [H.sapiens]	2.9
	109450	AA232183	Hs.173042	ESTs; Weakly similar to III ALU SUBFAMILY J	2.9
	104685	AA010530	Hs.9599	Human BAC clone GS025M02 from 7q21-q22	2.9
	108677	AA115629	Hs.118531	ESTs	2.9
	116028	AA452112	Hs.42644	thioredoxin-like	2.9
75	105404	AA243303	Hs.21187	ESTs	2.9
	132365	AA598694	Hs.46541	Homo sapiens PAC clone DJ0894A10 from 7q32-q3	2.9
	119638	W52480	Hs.55148	ESTs; Moderately similar to NY-REN-58 antigen	2.9
	124637	N80716	Hs.75798	Human DNA sequence from clone 1183121 on chro	2.9
	130588	AA287735	Hs.16411	Human DNA sequence from clone 1189B24 on chro	2.9
80	105640	AA281623	Hs.7525	ESTs; Weakly similar to KIAA0742 protein [Hs	2.9
	131818	Z39297	Hs.3281	neuronal pentraxin II	2.9
	119298	T23820	Hs.155478	cyclin T2	2.9
	128742	D00763	Hs.251531	proteasome (prosome; macropain) subunit; alph	2.9
	115089	AA255876	Hs.86919	ESTs; Weakly similar to III ALU SUBFAMILY J	2.9

5	100468	D89289	Hs.118722	fucosyltransferase 8 (alpha (1-6) fucosyltran	2.8
	132920	U06133	Hs.606	ATPase; Cu++ transporting; alpha polypeptide	2.8
	113490	T88700	Hs.173374	ESTs	2.8
	133451	Y00764	Hs.73818	ubiquinol-cytochrome c reductase hinge protel	2.8
	128770	H98645	Hs.143460	protein kinase C; nu	2.8
	129122	N62515	Hs.108790	ESTs	2.8
	104827	AA035630	Hs.8551	PRP4/STKAWD splicing factor	2.8
	111348	N90041	Hs.9585	ESTs	2.8
10	130987	R45698	Hs.21893	ESTs; Weakly similar to cAMP inducible 2 prot	2.8
	102139	U15932	Hs.2128	dual specificity phosphatase 5	2.8
	114902	AA236359	Hs.39504	ESTs	2.8
	106094	AA419461	Hs.18127	ESTs	2.8
	126438	N93125	Hs.137300	ESTs	2.8
15	107129	AA620553	Hs.4756	flap structure-specific endonuclease 1	2.8
	104491	N71513	Hs.39328	ESTs	2.8
	105043	AA132239	Hs.11810	ESTs; Weakly similar to CD4.2 [C.elegans]	2.8
	106855	AA486182	Hs.17975	ESTs	2.8
	109695	F09530	Hs.180591	ESTs; Weakly similar to R06F6.5b [C.elegans]	2.8
20	120455	AA251083	Hs.104347	ESTs	2.8
	130861	N23393	Hs.20509	ESTs	2.8
	131649	AA481254	Hs.30120	ESTs	2.8
	128517	AA280617	Hs.100861	ESTs; Weakly similar to p60 katanin [H.sapien	2.8
	100486	HG1112-HT1112		Ras-Like Protein Tc4	2.8
25	116729	F13700	Hs.115823	ribonuclease P; 40kD subunit	2.8
	101851	M94250	Hs.82045	midkine (neurite growth-promoting factor 2)	2.8
	115465	AA286941	Hs.43691	ESTs	2.8
	100137	D13627	Hs.15071	chaperonin containing TCP1; subunit 8 (theta)	2.8
	125837	H05323	Hs.146401	endothelial monocyte-activating polypeptide	2.8
30	131562	U90551	Hs.28777	H2A histone family; member L	2.8
	129445	AA306121	Hs.111615	ESTs; Weakly similar to predicted using Genef	2.8
	129239	D31544	Hs.109701	ESTs; Moderately similar to weak similarity t	2.8
	106507	AA452584	Hs.91585	protein phosphatase 1; regulatory (inhibitor)	2.8
	101684	M60752	Hs.121017	H2A histone family; member A	2.8
35	129428	AA412087	Hs.168272	EST; Highly similar to protein inhibitor of a	2.8
	103437	X98260	Hs.82254	M-phase phosphoprotein 11	2.8
	129821	F11019	Hs.12696	coractin SH3 domain-binding protein	2.8
	130160	Z39228	Hs.151344	UDP-GalbetaGlcNAc beta 1,3-galactosyltransfe	2.8
	104257	AF006265	Hs.9222	estrogen receptor-binding fragment-associated	2.8
40	116204	AA465701	Hs.108648	ESTs	2.8
	125914	AA262925	Hs.180034	cleavage stimulation factor; 3' pre-RNA; subu	2.8
	131510	AA207114	Hs.27842	ESTs; Weakly similar to similar to 1-acyl-gly	2.8
	106291	AA435551	Hs.30824	ESTs	2.8
	122761	AA459298	Hs.105039	ESTs; Weakly similar to HLL ALU SUBFAMILY J	2.8
45	107056	AA600310	Hs.18720	programmed cell death 8 (apoptosis-inducing f	2.8
	108535	AA084505	Hs.226440	Homo sapiens clone 24881 mRNA sequence	2.8
	116226	AA478729	Hs.76450	ESTs	2.8
	120268	AA173939	Hs.193902	ESTs; Weakly similar to inner centromere prot	2.8
	128654	H20689	Hs.103180	actin-like 6	2.8
50	116726	F13681	Hs.42309	ESTs	2.7
	132840	U33821		Tax1 (human T-cell leukemia virus type I) bin	2.7
	133273	AA147725	Hs.69469	dendritic cell protein	2.7
	108846	AA132983	Hs.44155	DKFZP586G1517 protein	2.7
	105621	AA280865	Hs.6375	Homo sapiens mRNA; cDNA DKFZp564K0222 (from c	2.7
55	129164	AA282183	Hs.109045	ESTs	2.7
	133618	U78524	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding prot	2.7
	120521	AA258785	Hs.107476	ATP synthase; H+ transporting; mitochondrial	2.7
	116429	AA609710	Hs.82837	Human chromosome 3p21.1 gene sequence	2.7
	110984	N52006	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polypeptid	2.7
60	100372	D79997	Hs.184339	KIAA0175 gene product	2.7
	125134	W19228	Hs.100748	ESTs	2.7
	129254	AA453624	Hs.10398	deoxynucleotidyltransferase; terminal	2.7
	102339	U37022	Hs.95577	cyclin-dependent kinase 4	2.7
	106589	AA456646	Hs.28661	ESTs	2.7
65	119118	R44122	Hs.42743	ESTs; Weakly similar to predicted using Genef	2.7
	105973	AA406320	Hs.21201	DKFZP566B0846 protein	2.7
	106317	AA436568	Hs.172140	ESTs	2.7
	115551	AA365527	Hs.177861	ESTs; Highly similar to CGI-110 protein [H.sa	2.7
	103789	AA096178	Hs.70337	immunoglobulin superfamily; member 4	2.7
70	105079	AA143190	Hs.12677	ESTs; Highly similar to CGI-147 protein [H.sa	2.7
	109299	AA205649	Hs.86371	zinc finger protein 254	2.7
	122089	AA432136	Hs.98682	ESTs	2.7
	129108	L20321	Hs.1087	serine/threonine kinase 2	2.7
	129385	D82675	Hs.110950	Homo sapiens clone 25007 mRNA sequence	2.7
75	131412	U34044	Hs.124027	SELENOPHOSPHATE SYNTHETASE; Human selenium d	2.7
	104052	AA393164	Hs.97644	mammaglobin 2	2.7
	116254	AA481146	Hs.41086	ESTs; Weakly similar to OXYSTEROL-BINDING PRO	2.7
	106878	AA488872	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (from c	2.7
	114852	AA101416	Hs.107149	ESTs; Weakly similar to PTB-ASSOCIATED SPLI	2.7
80	106831	AA482014	Hs.29463	centrin; EF-hand protein; 3 (CDC31 yeast homo	2.7
	101445	M21259	Hs.1066	small nuclear ribonucleoprotein polypeptide E	2.7
	124428	N36881	Hs.82202	ribosomal protein L17	2.7
	114471	AA028074	Hs.103387	ESTs	2.7
	102051	U07550	Hs.1197	heat shock 10kD protein 1 (chaperonin 10)	2.7
	106916	AA490814	Hs.24170	ESTs; Weakly similar to ribosomal S1 protein	2.7

5	116142	AA460649	Hs.39457	ESTs	2.7
	109912	H05509	Hs.24639	ESTs	2.7
	103193	X70476	Hs.75724	coarctin protein complex; subunit beta 2 (bet	2.7
	102046	U07151	Hs.182215	ADP-ribosylation factor-like 3	2.7
	104567	R64534	Hs.101469	ESTs	2.7
	112996	T23539	Hs.7165	zinc finger protein 259	2.7
	118138	N57773	Hs.93560	ESTs; Weakly similar to brg [R.norvegicus]	2.7
	123095	AA485724	Hs.192119	ESTs	2.7
10	124315	H94892	Hs.6906	v-rat simian leukemia viral oncogene homolog	2.7
	124447	M48000	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (from cl	2.7
	132834	H77546	Hs.57898	ESTs; Highly similar to NY-REN-49 antigen [H.	2.7
	107529	Y12065	Hs.5092	nucleolar protein (KKE/D repeat)	2.7
	130648	AA075427	Hs.17296	ESTs; Weakly similar to Jprediction	2.7
15	106685	AA461551	Hs.16251	ESTs; Highly similar to 73 kDa subunit of cle	2.6
	133848	AA093287	Hs.76728	ESTs	2.6
	134880	AA092376	Hs.90606	15 kDa selenoprotein	2.6
	128871	AA400271	Hs.106778	Homo sapiens mRNA for putative Ca2+-transport	2.6
	106846	AA465223	Hs.34892	ESTs	2.6
20	119892	W84548	Hs.94896	ESTs	2.6
	132309	AA460917	Hs.2780	jun D proto-oncogene	2.6
	132923	U21858	Hs.60679	TATA box binding protein (TBP)-associated fac	2.6
	114365	Z41688	Hs.18653	ESTs	2.6
	114162	Z38909	Hs.22265	ESTs	2.6
25	133370	AA156897	Hs.72157	DKFZP564I1922 protein	2.6
	106818	AA480890	Hs.3542	ESTs	2.6
	133501	W16684	Hs.74284	ESTs; Moderately similar to Similar to S.cere	2.6
	100530	HG1869-HT1904		Male Enhanced Antigen	2.6
	130553	AA430032	Hs.252587	pituitary tumor-transforming 1	2.6
30	108917	AA137078	Hs.173648	ESTs	2.6
	122249	AA436679	Hs.258543	ESTs; Highly similar to CGI-07 protein [H.sap	2.6
	119598	W45531	Hs.94642	ESTs	2.6
	119902	W84865	Hs.40094	Human DNA sequence from clone 167A19 on chrom	2.6
	133272	AA465016	Hs.59423	kallikrein 10	2.6
35	132575	AA045365	Hs.5188	ESTs; Weakly similar to 60S RIBOSOMAL PROTEIN	2.6
	130459	AA460264	Hs.155983	KIAA0677 gene product	2.6
	133083	N70633	Hs.6456	chaperonin containing TCP1; subunit 2 (beta)	2.6
	131130	T19399	Hs.23255	nucleoporin 155kD	2.6
	112043	R43317	Hs.26312	glioma amplified on chromosome 1 protein (leu	2.6
40	116146	AA460701	Hs.193200	ESTs	2.6
	122378	AA446100	Hs.103617	ESTs	2.6
	103134	X65724	Hs.2839	Norrie disease (pseudoglioma)	2.6
	133395	AA491296	Hs.72805	ESTs	2.6
	115652	AA405098	Hs.38178	ESTs	2.6
45	104975	AA086071	Hs.50758	chromosome-associated polypeptide C	2.6
	134691	M59979	Hs.88474	prostaglandin-endoperoxide synthase 1 (prosta	2.6
	112869	T03313	Hs.4747	dyskeratosis congenita 1; dyskerin	2.6
	100092	AF000231	Hs.75618	RAB11A; member RAS oncogene family	2.6
	102635	U66838	Hs.79378	cyclin A1	2.6
50	104490	N71503	Hs.43087	ESTs; Weakly similar to dysferlin [H.sapiens]	2.6
	106813	AA479922	Hs.181022	ESTs	2.6
	106872	AA487907	Hs.18282	ESTs; Highly similar to unknown [H.sapiens]	2.6
	107022	AA599041	Hs.28866	programmed cell death 10	2.6
	107113	AA610073	Hs.23900	ESTs; Weakly similar to oligophrenin-1 like p	2.6
55	113281	T66300	Hs.112356	Homo sapiens mRNA for lipoyltransferase; comp	2.6
	115586	AA399218	Hs.92423	ESTs	2.6
	115779	AA424183	Hs.70945	ESTs	2.6
	122895	AA469946	Hs.105325	ESTs	2.6
	124726	R15740	Hs.104576	carbohydrate (keratan sulfate Gal-6) sulfotra	2.6
60	129775	R94659	Hs.12420	ESTs	2.6
	131991	AA251909	Hs.36708	budding uninhibited by benzimidazoles 1 (yeas	2.6
	132518	D57975	Hs.5064	ESTs	2.6
	134612	AA451712	Hs.171581	ESTs; Highly similar to ubiquitin C-terminal	2.6
	130313	AA620323	Hs.154320	ubiquitin-activating enzyme E1C (homologous t	2.6
65	131971	R70167	Hs.3811	ESTs	2.6
	133175	AA134767	Hs.68666	ESTs	2.6
	102083	U10323	Hs.75117	interleukin enhancer binding factor 2; 45kD	2.6
	125670	AI432621	Hs.82685	CD47 antigen (Rb-related antigen; integrin-as	2.6
	121822	AA425107	Hs.97016	ESTs; Moderately similar to SH3 domain-bindin	2.6
70	106719	AA465171	Hs.236844	ESTs	2.6
	130029	AA236412	Hs.236510	ESTs; Moderately similar to PFT27 [M.musculus	2.6
	124328	H97781	Hs.14415	ESTs; Highly similar to CGI-108 protein [H.s	2.6
	105387	AA236951	Hs.108636	chromosome 1 open reading frame 9	2.6
	103073	X59417	Hs.74077	proteasome (prosome; macropain) subunit; alph	2.6
75	116294	AA489000	Hs.93748	ESTs; Moderately similar to TRANSCRIPTION FAC	2.6
	135339	D59269	Hs.127842	Homo sapiens mRNA full length insert cDNA clo	2.6
	125390	H95094	Hs.75187	translocase of outer mitochondrial membrane 2	2.6
	102504	U52077	Hs.247948	Human mariner1 transposase gene; complete con	2.6
	131076	H44386	Hs.22666	ESTs	2.6
80	114096	Z38342	Hs.27007	chromosome condensation 1-like	2.6
	120402	AA234339	Hs.50282	GTP-binding protein ragB	2.6
	102125	U14550	Hs.107573	slatyltransferase	2.6
	134653	AA452818	Hs.87385	ESTs	2.6
	101959	S80343	Hs.180832	arginyl-tRNA synthetase	2.6
	116766	H13260	Hs.95097	ESTs	2.6

5	104954	AA074514	Hs.26213	ESTs; Weakly similar to protein [H.sapiens]	2.5
	108771	AA127924	Hs.71034	ESTs	2.5
	116439	AA610068	Hs.43913	PIBF1 gene product	2.5
	133859	U86782	Hs.178761	26S proteasome-associated pad1 homolog	2.5
	132792	AA401903	Hs.242985	hemoglobin; gamma G	2.5
	129620	AA010686	Hs.239720	ESTs; Weakly similar to KIAA0691 protein [H.s]	2.5
	120296	AA191353	Hs.22385	ESTs; Weakly similar to KIAA0970 protein [H.s]	2.5
	115615	AA401186	Hs.48617	ESTs	2.5
10	102983	X17620	Hs.118638	non-metastatic cells 1; protein (NM23A) expe	2.5
	106288	AA435636	Hs.24336	ESTs	2.5
	107444	W28391	Hs.5181	proliferation-associated 2G4; 38kD	2.5
	104525	R16007	Hs.75355	ubiquitin-conjugating enzyme E2N (homologous	2.5
	128917	AA204876	Hs.206097	oncogene TC21	2.5
15	102299	U32907	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	2.5
	115363	AA282071	Hs.152759	activator of S phase kinase	2.5
	130399	AAA49417	Hs.155356	Homo sapiens mRNA for putative glucosyltransf	2.5
	130752	D50927	Hs.18895	toasted-like kinase 1	2.5
	132724	AA417962	Hs.55498	geranylgeranyl diphosphate synthase 1	2.5
20	106743	AA476352	Hs.21938	ESTs; Weakly similar to KIAA0704 protein [H.s]	2.5
	128949	AA180993	Hs.8850	a disintegrin and metalloproteinase domain 12	2.5
	125685	AJ040346	Hs.4943	hepatocellular carcinoma associated protein;	2.5
	105826	AA398243	Hs.21806	ESTs; Moderately similar to similar to NEDD-4	2.5
	110841	N31610	Hs.18645	ESTs; Weakly similar to partial CDS [C.elegan	2.5
25	111987	R42036	Hs.6763	KIAA0942 protein	2.5
	132669	AA188378	Hs.54602	ESTs; Weakly similar to 60S RIBOSOMAL PROTEIN	2.5
	100398	D84557	Hs.155462	minichromosome maintenance deficient (mis5; 6	2.5
	130800	AA223386	Hs.19574	ESTs; Weakly similar to katanin p80 subunit [2.5
	114481	AA033562	Hs.151572	ESTs	2.5
30	113404	T82323	Hs.70337	immunoglobulin superfamily; member 4	2.5
	100260	D38491	Hs.174135	KIAA0117 protein	2.5
	103563	Z22534	Hs.150402	activin A receptor; type I	2.5
	104573	R68952	Hs.29780	ESTs	2.5
	105025	AA126336	Hs.22744	ESTs; Weakly similar to ZINC FINGER PROTEIN 1	2.5
35	105524	AA258158	Hs.22153	ESTs; Weakly similar to KIAA0352 [H.sapiens]	2.5
	106157	AA425367	Hs.32094	ESTs	2.5
	107243	D59489	Hs.34727	ESTs	2.5
	109920	H05733	Hs.30558	ESTs	2.5
	109981	H09552	Hs.26090	ESTs; Weakly similar to T20B12.1 [C.elegans]	2.5
40	114518	AA046407	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like 1	2.5
	114768	AA149007	Hs.182339	Ets homologous factor	2.5
	118906	N91000	Hs.94433	ESTs	2.5
	119025	N98926	Hs.55209	ESTs; Weakly similar to DMR-N9 PROTEIN [H.sap	2.5
	131712	N29502	Hs.30991	KIAA0957 protein	2.5
45	132233	X04706	Hs.93574	homeo box D3	2.5
	132740	AA227751	Hs.55896	ESTs	2.5
	115239	AA278650	Hs.73291	ESTs; Weakly similar to similar to the beta 1	2.5
	128820	F10338	Hs.106309	Friend of GATA2	2.5
	124049	F10523	Hs.74519	primase; polypeptide 2A (58kD)	2.5
50	128781	X85372	Hs.105465	small nuclear ribonucleoprotein polypeptide F	2.5
	121361	AA405494	Hs.183052	ESTs	2.5
	134133	X93920	Hs.180383	dual specificity phosphatase 6	2.5
	102502	U51678	Hs.78050	small acidic protein	2.5
	115875	AA433943	Hs.43946	ESTs; Weakly similar to Weak similarity to Ye	2.5
55	132874	AA425776	Hs.58609	ESTs	2.5
	109646	F04543	Hs.5028	DKFZP564O0423 protein	2.5
	111197	N68093	Hs.22909	ESTs	2.5
	102968	X16396	Hs.154672	methylene tetrahydrofolate dehydrogenase (NAD	2.5
60	124911	R88992	Hs.123645	ESTs	2.5
	106628	AA459657	Hs.12311	Homo sapiens clone 23570 mRNA sequence	2.5
	116988	H82527		ys69e12.s1 Soares retina N2b4HR Homo sapiens	2.5
	131075	Y00757	Hs.2265	secretory granule; neuroendocrine protein 1 (2.5
	133578	X78627	Hs.75066	translin	2.5
	100420	D86983	Hs.118893	p53-responsive gene 2	2.5
65	130743	W87710	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (from cl	2.5
	122465	AA448164	Hs.99153	ESTs; Highly similar to CGI-73 protein [H.sap	2.5
	115117	AA256492	Hs.49007	poly(A) polymerase	2.5
	124582	N68477	Hs.108408	ESTs; Highly similar to CGI-78 protein [H.sap	2.5
	104771	AA025911	Hs.24994	ESTs; Highly similar to CGI-53 protein [H.sap	2.5
70	108059	AA043944	Hs.62663	ESTs	2.5
	105628	AA281251	Hs.35696	ESTs; Weakly similar to putative zinc finger	2.5
	109261	AA195255	Hs.61779	ESTs	2.5
	119789	W73140	Hs.50915	kallikrein 5	2.5
	130512	AA045304	Hs.181271	ESTs; Highly similar to CGI-120 protein [H.s	2.5
75	134402	U25165	Hs.82712	fragile X mental retardation; autosomal homol	2.5
	104769	AA025887	Hs.114774	ESTs; Weakly similar to III ALU SUBFAMILY J	2.5
	125787	AA744748	Hs.29403	ESTs; Weakly similar to PROBABLE ATP-DEPEND	2.5
	131775	AA459555	Hs.31921	KIAA0648 protein	2.5

TABLE 7B:

Key: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

100352 37786_1 AL133887 D64159 AF112218 AF1766633 AL039303 AL133888 BE620604 AW976259 AW262792 AW591383 AI365413 N36652 AA807027
 101084 13883_1 AW42041 BE620065
 AW409934 AW245855 AU077157 AW163245 AW161434 AW250083 AA316055 BE621134 AA171883 BE272494 L05425 BE250310
 NM_013285 BE311494 AA858436 AA308223 AW362598 AA373618 BE394454 AA126101 AA581348 AA303227 AA058438 AA126544
 AL135350 AW996947 AA403201 AA446682 W79685 AW246249 AW577783 AW002316 AA320025 AW753913 AI798554 AW070650
 BE250413 AW250835 BE076336 AI925558 AI907634 AW804193 AW804270 AA902387 AW804232 AW804255 AW607751 AI909114
 AW157242 AA934590 AI628921 AI470650 AW409935 AW172793 AA401208 AW162279 AA888018 BE206452 AI826742 AA857353
 AA483514 AA126418 AA722289 AA780182 AW768894 AW183614 AW156969 AI244063 AA863491 AI376281 AA582490 AA846248
 AI474094 AW246802 AA446557 AA126000 AI699045 AI702310 AI253092 AA171554 AA831455 AW118384 AI954511 AI760439 AI867001
 AA493881 W81287 AA515590 AA658297 AA635139 AA659293 AA766044 AA196109 N32569 AI907635
 100502 26409_1 U15979 X17544 W52755 NM_003835 Z12172 AW370136 BE262564 T49116 AA333753 BE262238 BE313737 H38153 AW583056 R28890
 BE259532 D16897 AA885610 AA911293 AA319527 R94472 R29022 AA443405 R96397 W04904 W01746 W01204 N74203 N58621
 AA701998 AW418723 N53220 AA602813 AA576129 AA593786 AA911577 AA575957 AI149135 AW573058 AA772985 AI188918 AI372065
 AA575838 W60010 AI004576 AI131265 AA319845 T50070 AI335742 AA235245 W32706 AA447372 R96355 N58573 AA904616 AI291224
 BE467454 T49117 AI268620 AA928248 AA449494 AA318817 T49929 R94473 H38154 AI076649 AW935307 AW605112 AW935433
 AW935342 AW935310 AW935345 AI296308 AW935395 AW935384 AI184857 AA319871 T29465 C21134 Z19785 AA329107 T52079
 AW935346 C06234 AI951555 T49928 AA371745 AA365296 AA346673 R82547 T50006
 102398 entrez_U42359 U42359

Table 8A lists about 54 genes up-regulated in ovarian cancer compared to normal adult tissues. These were selected from 35403 probesets on the Affymetrix/Eos-Hu01 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 4.0. The "average" ovarian cancer level was set to the 3rd highest amongst various ovarian cancers. The "average" normal adult tissue level was set to the 4th highest amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 8A: ABOUT 54 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES

Pkey: Primekey

Ex. Accn: Exemplar Accession

UG ID: UniGene ID

Title: UniGene Title

ratio: ration tumor vs. normal tissues

Pkey	Ex. Accn	UG ID	Title	ratio
130941	D49394	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3A	12.1
101249	L33881	Hs.1904	protein kinase C; iota	11.8
132528	AA283008	Hs.50758	chromosome-associated polypeptide C	11.5
102610	U65011	Hs.30743	preferentially expressed antigen in melanoma	11.0
115536	AA347193	Hs.62180	ESTs	10.0
129571	X51630	Hs.1145	Wilms tumor 1	9.3
105298	AA233459	Hs.26369	ESTs	7.8
121779	AA422038	Hs.98367	ESTs	7.3
104301	D45332	Hs.6783	ESTs	6.9
132191	AA449431	Hs.158688	KIAA0741 gene product	6.7
102136	U15552	Hs.85769	acidic 82 kDa protein mRNA	6.6
101804	M86699	Hs.169840	TTK protein kinase	6.5
132572	AA448297	Hs.237825	signal recognition particle 72kD	5.9
106738	AA470145	Hs.25130	ESTs	5.8
108857	AA133250	Hs.62180	ESTs	5.8
115291	AA278943	Hs.122579	ESTs	5.8
132632	N59764	Hs.5398	guanine-monophosphate synthetase	5.8
116401	AA599863	Hs.59698	ESTs	5.7
132725	L41887	Hs.184167	splicing factor, arginine/serine-rich 7 (35kD)	5.7
129097	S50223		KIR-T1=Kruppel-like zinc finger protein (huma	5.6
134520	N21407	Hs.257325	ESTs	5.5
108778	AA128548	Hs.90847	general transcription factor IIC; polypeptid	5.4
131228	AA279157	Hs.24485	chondroitin sulfate proteoglycan 6 (barnacan)	5.2
116238	AA479362	Hs.47144	DKFZP586N0819 protein	5.2
108055	AA043562	Hs.62637	ESTs	5.1
132939	U76189	Hs.61152	exostoses (multiple)-like 2	5.1
115909	AA436666	Hs.59761	ESTs	5.0
120438	AA243441	Hs.99488	ESTs; Weakly similar to ORF YKR074w [S.cerev]	5.0
123494	AA599786	Hs.112110	ESTs	5.0
109648	F04600	Hs.7154	ESTs	4.9
132624	AA164819	Hs.53631	ESTs	4.9
111234	N69287	Hs.21943	ESTs; Weakly similar to ORF YGL221c [S.cerev]	4.9
135242	M74093	Hs.9700	cyclin E1	4.9
123005	AA479726	Hs.105577	ESTs	4.8
116298	AA489033	Hs.62601	Homo sapiens mRNA; cDNA DKFZp586K1318 (from c	4.7
100661	HG2874-HT3018		Ribosomal Protein L39 Homolog	4.6
111345	N89820	Hs.14559	ESTs	4.6
102627	U66561	Hs.158174	zinc finger protein 184 (Kruppel-like)	4.5
106459	AA449741	Hs.4029	glioma-amplified sequence-41	4.5
102305	U33286	Hs.90073	chromosome segregation 1 (yeast homolog)-like	4.5
129229	AA211941	Hs.109643	polyadenylate binding protein-interacting pro	4.5
130376	R40873	Hs.155174	KIAA0432 gene product	4.4
120619	AA284372	Hs.111471	ESTs	4.4
122802	AA460530	Hs.255579	ESTs	4.4
116416	AA609219	Hs.39982	ESTs	4.3
115094	AA255921	Hs.88095	ESTs	4.2
126802	AA947601	Hs.97056	ESTs	4.2
126892	AI160190	Hs.76127	hact (homologous to the E6-AP (UBE3A) carboxy	4.2
105516	AA257971	Hs.21214	ESTs	4.1
131985	AA434329	Hs.36563	ESTs	4.1

122802	287993_1	AI783813 AI769315 AI743691 AI915645 AA479473 C21435 N50944 N50902 AW978102 H23837 BE087538 AA316516 AI687303 AW571681 AI554465 AI684252 AI581056 AA604098 AI628160 AI859843 AA424021 AA460530 BE042778 AW273200 AW273223 AW167288 AW083347 AI654306 AW517496 AW104706 AW273214 BE139512 AW169487 AW130822 AW167419 AI289485 AW150010 H88004 AI743745 AW088710
123494	21202_1	AW179019 AW179011 AF135160 NM_014050 AF078860 BE018005 AK000285 AF151038 BE245156 AW179007 AA345114 BE619758 BE619209 W25509 AA314339 AA336674 AA337956 AW954843 AW390412 N46796 AA316235 AA314286 R15686 BE535633 N57134 N46483 AW358462 AA923517 AA665223 AI418513 AA837523 AI359320 AI309273 AI522278 N40939 AA904977 AA938272 N30240 AA887965 AI671972 AI028109 AA094652 AA883262 AA887781 AI744447 AW592944 AI077790 AW860883 AW148667 N89861 AA557195 AI191824 AI433166 AI719760 AA453089 AA630656 AA300976 AA639620 AW675033 AA284393 AW866987 AI476335 AI332939 BE301513 AA452920 AW674302 AI925483 AW170412 AI698717 AI375985 BE220535 AI688151 AW514809 AW062346 AA599786 BE350848 AI560848 AI023075 AA864875 AA166871 AI807947 AW514579 AI978602 AI860340 AA830886 AI374788 AI283592 AA683152 AA743159 AI379932 AI432056 AI128904 AW150433 N38909
116296	11967_2	AW149502 Z43342 AW002826 AL049382 AA442545 AW971471 BE220243 AW968952 AA043607 AW299245 AA659892 AI038768 H26330 BE463534 AI628252 AA836139 AI277291 AA489033 AA741239 AI209064 AI300253 AI275761 Z39417 C01835

Table 9A lists about 382 genes up-regulated in ovarian cancer compared to normal ovaries. These were selected from 35403 probesets on the Affymetrix/Eos-Hu01 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult ovaries was greater than or equal to 10. The "average" ovarian cancer level was set to the 2nd highest amongst various ovarian cancers. The "average" normal adult ovaries level was set to the arithmetic mean amongst various non-malignant ovaries. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues (see Table 7A) was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 9A: 382 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY

Pkey: Primekey

Ex. Accn: Exemplar Accession

UG ID: UniGene ID

Title: UniGene title

ratio: ratio tumor vs. normal tissues

Pkey	Ex. Accn	UG ID	Title	ratio
134454	L33930	Hs.173996	CD24 antigen (small cell lung carcinoma clust	86.2
102927	X12876	Hs.65114	keratin 18	84.7
115909	AA436666	Hs.59781	ESTs	72.3
123169	AA486892	Hs.104472	ESTs; Weakly similar to Gag-Pol polyprotein [66.8
115674	AA406542	Hs.71520	ESTs	65.4
102193	U20758	Hs.313	secreted phosphoprotein 1 (osteopontin; bone	63.1
101839	M93036	Hs.692	membrane component; chromosomal 4; surface ma	56.8
115221	AA262942	Hs.79741	ESTs	56.1
108059	AA043944	Hs.62663	ESTs	52.3
121853	AA425887	Hs.98502	ESTs	47.8
133504	W95070	Hs.74316	desmoplakin (DPI; DP1)	47.0
103546	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	46.5
100147	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin I-lik	45.5
102979	X17042	Hs.1908	proteoglycan 1; secretory granule	44.6
130967	AA134138	Hs.182579	Homo sapiens leucine aminopeptidase mRNA; com	44.5
102009	U02680	Hs.82643	protein tyrosine kinase 9	40.4
126960	AA317900	Hs.161758	ESTs	39.6
103111	X63187	Hs.2719	epididymis-specific; whey-acidic protein type	39.1
133829	AA453783	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (from c	39.0
111223	N68921	Hs.34808	ESTs; Weakly similar to neogenin [H.sapiens]	38.9
102803	U89916	Hs.26126	claudin 10	38.8
104943	AA065217	Hs.169574	ESTs	38.7
106605	AA457718	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (from cl	38.4
120555	AA287347	Hs.238205	ESTs	38.1
102968	X16396	Hs.154672	methylene tetrahydrofolate dehydrogenase (NAD	36.3
104052	AA393164	Hs.97644	mammaglobin 2	36.0
109166	AA179845	Hs.73625	RAB6 interacting; kinesin-like (rakinesin6)	35.9
101332	L47276	Hs.147276	Homo sapiens (cell line HL-6) alpha topoisoma	35.0
106187	AA425906	Hs.7956	ESTs	34.5
101042	J05428	Hs.10319	UDP glycosyltransferase 2 family; polypeptide	34.3
125852	H09290	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (from c	33.7
101201	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin; uteri	32.3
126410	R51912	Hs.12409	somatostatin	32.1
134326	U16306	Hs.81800	chondroitin sulfate proteoglycan 2 (versican)	32.0
125739	AA428557	Hs.92137	v-myc avian myelocytomatosis viral oncogene h	31.6
132254	L20826	Hs.430	plastin 1 (I isoform)	31.4
112610	R79392	Hs.23643	ESTs	30.9
101441	M21005	Hs.100000	S100 calcium-binding protein A8 (calgranulin	30.6
116345	AA496981	Hs.199067	HER3 receptor tyrosine kinase (c-erbB3; ERBB3	30.1
108860	AA133334	Hs.129911	ESTs	29.8
133859	U86782	Hs.178761	26S proteasome-associated pad1 homolog	29.2
107295	T34527	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polypeptid	28.9
106210	AA428239	Hs.10338	ESTs	28.9
134711	X04011	Hs.88974	cytochrome b-245; beta polypeptide (chronic g	28.0
125769	AI382972	Hs.82128	5T4 oncofetal trophoblast glycoprotein	27.5
107222	D51235	Hs.82689	tumor rejection antigen (gp96) 1	27.4
102260	U28386	Hs.159557	karyopherin alpha 2 (RAG cohort 1; importin a	26.9
134691	M59979	Hs.88474	prostaglandin-endoperoxide synthase 1 (prosta	26.8
105588	AA279215	Hs.10867	ESTs	26.3
130718	N70196	Hs.18376	ESTs	26.3
111185	N67551	Hs.12844	EGF-like domain; multiple 6	25.6
131965	W90146	Hs.35962	ESTs	25.6
132903	AA235404	Hs.5985	Homo sapiens clone 25186 mRNA sequence	25.6
114359	Z41589	Hs.153483	ESTs; Moderately similar to H1 chloride chann	25.5

	101185	L19872	Hs.170087	aryl hydrocarbon receptor	25.2
	128742	D00763	Hs.251531	proteasome (prosome; macropain) subunit; alph	25.1
	116724	F13665	Hs.65641	ESTs	24.9
5	111929	R40057	Hs.112360	prominin (mouse)-like 1	24.9
	102915	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin 2)	24.8
	131210	AA430047	Hs.24248	ESTs	24.7
	101714	M68874		Human phosphatidylcholine 2-acylhydrolase (cP	24.6
	100154	D14657	Hs.81892	KIAA0101 gene product	24.6
10	134656	X14787	Hs.87409	thrombospondin 1	24.3
	100294	D49396	Hs.75454	antioxidant protein 1	23.9
	104080	AA402971	Hs.57771	kallikrein 11	23.7
	107056	AA600310	Hs.18720	programmed cell death 8 (apoptosis-inducing f	23.7
	115697	AA411502	Hs.63325	ESTs; Weakly similar to airway trypsin-like p	23.7
	130350	U02020	Hs.239138	pre-B-cell colony-enhancing factor	23.7
15	105870	AA399623	Hs.23505	ESTs	23.6
	118528	N67889	Hs.49397	ESTs	23.4
	105309	AA233790	Hs.4104	ESTs; Weakly similar to cDNA EST yk386g7.5 co	23.2
	109680	F09255	Hs.4993	ESTs	23.2
20	131501	AA121127	Hs.181307	H3 histone; family 3A	23.2
	100824	HG4058-HT4328		Oncogene Aml1-Evl-1, Fusion Activated	23.1
	111890	R38678	Hs.12365	ESTs	23.0
	101543	M31166	Hs.2050	pentoxin-related gene; rapidly induced by IL-	22.8
	102095	U11313	Hs.75760	sterol carrier protein 2	22.8
25	114988	AA251089	Hs.94576	ESTs; Weakly similar to phosphatidylcholine [H	22.8
	120695	AA291468		ESTs	22.8
	130941	D49394	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3A	22.8
	106654	AA460449	Hs.3784	ESTs; Highly similar to phosphoserine aminotr	22.7
	109141	AA176428	Hs.193380	ESTs	22.6
30	102345	U37283	Hs.58882	Microfibril-associated glycoprotein-2	22.6
	116652	AA405098	Hs.38178	ESTs	22.4
	100103	AF007875	Hs.5085	dolichyl-phosphate mannosyltransferase polype	22.3
	105463	AA253370	Hs.32846	ESTs	22.2
	132624	AA164819	Hs.53631	ESTs	22.2
35	119743	W70242	Hs.58086	ESTs	22.0
	132528	AA283006	Hs.50758	chromosome-associated polypeptide C	22.0
	107174	AA621714	Hs.25338	ESTs	21.8
	134495	D63477	Hs.84087	KIAA0143 protein	21.8
	131985	AA434329	Hs.36563	ESTs	21.5
40	105832	AA398346	Hs.21898	ESTs	21.2
	126160	N90960	Hs.247277	ESTs; Weakly similar to transformation-relate	21.2
	114846	AA234929	Hs.44343	ESTs	20.9
	109703	F09684	Hs.24792	ESTs; Weakly similar to ORF YOR283w [S.cerevi	20.9
	135154	AA126433	Hs.173242	sorting nexin 4	20.8
45	131185	M25753	Hs.23960	cyclin B1	20.7
	105616	AA280670	Hs.24968	ESTs	20.5
	131148	C00038	Hs.23579	ESTs	20.2
	129337	R63542	Hs.110488	KIAA0990 protein	20.2
50	133640	D83004	Hs.75355	ubiquitin-conjugating enzyme E2N (homologous	20.1
	127479	AA513722	Hs.179729	collagen; type X; alpha 1 (Schmid metaphyseal	19.9
	133711	J04130	Hs.75703	small inducible cytokine A4 (homologous to mo	19.8
	131818	Z39297	Hs.3281	neuronal pentraxin II	19.7
	125303	Z39821	Hs.107296	ESTs	19.6
	109112	AA169379	Hs.72865	ESTs	19.5
55	105376	AA236559	Hs.8768	ESTs; Weakly similar to IIII ALU SUBFAMILY SQ	19.2
	103605	Z35402	Hs.194657	cadherin 1; E-cadherin (epithelial)	19.1
	100661	HG2874-HT3018		Ribosomal Protein L39 Homolog	19.1
	129571	X51630	Hs.1145	Wilms tumor 1	19.0
	115239	AA278650	Hs.73291	ESTs; Weakly similar to similar to the beta t	18.9
60	131562	U90551	Hs.28777	H2A histone family; member L	18.9
	131272	AA423884	Hs.139033	paternally expressed gene 3	18.9
	130343	AA490262	Hs.15485	ESTs; Weakly similar to APICAL-LIKE PROTEIN I	18.8
	103245	X76648	Hs.28988	glutaredoxin (thioltransferase)	18.7
	101809	M86849		Homo sapiens connexin 26 (GJB2) mRNA, complet	18.6
65	105344	AA235303	Hs.8645	ESTs	18.4
	135225	AA455988	Hs.9667	butyrobetaine (gamma); 2-oxoglutarate dioxyge	18.4
	118788	H25836	Hs.83429	tumor necrosis factor (ligand) superfamily; m	18.3
	131510	AA207114	Hs.27842	ESTs; Weakly similar to similar to 1-acyl-gly	18.2
	124059	F13673	Hs.99769	ESTs	18.0
70	103352	X89398	Hs.78853	uracil-DNA glycosylase	17.9
	132742	AA490862	Hs.55901	ESTs; Weakly similar to C43H8.1 [C.elegans]	17.9
	135242	M74093	Hs.9700	cyclin E1	17.9
	123494	AA599786	Hs.112110	ESTs	17.8
	129168	T90621	Hs.109052	chromosome 14 open reading frame 2	17.7
75	128517	AA280617	Hs.100861	ESTs; Weakly similar to p60 katanin [H.sapien	17.6
	130160	Z39228	Hs.151344	UDP-Gal-beta-GlcNAc beta 1;3-galactosyltransfe	17.6
	103448	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	17.5
	119708	W67810	Hs.57904	mago-nashi (Drosophila) homolog; proliferatio	17.5
	122946	AA477445	Hs.105341	ESTs	17.5
80	125819	AA044840	Hs.251871	CTP synthase	17.5
	131689	AA599653	Hs.30696	transcription factor-like 5 (basic helix-loop	17.5
	115061	AA253217	Hs.41271	ESTs	17.3
	113702	T97307	Hs.161720	ESTs; Moderately similar to IIII ALU SUBFAMIL	17.3
	115291	AA279943	Hs.122579	ESTs	17.3
	102567	U59863	Hs.146847	TRAF family member-associated NFKB activator	17.2

	129229	AA211941	Hs.109643	polyadenylate binding protein-interacting pro	17.2
	129351	AA167268	Hs.62349	Human ras inhibitor mRNA; 3' end	17.2
	110769	N22222		yw34b06.s1 Morton Fetal Cochlea Homo sapiens	17.1
5	113182	T55234	Hs.9676	Human DNA sequence from clone 30M3 on chromos	17.0
	115892	AA435946	Hs.50831	ESTs	17.0
	123114	AA488407	Hs.105235	ESTs; Moderately similar to KIAA0454 protein	17.0
	123442	AA598803	Hs.111496	ESTs	17.0
	123339	AA504253	Hs.101615	ESTs	16.9
10	123689	AA609556	Hs.256562	ESTs	16.9
	131941	D62657	Hs.35086	ubiquitin-specific protease 1	16.8
	120649	AA287115	Hs.99697	ESTs	16.8
	102139	U15932	Hs.2128	dual specificity phosphatase 5	16.8
	115522	AA331393	Hs.47378	ESTs	16.7
15	135243	AA215333	Hs.97101	putative G protein-coupled receptor	16.6
	131257	AA256042	Hs.24908	ESTs	16.5
	109508	AA233892	Hs.55902	ESTs; Weakly similar to IIII ALU SUBFAMILY SX	16.3
	132701	AA279359	Hs.55220	BCL2-associated atlanogene 2	16.3
	134449	L31155	Hs.83450	laminin; alpha 3 (niceln (150kD); kalinin (16	16.3
20	126180	R18070	Hs.3712	ubiquinol-cytochrome c reductase; Rieske iron	16.3
	106124	AA423987	Hs.7587	ESTs	16.2
	115363	AA282071	Hs.152759	activator of S phase kinase	16.2
	117588	N34895	Hs.44648	ESTs	16.1
	131245	AA620599	Hs.24766	DKFZP564E1962 protein	16.1
25	101674	M61916	Hs.82124	laminin; beta 1	16.0
	126819	AA305536	Hs.161489	ESTs	16.0
	134039	S78569	Hs.78672	laminin; alpha 4	16.0
	130648	AA075427	Hs.17298	ESTs; Weakly similar to /prediction	15.9
	102823	U90914	Hs.5057	carboxypeptidase D	15.8
30	128470	AA447604	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (from cl	15.8
	115844	AA430124	Hs.234607	ESTs	15.7
	132543	AA417152	Hs.5101	protein regulator of cytokinesis 1	15.7
	130155	L33404	Hs.151254	kallikrein 7 (chymotryptic; stratum corneum)	15.7
	101008	J04162	Hs.763	Fc fragment of IgG; low affinity IIa; recept	15.7
35	120472	AA251875	Hs.104472	ESTs; Weakly similar to Gag-Pol polyprotein [15.6
	116844	H54938	Hs.38331	ESTs	15.6
	106753	AA476944	Hs.7331	ESTs	15.6
	114767	AA148885	Hs.154443	minichromosome maintenance deficient (S. cere	15.5
	114768	AA149007	Hs.182339	Ets homologous factor	15.5
40	127370	A1024352	Hs.70337	immunoglobulin superfamily; member 4	15.5
	101507	M27492	Hs.82112	Interleukin 1 receptor; type I	15.4
	102519	U52959	Hs.80296	Purkinje cell protein 4	15.4
	102610	U65011	Hs.30743	preferentially expressed antigen in melanoma	15.4
	111244	N69556	Hs.24724	MFH-amplified sequences with leucine-rich tan	15.4
45	120404	AA234921	Hs.96427	KIAA1013 protein	15.3
	130455	X17059	Hs.155956	N-acetyltransferase 1 (arylamine N-acetyltran	15.2
	129519	AA298786	Hs.112242	ESTs	15.1
	106553	AA454967	Hs.5887	ESTs; Highly similar to RNA binding motif pro	15.0
	109502	AA233837	Hs.44755	ESTs; Weakly similar to membrane glycoprotein	14.9
50	115967	AA446887	Hs.42911	ESTs	14.9
	104636	AA004415	Hs.106106	ESTs	14.9
	134133	X33920	Hs.180383	dual specificity phosphatase 6	14.9
	134444	X04470	Hs.251754	secretory leukocyte protease inhibitor (antil	14.8
	132698	Y00062	Hs.170121	protein tyrosine phosphatase; receptor type;	14.8
55	131997	D82399	Hs.136644	Homo sapiens clone 23714 mRNA sequence	14.8
	134056	R27358	Hs.7886	ESTs; Weakly similar to Pelle associated prot	14.6
	101249	L33881	Hs.1904	protein kinase C; tota	14.5
	105298	AA233459	Hs.26369	ESTs	14.5
	107119	AA620307	Hs.27379	ESTs	14.5
60	115839	AA429038	Hs.40541	ESTs	14.5
	122802	AA460530	Hs.256579	ESTs	14.5
	129896	AA043021	Hs.13225	UDP-GalbetaGlcNAc beta 1;4- galactosyltransf	14.3
	130269	AA284694	Hs.168352	nucleoporin-like protein 1	14.3
	134374	D62633	Hs.8236	ESTs	14.3
65	106370	AA443841	Hs.18676	sprouty (Drosophila) homolog 2	14.2
	130919	AA291710	Hs.21276	collagen; type IV; alpha 3 (Goodpasture antig	14.1
	132923	U21858	Hs.60679	TATA box binding protein (TBP)-associated fac	14.1
	107968	AA034020	Hs.61539	ESTs	14.1
	125390	H95094	Hs.75187	translocase of outer mitochondrial membrane 2	14.1
70	107148	AA621131	Hs.5889	ESTs; Weakly similar to W01A11.2 gene product	14.1
	110788	N24730	Hs.15420	ESTs	14.0
	109481	AA233342	Hs.90680	ESTs; Weakly similar to WD40 protein Ciao 1 [13.9
	105646	AA282147	Hs.5888	ESTs	13.9
	106030	AA412251	Hs.12802	development and differentiation enhancing fac	13.8
75	132618	AA253330	Hs.5344	adaptor-related protein complex 1; gamma 1 su	13.7
	133230	S82240	Hs.6838	ras homolog gene family; member E	13.7
	124803	R45480	Hs.164866	cyclin K	13.6
	121381	AA405747	Hs.97865	ESTs; Weakly similar to WASP-family protein [13.6
	105200	AA195399	Hs.24641	ESTs	13.5
80	105627	AA281245	Hs.23317	ESTs	13.5
	114986	AA251010	Hs.87807	ESTs	13.5
	118036	N52844	Hs.196008	ESTs	13.5
	134672	N79749	Hs.87627	ESTs; Weakly similar to cDNA EST EMBL-T00542	13.5
	110915	N46252	Hs.29724	ESTs	13.3
	117984	N51919	Hs.47368	ESTs	13.3

	132550	AA029597	Hs.170195	bone morphogenetic protein 7 (osteogenic prot	13.3
	124315	H94892	Hs.6906	v-rat simian leukemia viral oncogene homolog	13.2
	102547	U57911	Hs.46638	chromosome 11 open reading frame 8	13.2
5	125134	W19228	Hs.100748	ESTs	13.2
	111806	R33468	Hs.24651	ESTs	13.1
	106983	AA521195	Hs.10887	similar to lysosome-associated membrane glyco	13.0
	106498	AA452141	Hs.7171	ESTs	13.0
	110787	N24718	Hs.12244	ESTs; Weakly similar to C4489.1 [C.elegans]	13.0
10	122860	AA464414	Hs.112159	ESTs	13.0
	131535	AA504842	Hs.28436	ESTs; Weakly similar to coded for by C. eleg	13.0
	116188	AA464728	Hs.184598	ESTs	13.0
	107243	D59489	Hs.34727	ESTs	12.9
	129300	C20976	Hs.110165	ESTs; Highly similar to ribosomal protein L26	12.9
15	134487	R38185	Hs.83954	Homo sapiens unknown mRNA	12.8
	102348	U37519	Hs.87539	aldehyde dehydrogenase 8	12.8
	131839	H80622	Hs.33010	KIAA0633 protein	12.8
	118620	W47620	Hs.56009	2'-5'-oligoadenylate synthetase 3	12.8
	120802	AA343533	Hs.128777	ESTs; Weakly similar to predicted using Genef	12.7
20	102250	U28014	Hs.74122	caspase 4; apoptosis-related cysteine proteas	12.7
	105539	AA258873	Hs.25242	ESTs	12.7
	114965	AA250737	Hs.72472	ESTs	12.7
	118001	N52151	Hs.47447	ESTs	12.7
	100448	D87469	Hs.57652	EGF-like-domain; multiple 2	12.6
25	130920	D50975	Hs.75525	cathectin	12.6
	131075	Y00757	Hs.2265	secretory granule; neuroendocrine protein 1 (12.6
	105496	AA256323	Hs.25264	DKFZP434N126 protein	12.5
	109235	AA193592	Hs.42300	ESTs; Weakly similar to [H] ALU SUBFAMILY SQ	12.5
	118216	N62185	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A synthas	12.5
30	134388	M15841	Hs.82575	small nuclear ribonucleoprotein polypeptide B	12.5
	106897	AA489790	Hs.167496	RAN binding protein 6	12.4
	133050	S67325	Hs.63788	propionyl Coenzyme A carboxylase; beta polype	12.4
	109683	F09308	Hs.27607	ESTs	12.3
	121463	AA411745	Hs.239681	ESTs; Weakly similar to KIAA0554 protein [Hs	12.3
35	102876	X03663	Hs.174142	colony stimulating factor 1 receptor; formerl	12.2
	101804	M86699	Hs.169840	TTK protein kinase	12.2
	129017	H13108	Hs.107968	ESTs	12.1
	105812	AA394126	Hs.20814	ESTs; Highly similar to CGI-27 protein [Hsap	12.1
	106459	AA49741	Hs.4029	glioma-amplified sequence-41	12.0
40	107059	AA608545	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli RacA ho	12.0
	107080	AA609210	Hs.19221	ESTs	12.0
	107799	N26101	Hs.7838	Human ring zinc-finger protein (ZNF127-Xp) ge	12.0
	112253	R51818	Hs.104222	Homo sapiens mRNA; cDNA DKFZp566L034 (from cl	12.0
	116760	H11054	Hs.155342	protein kinase C; delta	12.0
45	120314	AA194166	Hs.221040	KIAA1038 protein	12.0
	123005	AA479726	Hs.105577	ESTs	12.0
	132572	AA448297	Hs.237825	signal recognition particle 72kD	12.0
	110661	H59617	Hs.5199	ESTs; Weakly similar to UBIQUITIN-CONJUGATING	12.0
	101823	S75256		HNL=neutrophil lipocalin [human, ovarian canc	11.9
50	134992	H05625	Hs.92414	ESTs	11.8
	105516	AA257971	Hs.21214	ESTs	11.8
	105248	AA226968	Hs.22826	ESTs	11.7
	109130	AA172040	Hs.20161	ESTs; Weakly similar to IgE receptor beta sub	11.7
	115955	AA446121	Hs.44198	Homo sapiens BAC clone RG054D04 from 7q31	11.7
55	116135	AA460314	Hs.94179	ESTs	11.7
	116284	AA487252	Hs.237809	ESTs; Weakly similar to hypothetical protein	11.7
	132384	AA479933	Hs.46967	Human DNA sequence from clone 167A19 on chrom	11.7
	134753	Y09216	Hs.173135	dual-specificity tyrosine-(Y)-phosphorylation	11.7
	125136	W31479	Hs.129051	ESTs	11.7
60	133928	N34096	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homologou	11.6
	117395	N26330	Hs.93701	ESTs	11.5
	127007	AA289360		EST11857 Uterus tumor I Homo sapiens cDNA 5'	11.5
	130567	L07493	Hs.1608	replication protein A3 (14kD)	11.5
	135073	AA452000	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (from c	11.5
65	115140	AA258030	Hs.55356	ESTs; Weakly similar to supported by GENSCAN	11.4
	115536	AA347193	Hs.62180	ESTs	11.4
	133240	D31161	Hs.68613	ESTs	11.3
	106521	AA453431	Hs.14732	malic enzyme 1; NADP(+)-dependent; cytosolic	11.3
	107674	AA011027	Hs.41143	KIAA0581 protein	11.3
70	114149	Z38814	Hs.27196	ESTs	11.3
	132478	H20906	Hs.49500	KIAA0746 protein	11.2
	104252	AF002246	Hs.210863	cell adhesion molecule with homology to L1CAM	11.2
	102436	U46499	Hs.790	microsomal glutathione S-transferase 1	11.2
	106726	AA465339	Hs.7141	ESTs	11.2
	100116	D00654	Hs.77443	actin; gamma 2; smooth muscle; enteric	11.2
75	110970	N51374	Hs.96870	Homo sapiens mRNA full length insert cDNA clo	11.2
	130417	U58522	Hs.155485	huntingtin-interacting protein 2	11.2
	132906	AA142857	Hs.234896	ESTs; Highly similar to gominin [Hsapians]	11.2
	107853	AA024427	Hs.59461	DKFZP434C245 protein	11.2
80	103467	Y00451	Hs.78712	aminolevulinatase; delta; synthase 1	11.1
	100438	D87448	Hs.91417	topoisomerase (DNA) II binding protein	11.1
	102654	U68494	Hs.24385	Human hbc647 mRNA sequence	11.1
	103172	X68742	Hs.116774	integrin; alpha 1	11.1
	106856	AA486183	Hs.15839	ESTs; Weakly similar to similar to oxysterol-	11.1
	108255	AA063157	Hs.172608	ESTs	11.1

	124308	H93575	Hs.227146	Homo sapiens mRNA; cDNA DKFZp564J142 (from cl	11.1
	129057	X62466	Hs.214742	CDWS2 antigen (CAMPATH-1 antigen)	11.1
	128845	AA455658	Hs.10649	basement membrane-induced gene	11.1
5	129025	AA420992	Hs.103441	ESTs; Weakly similar to testicular teklin B1-	11.0
	107638	AA009528	Hs.42743	ESTs; Weakly similar to predicted using Genef	11.0
	134480	AA024664	Hs.83916	NADH dehydrogenase (ubiquinone) 1 alpha subco	11.0
	115262	AA279112	Hs.88594	ESTs	11.0
	102580	U60808	Hs.152981	CDP-diacylglycerol synthase (phosphatidate cy	10.9
10	106614	AA458934	Hs.179912	ESTs	10.9
	107115	AA610108	Hs.27693	ESTs; Highly similar to CGI-124 protein [H.s	10.9
	115764	AA421562	Hs.91011	anterior gradient 2 (Xenopus laevis) homolog	10.9
	121770	AA421714	Hs.11469	KIAA0896 protein	10.9
	132191	AA449431	Hs.158688	KIAA0741 gene product	10.9
	133214	Y10659	Hs.250911	interleukin 13 receptor; alpha 1	10.9
15	133914	N32811	Hs.77542	ESTs	10.8
	101973	S82597	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polypeptid	10.8
	102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	10.8
	104147	AA451992	Hs.226799	ESTs; Highly similar to HSPC039 protein [H.s	10.8
20	106474	AA450212	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (from cl	10.8
	115881	AA435577	Hs.184942	G protein-coupled receptor 64	10.8
	129950	M31516	Hs.1369	decay accelerating factor for complement (CD5	10.8
	132783	N74897	Hs.5683	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide	10.8
	133784	AA214305	Hs.76173	ESTs	10.8
25	134248	AA292677	Hs.80624	ESTs	10.8
	105565	AA278302	Hs.18349	ESTs; Weakly similar to partial CDS [C.elegan	10.8
	127999	AA837495	Hs.69851	ESTs; Weakly similar to Wiskott-Aldrich syndr	10.8
	108040	AA041551	Hs.48644	ESTs	10.7
	130367	Z38501	Hs.8768	ESTs; Weakly similar to IIII ALU SUBFAMILY SQ	10.7
30	108539	AA084677	Hs.54558	ESTs; Weakly similar to protein B [H.sapiens]	10.7
	111345	N89820	Hs.14559	ESTs	10.7
	115583	AA398913	Hs.45231	LDOC1 protein	10.7
	128965	T17440	Hs.107418	ESTs	10.7
	101396	M15796	Hs.78996	proliferating cell nuclear antigen	10.6
35	132164	U84573	Hs.41270	procollagen-lysine; 2-oxoglutarate 5-dioxygen	10.6
	101275	L37936	Hs.3273	Ts translation elongation factor; mitochondri	10.6
	104660	AA007160	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (from cl	10.6
	108609	AA100694	Hs.69499	Human DNA sequence from BAC 15E1 on chromosom	10.6
	112041	R43300	Hs.22829	ESTs	10.6
40	114208	Z39301	Hs.7859	ESTs	10.6
	118537	N67974	Hs.75431	fibrinogen; gamma polypeptide	10.6
	106919	AA490885	Hs.21766	ESTs	10.6
	115984	AA447687	Hs.91109	ESTs	10.6
	105538	AA258860	Hs.32597	ring finger protein (C3H2C3 type) 6	10.6
45	102200	U21551	Hs.157205	branched chain aminotransferase 1; cytosolic	10.5
	116710	F10577	Hs.70312	ESTs	10.5
	119780	W72967	Hs.191381	ESTs; Weakly similar to hypothetical protein	10.5
	112996	T23539	Hs.7165	zinc finger protein 259	10.5
	103029	X54489	Hs.789	GRO1 oncogene (melanoma growth stimulating ac	10.5
50	101255	L34600	Hs.149894	mitochondrial translational initiation factor	10.4
	107032	AA599472	Hs.247309	succinate-CoA ligase; GDP-forming; beta subun	10.4
	125617	A1287461	Hs.164950	ESTs	10.4
	131475	Z39053	Hs.27263	ESTs	10.4
	132073	N67408	Hs.38516	ESTs	10.4
55	101469	M22877	Hs.169248	Human somatic cytochrome c (HCS) gene; comple	10.3
	102437	U46569	Hs.221986	aquaporin 5	10.3
	104301	D45332	Hs.6783	ESTs	10.3
	127236	A1341818	Hs.98658	budding uninhibited by benzimidazoles 1 (yeas	10.3
	101465	M22612	Hs.241395	protease; serine; 1 (trypsin 1)	10.3
60	113805	W42957	Hs.250617	ESTs	10.2
	133538	Y00264	Hs.177486	amyloid beta (A4) precursor protein (protease	10.2
	109799	F10770	Hs.180378	Homo sapiens clone 669 unknown mRNA; complete	10.2
	113523	T90037	Hs.16686	ESTs	10.2
	116195	AA465148	Hs.72402	ESTs	10.2
65	134542	X57025	Hs.85112	Insulin-like growth factor 1 (somatomedin C)	10.2
	125298	Z39255	Hs.235350	YDD19 protein	10.2
	119367	T78324	Hs.90905	ESTs	10.2
	134470	X54942	Hs.83758	CDC28 protein kinase 2	10.2
	134288	AA430008	Hs.8117	ESTs	10.1
70	105127	AA158132	Hs.11817	ESTs; Weakly similar to contains similarity t	10.1
	110627	H70485	Hs.35225	ESTs; Weakly similar to MBNL protein [H.sapia	10.1
	115188	AA261819	Hs.88367	ESTs	10.1
	132632	N59764	Hs.5398	guanine-monophosphate synthetase	10.1
	124049	F10523	Hs.74519	primase; polypeptide 2A (58kD)	10.1
75	100079	AB002365	Hs.23311	KIAA0367 protein	10.0
	113987	W87494	Hs.9841	ESTs; Moderately similar to COMPLEMENT C1Q SU	10.0
	117280	N22107	Hs.172241	ESTs	10.0

TABLE 98:

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey	CAT Number	Accession
100661	23182_1	BE623001 L05096 AA383604 AW966416 N53295 AA460213 AW571519 AA603655

101332	25130_1	J04088 NM_001067 AF071747 AJ011741 NB5424 AL042407 AA218572 BE296748 BE083981 AL040877 AW499918 AW675045 H17813 BE081283 AA670403 AW504327 BE094229 AA104024 A1471482 A1970337 AA737616 A1827444 AW003286 A1742333 A1344044 A1765634 A1948838 AW235336 AW172827 AA095289 BE046383 A1734240 W16699 A1660329 A1289433 AA933778 AW489242 AA468838 AA808983 AA625873 W78031 BE206307 AA550803 A1743147 A1990075 AA948274 AA129533 A1635399 AA605313 A1624669 AW594319 A1221834 A1337434 AA307706 BE550282 A1760467 A1630636 A1221521 AW674314 AW078889 A1933732 A1686969 A1186928 AW074595 A1127486 AL079544 A1910815 H17814 AA310903 AW137854 T19279 AA026682 AA306035 AW383390 AW383389 AW383422 AW383427 AW383395 H09977 AA306247 AA352501 AW403639 F05421 AA224473 AA305321 H83904 AA089612 AW391543 AW029155 AW173382 AW402701 AW403113 R94438 N73126 H93466 AA090928 AA095051 T29025 AW951071 L47277 L47276 A1375913 BE384156 W24652 AA746288 AA568223 BE090591 H93033 N57027 AA504348 AA327653 AW959913 N53767 AA843715 A1453437 AW263710 A1076594 AA583483 AW873194 AW575166 A1128799 A1803319 AL042776 AW074313 A1887722 A1032284 AA447521 A1123885 N23334 A1354911 AW090687 AA236763 AA435535 AA236910 AA047124 AA236734 AW514610 H83467 AA962007 AA446783 AA127259 A1613495 A1686720 A1587374 AA936731 AA702453 A1859757 AA216786 A1251819 A1469227 AA806022 A1092324 N71868 AA968782 AA236919 AA809450 AA227220 AA765284 A1192007 AA768810 AA805794 AA729280 AA806238 AW768817 N71879 A1050686 AA505822 AA688974 A1688160 BE045915 AW466315 AA731314 AA649568 AA834316 AW591901 AW063876 AW294770 A1300266 A1336094 A1560380 AA721755 H09978 D20305 D29155 AW821790 BE150864 F01675 A1457474 AW466316 AA550969 AA630788 A1383237 A1521317 A1761348 AF025841 D43968 AW994587 L34598 AF025841 D89789 D89788 D89790 AW998932 A971742 A1310238 X09076 AW139668 AW674280 A1365552 AA877452 AV657554 C75229 AA376077 A1780656 AW609213 W25586 H30149 BE075089 BE075190 AW580858 H99598 AA425238 AA133916 AW363478 BE158121 BE158127 AW467960 BE158135 BE158128 BE158145 N92860 AA847248 A1961688 A1361423 AA878154 AA043767 A1863712 A1559226 AW339007 A1371266 A1688901 AA046624 AA134739 AW449154 AA130232 A1458720 AA962511 A1070627 R70437 AW004008 AA045229 A1671572 H99599 AA043768 A1685454 A1871685 N29937 X09077 AA524240 A1142114 A1825750 A1567805 A1631365 A1347893 AA134740 F20669 AA046707 AW793216 AW963298 AW959380 AA363265 A1784593 A1268201 R69451 AV657618 A1695588 M68874 AL022147 M72393 AL049797 BE439441 T27650 A1766240 AW150345 AW778943 A1627464 BE439479 AA587049 A1277800 A1984983 A1630935 M86849 AA315280 NM_004004 AA315269 BE142653 AA461400 AW802042 BE152893 AW383155 AA490688 AW117930 AW384563 AW384544 AW384566 AW378307 AW378323 AW383085 AA257102 AW378317 AW276060 AW271245 AW378298 AW384497 A1598114 AW264544 A1018136 AW021810 AA961504 AW086214 AW771489 AW192483 A1290266 AW192488 AW384490 AW007451 AW890895 AA554460 AA613715 AW020066 A1783695 A1589498 A1917637 AW264471 AW384491 A1816732 AW368530 AW368521 AW368463 AA461087 A1341438 A1970613 A1040737 A1418400 AA947181 AA962716 A1280695 AW769275 AW023591 A1160977 AA055400 N71882 AA490466 AW243772 AW316636 A1076554 AW511702 N69323 H88912 AA257017 A1952506 H88913 A1912481 AA600714 BE465701 N64149 C00523 N64240 AA677120 X99133 X83006 W38398 AA401137 A1298242 AA366738 AA308126 AW583781 AA298668 AW845024 BE140204 AW845005 U47734 AA837575 NM_005564 AA329732 AA421943 BE171567 S75256 A1750047 A1762213 AA100735 AW612993 A1474120 AW062884 A1940001 AW062852 AW062899 BE182639 AW778875 AA528093 AW517424 A1939989 AA076188 BE182636 AA169569 AA167439 A1283967 A1677783 AA076140 A1749649 AA166792 A1708618 AA400973 AA514773 AA514789 AA164458 AA167440 AA074845 AA421944 AA514874 AA079557 AA102361 AA587027 AA642930 AA878029 AA164459 AW176400 AW475086 AA857522 AA148193 AA838234 AA593897 A1284506 AW193324 AA148194 AW583341 A1669077 AW264913 AA074902 A1680515 AA169874 AA169614 AA079551 AW591737 AW190644 AA076565 AA662747 AA075896 AA535642 N27757 A1306666 AA074727 N79823 AA524360 A1826800 AA173827 BE140374 BE004062 AW265060 BE184103 A1199258 AA857853 AA299459 AA837890 A1626104 AA503624 BE183618 BE183717 AA573267 A1833071 AW270590 AA506601 BE004010 AA837854 A1675895 A1810491 A1184883 AW664712 AA076046 AA515574 AW352267 A1797418 AA172395 A1749194 A1559933 AA502597 AA321220 A1866124 A1695633 AA494293 AW085635 AA165649 AA165663 AB037771 BE005079 AA394189 AW959650 AA299360 AA398081 W37627 AW750817 AW630138 A1522058 BE326323 AA374890 AW418534 AW997510 AW995214 AW959649 AA504426 D79223 D79621 A1276062 A1973155 AA653470 AA337887 A1382521 AW084427 D57078 W37628 A1610506 Z30230 A1567034 AA766091 H25097 H25078 AW991507 AA319736 BE000831 AA541787 AW173038 AA327831 AW117510 AW664665 A1066624 A1478955 A1863075 A1073744 AA490170 R46651 A1075653 F02865 N22222 AW972956 AA976503 A1917802 AA953664 AA404613 AA428771 BE280542 AW194691 A1927301 A1740458 A1796100 A1935603 AW052210 AA970201 A1633384 AA425910 A1017004 A1241295 AA402816 AA281468
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Table 10A lists about 733 genes up-regulated in ovarian cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" ovarian cancer level was set to be about the 80th percentile amongst various ovarian cancers. The "average" normal adult tissue level was set to be the 90th percentile value amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 10A: ABOUT 733 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES

Pkey: Primkey

Ex. Accn: Exemplar Accession

UG ID: UniGene ID

Title: UniGene title

ratio: ratio tumor vs normal tissues

Pkey	Ex. Accn	UG ID	Title	ratio
432938	T27013	Hs.3132	steroidogenic acute regulatory protein	56.1
418179	X51630	Hs.1145	Wilms tumor 1	33.5
400292	AA250737	Hs.72472	BMPLR-1b; bone morphogenetic protein receptor	30.0
452838	U65011	Hs.30743	Preferentially expressed antigen in melanoma	29.5
415511	A1732617	Hs.182362	ESTs	28.1
422956	BE545072	Hs.122579	ESTs	28.1
410929	H47233	Hs.30643	ESTs	27.4
400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromelysin 2)	25.2
449034	A1624049	Hs.277523	ghbts41a09.x1 NC1_CGAP_U1 Homo sapiens cDNA	23.7
427585	D31152	Hs.179729	collagen; type X; alpha 1 (Schmid metaphyseal	22.7
428392	H10233	Hs.2265	secretory granule, neuroendocrine protein 1	21.9
448243	AW369771	Hs.77496	ESTs	21.3
430691	C14187	Hs.103538	ESTs	21.2
444783	AK001468	Hs.62180	ESTs	20.8
407638	AJ404672	Hs.288693	EST	20.1
423739	AA398155	Hs.97600	ESTs	19.7
436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular matrix p	19.0
451110	A1955040	Hs.301584	ESTs	18.8
426427	M86699	Hs.169840	TTK protein kinase	18.7

	428227	AA321649	Hs.2248	INTERFERON-GAMMA INDUCED	18.3
	419854	AW664873	Hs.87836	Homo sapiens PAC clone RP5-1087M19 from 7q11.	18.3
	439706	AW872527	Hs.59761	ESTs	18.3
5	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	17.4
	410247	AF181721	Hs.61345	RU2S	17.0
	428153	AW513143	Hs.98367	hypothetical protein FLJ22252 similar to SRY-	16.9
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	16.6
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolog)	16.6
10	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related kinase	16.2
	423685	BE350494	Hs.49753	Homo sapiens mRNA for KIAA1551 protein, part	15.9
	428187	AI687303	Hs.285529	ESTs	15.9
	438817	AI023799	Hs.163242	ESTs	15.9
	424906	AI565086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3' untr	15.9
15	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphorylation	15.7
	412723	AA648459	Hs.179912	ESTs	15.3
	424717	H03754	Hs.152213	wingless-type MMTV integration site family, m	15.2
	443646	AI085198	Hs.298699	ESTs	15.1
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fs, clone NT2RP20	14.8
20	428976	AL037824	Hs.194695	ras homolog gene family, member 1	14.6
	418738	AW388633	Hs.6682	solute carrier family 7, member 11	14.3
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to M	14.2
	436209	AW850417	Hs.254020	ESTs, Moderately similar to unnamed protein p	14.1
	427356	AW023482	Hs.97849	ESTs	13.9
25	418601	AA279490	Hs.86368	calmeglin	13.8
	416681	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	13.7
	428532	AF157326	Hs.184786	TBP-interacting protein	13.6
	402408			0	13.6
	447350	AI375572	Hs.172634	ESTs; HER4 (c-erb-B4)	13.4
30	451807	W52854	Hs.27099	DKFZP564J0863 protein	13.4
	423575	C18863	Hs.163443	ESTs	13.2
	443211	AI128388	Hs.143655	ESTs	13.2
	437872	AK002015	Hs.5887	RNA binding motif protein 7	13.0
	451659	BE379761	Hs.14248	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	12.7
35	452904	AL157581	Hs.30957	Homo sapiens mRNA; cDNA DKFZp434E0628 (from c	12.7
	442655	AW027457	Hs.30323	ESTs	12.5
	452096	BE394901	Hs.226785	ESTs	12.4
	414972	BE263782	Hs.77695	KIAA0008 gene product	12.3
	435039	AW043921	Hs.130526	ESTs	12.3
40	447033	AI357412	Hs.157601	EST - not in UniGene	12.3
	433764	AW753676	Hs.39982	ESTs	12.2
	442611	BE077155	Hs.177537	ESTs	12.0
	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein, part	11.9
	427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3A	11.8
45	421478	AI683243	Hs.97258	ESTs	11.8
	426635	BE395109	Hs.129327	ESTs	11.8
	415989	AI267700	Hs.111128	ESTs	11.7
	433159	AB035898	Hs.150587	kinesin-like protein 2	11.5
	452249	BE394412	Hs.61252	ESTs	11.4
50	418506	AA084248	Hs.85339	G protein-coupled receptor 39	11.3
	442353	BE379594	Hs.49136	ESTs	11.3
	447700	AI420183	Hs.171077	ESTs, Weakly similar to similar to serine/thr	11.3
	450480	X82125	Hs.25040	zinc finger protein 239	11.3
	425176	AW015644	Hs.301430	ESTs, Moderately similar to TEF1_HUMAN TRANSC	11.2
55	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-related	11.2
	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated protein	11.1
	445258	AI635931	Hs.147613	ESTs	11.1
	432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polypeptid	11.0
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain-bind	10.9
60	404567			0	10.8
	423811	AW299598	Hs.50895	homeo box C4	10.7
	452891	N75582	Hs.212875	ESTs, Weakly similar to KIAA0357 [H.sapiens]	10.6
	441627	AA947552	Hs.58066	ESTs	10.3
	443555	N71710	Hs.21398	ESTs, Moderately similar to GNPI_HUMAN GLUCOS	10.3
65	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkinesin6)	10.2
	427469	AA403084	Hs.269347	ESTs	10.1
	415227	AW821113	Hs.72402	ESTs	10.1
	445413	AA151342	Hs.12677	CGI-147 protein	10.0
	425734	AF056208	Hs.159396	peptidylglycine alpha-amidating monooxygenase	10.0
70	421451	AA291377	Hs.50831	ESTs	10.0
	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leucine h	9.8
	427878	C05766	Hs.181022	CGI-07 protein	9.7
	408460	AA054726	Hs.285574	ESTs	9.7
	422972	N59319	Hs.145404	ESTs	9.7
75	443715	AI583187	Hs.9700	cyclin E1	9.7
	440901	AA909358	Hs.128612	ESTs	9.6
	453160	AI263307	Hs.146228	ESTs	9.6
	415211	R84730.comp	Hs.155986	ESTs; Highly similar to SPERM SURFACE PROTEIN	9.5
	425282	AW163518	Hs.155485	huntingtin interacting protein 2	9.5
80	400250			0	9.5
	410568	AW162948	Hs.64542	pre-mRNA cleavage factor Im (68kD)	9.3
	442957	AB949552	Hs.49397	ESTs	9.3
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1 (yeas	9.3
	434401	AI864131	Hs.71119	Putative prostate cancer tumor suppressor	9.2
	453628	AW243307	Hs.170187	ESTs	9.1

	452055	AI377431	Hs.293772	ESTs	9.1
	424088	AI351010	Hs.102267	lysyl oxidase	9.1
	442875	BE623003	Hs.23625	Homo sapiens clone TCCTA00142 mRNA sequence	9.1
5	416208	AW291168	Hs.41295	ESTs	9.0
	407168	RA5175	Hs.117183	gb:yg40101.s1 Soares infant brain 1N1B Homo s	9.0
	445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	8.9
	409269	AA576953	Hs.22972	Homo sapiens cDNA FLJ13352 fis, clone OVARC10	8.9
	433527	AW235613	Hs.133020	ESTs	8.9
10	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	8.8
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	8.7
	425665	AK001050	Hs.159066	ESTs	8.6
	443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT2RP30	8.6
	449433	AJ672096	Hs.9012	ESTs	8.6
	453878	AW964440	Hs.19025	ESTs	8.6
15	450505	NM_004572	Hs.25051	plakophilin 2	8.6
	407001	U12471	Hs.247954	Human thrombospondin-1 gene, partial cds	8.5
	414315	Z24878		gb:HSB65D052 STRATAGENE Human skeletal muscle	8.5
	425492	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	8.5
20	435181	AA669339	Hs.28838	KIAA1571 protein	8.5
	436396	AJ683487	Hs.299112	Homo sapiens cDNA FLJ11441 fis, clone HEMBA10	8.5
	418384	AW149266	Hs.25130	ESTs	8.4
	453370	AJ470523	Hs.182356	ESTs, Moderately similar to translation Init	8.4
	409041	AB033025	Hs.50081	KIAA1199 protein	8.4
25	447078	AW885727	Hs.301570	ESTs	8.4
	448674	W31178	Hs.154140	ESTs	8.3
	433393	AF038564	Hs.98074	atrophin-1 interacting protein 4	8.3
	433496	AF064254	Hs.49765	VERY-LONG-CHAIN ACYL-COA SYNTHETASE	8.3
	421155	H87879	Hs.102287	lysyl oxidase	8.2
30	438394	BE379623	Hs.27693	CGI-124 protein	8.2
	400298	AA032279	Hs.61635	STEAP1	8.1
	409092	AJ735283	Hs.172608	ESTs	8.1
	440250	AA876179	Hs.134650	ESTs	8.1
	409143	AW025980	Hs.138965	ESTs	8.1
35	407771	AL138272	Hs.62713	ESTs	8.1
	419088	AI538323	Hs.77496	ESTs	8.1
	431725	XG5724	Hs.2639	Norrie disease (pseudoglioma)	7.9
	431750	AA514988	Hs.283705	ESTs	7.9
	456335	AF220050	Hs.181385	uncharacterized hematopoietic stem/progenitor	7.9
40	441826	AW503603	Hs.129915	phosphotriesterase related	7.9
	417728	AW138437	Hs.24790	KIAA1573 protein	7.8
	418845	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alpha)	7.8
	421039	NM_003478	Hs.101299	cutlin 5	7.8
	446999	AA151520	Hs.279525	hypothetical protein PRO2605	7.8
45	429609	AF002246	Hs.210863	cell adhesion molecule with homology to L1CAM	7.8
	415139	AW975942	Hs.48524	ESTs	7.7
	450192	AA263143	Hs.24596	RAD51-interacting protein	7.7
	423992	AW898292	Hs.137206	Homo sapiens mRNA; cDNA DKFZp564H1663 (from c	7.7
	436211	AK001581	Hs.80961	polymerase (DNA directed), gamma	7.7
50	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	7.5
	426921	AA037145	Hs.172855	cleavage stimulation factor, 3' pre-RNA, subu	7.5
	433330	AW207084	Hs.132816	ESTs	7.5
	439759	AL359055	Hs.67709	Homo sapiens mRNA, full length insert cDNA clo	7.5
	427660	AJ741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone CAE066	7.5
55	422095	AI868872	Hs.288966	ceruloplasmin (ferroxidase)	7.5
	436476	AA326108	Hs.53631	ESTs	7.5
	412170	D16532	Hs.73729	very low density lipoprotein receptor	7.4
	428954	AF100781	Hs.194678	WNT1 inducible signaling pathway protein 3	7.4
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	7.4
60	439262	AA832333	Hs.124399	ESTs	7.4
	435420	AB28513	Hs.59203	ESTs	7.3
	422892	AA988176	Hs.121553	hypothetical protein FLJ20641	7.3
	457030	AJ301740	Hs.173381	dihydropyrimidinase-like 2	7.3
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	7.2
65	409916	BE313625	Hs.57435	solute carrier family 11 (proton-coupled diva	7.2
	418007	M13509	Hs.83169	Matrix metalloprotease 1 (interstitial collag	7.2
	420900	AL045633	Hs.44269	ESTs	7.2
	424001	W67883	Hs.137476	KIAA1051 protein	7.2
	400301	XO3635	Hs.1657	Estrogen receptor 1	7.1
70	400238			0	7.1
	413573	AJ733859	Hs.149089	ESTs	7.1
	428071	AF212848	Hs.182339	transcription factor ESE-3B	7.1
	447164	AF026941	Hs.17518	Homo sapiens c1g5 mRNA, partial sequence	7.1
	453062	AW207538	Hs.61603	ESTs	7.1
75	456965	AW131888	Hs.172792	ESTs, Weakly similar to hypothetical protein	7.1
	442500	AJ619068	Hs.209122	ESTs	7.1
	446142	AJ754693	Hs.145968	ESTs	7.0
	417791	AW965339	Hs.111471	ESTs	7.0
	418524	AA300576	Hs.85769	acidic 82 kDa protein mRNA	7.0
80	451797	AW663858	Hs.56120	ESTs	7.0
	452909	NM_015368	Hs.30985	pannexin 1	7.0
	453616	NM_003462	Hs.33946	dynein, axonemal, light intermediate polypept	7.0
	436281	AW411194	Hs.120051	ESTs	7.0
	448897	AW819642	Hs.24135	transmembrane protein vezatin; hypothetical p	6.9
	414142	AW368397	Hs.150042	ESTs	6.9

	448776	BE302464	Hs.30057	transporter similar to yeast MRS2	6.9
	419423	D26488	Hs.90315	KIAA0007 protein	6.9
	420908	AL049974	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (from cl	6.8
5	452971	AI873878	Hs.91789	ESTs	6.8
	413597	AW302885	Hs.117183	ESTs	6.8
	415138	C18358	Hs.78045	tissue factor pathway inhibitor 2 TFPI2	6.8
	437478	AL390172	Hs.118811	ESTs	6.7
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	6.7
10	421184	NM_003616	Hs.102456	survival of motor neuron protein interacting	6.7
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	6.6
	446508	N75217	Hs.257848	ESTs	6.6
	438167	R28363	Hs.24288	ESTs	6.6
	445459	AI478629	Hs.158465	ESTs	6.6
15	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae, h	6.6
	410011	AB020641	Hs.57858	PFTAIRE protein kinase 1	6.6
	410292	AA843087	Hs.124194	ESTs	6.5
	415716	NS9294	Hs.301141	Homo sapiens cDNA FLJ11689 fis, clone HEMBA10	6.5
	424770	AA25562		gbzw46e05.1 Soares_t0tal_fetus_Nb2HF8_9w Ho	6.5
20	438122	AI620270	Hs.129837	ESTs	6.5
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDNA clo	6.5
	447473	AA045648	Hs.11817	nudix (nucleoside diphosphate linked molecu X	6.5
	450838	AK001826	Hs.25245	hypothetical protein FLJ11269	6.5
	418203	X54942	Hs.83758	CDC28 protein kinase 2	6.5
25	439901	N73885	Hs.124169	ESTs	6.5
	428758	AA433988	Hs.98502	Homo sapiens cDNA FLJ14303 fis, clone PLACE20	6.4
	404552			0	6.4
	404599			0	6.4
	418503	AA243642	Hs.137422	ESTs	6.4
30	420149	AA255920	Hs.88095	ESTs	6.4
	440411	N30258	Hs.156971	ESTs, Weakly similar to Weak similarity with	6.4
	449108	AI140683	Hs.98328	ESTs	6.4
	452097	AB002364	Hs.27916	ADAM-TS3 ; a disintegrin-like and metallopr	6.4
	453619	H87648	Hs.33922	H.sapiens novel gene from PAC 117P20, chromos	6.4
35	410273	BE326877	Hs.281523	ESTs	6.3
	434486	AA678818	Hs.117142	ESTs	6.3
	454036	AA374756	Hs.93560	ESTs, Weakly similar to unnamed protein produ	6.3
	403381			0	6.2
	412308	AA687322	Hs.192843	ESTs	6.2
40	419346	AI830417		gbwh94d12x1 NCL_CGAP_CLL1 Homo sapiens cDNA	6.2
	446140	AA356170	Hs.26750	Homo sapiens cDNA: FLJ21908 fis, clone HEP038	6.2
	453047	AW023798	Hs.286025	ESTs	6.2
	442573	H93366	Hs.7567	Branched chain aminotransferase 1, cytosolic,	6.1
	410102	AW248508	Hs.279727	ESTs;	6.1
45	410004	AI298027	Hs.289115	ESTs	6.1
	413335	AI613318	Hs.48442	ESTs	6.1
	429455	AI221919	Hs.173438	hypothetical protein FLJ10582	6.1
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, polypep	6.1
	451229	AW967707	Hs.48473	ESTs	6.1
50	452641	AW952893	Hs.237825	signal recognition particle 72kD	6.1
	433172	AB037841	Hs.102652	hypothetical protein ASH1	6.1
	425465	L18964	Hs.1904	protein kinase C; iota	6.1
	437117	AL049256	Hs.122593	ESTs	6.0
	423440	R25234	Hs.143434	contactin 1	6.0
55	430510	AW162916	Hs.241576	hypothetical protein PRO2577	6.0
	433252	AB040957	Hs.151343	KIAA1524 protein	6.0
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HEMBB10	6.0
	436954	AA740151	Hs.130425	ESTs	5.9
	436032	AA150797	Hs.109276	latexin protein	5.9
60	424590	AW966399	Hs.46821	hypothetical protein FLJ20086	5.9
	444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-bind	5.9
	418379	AA218940	Hs.137516	ldigetin-like 1	5.9
	438081	H49548	Hs.298964	ESTs	5.8
	443270	NM_004272	Hs.9192	Homer, neuronal immediate early gene, 1B	5.8
65	450459	AI697193	Hs.299254	ESTs	5.8
	433812	AF078184	Hs.61188	Homo sapiens Ku70-binding protein (KUB3) mRNA	5.8
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induced ge	5.8
	417251	AW015242	Hs.99488	ESTs; Weakly similar to ORF YKR074w [S.cerevi	5.7
	429181	AW979104	Hs.294009	ESTs	5.7
70	454933	BE141714		gb:QV0-HT0101-061099-032-c04 HT0101 Homo sapi	5.7
	456553	AA721325	Hs.189058	ESTs, Weakly similar to cAMP-regulated guanine	5.7
	430371	D87466	Hs.240112	KIAA0276 protein	5.7
	425371	D49441	Hs.155981	mesothelin	5.7
	424513	BE385864	Hs.149894	mitochondrial translational initiation factor	5.6
75	432015	AL157504	Hs.159115	ESTs	5.6
	438109	AI076621	Hs.71367	ESTs, Moderately similar to ALU7_HUMAN ALU SU	5.6
	407137	T97307	Hs.189067	v-erb-b2 avian erythroblastic leukemia viral	5.6
	407945	X69208	Hs.506	ATPase, Cu++ transporting, alpha polypeptide	5.6
	416565	AW000960	Hs.44970	ESTs	5.6
80	417830	AW504786	Hs.132808	epithelial cell transforming sequence 2 oncog	5.5
	419752	AA249573	Hs.152618	ESTs	5.5
	422093	AF151852	Hs.111449	CGI-94 protein	5.5
	424583	AF017445	Hs.150928	fructose-1-phosphate guanylyltransferase	5.5
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 20kD	5.5
	452534	AW083022	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HEMBB10	5.5

	453279	AW893940	Hs.59698	ESTs	5.5
	424188	AW954552	Hs.142634	zinc finger protein	5.5
	453884	AA355925	Hs.36232	KIAA0186 gene product	5.5
5	424841	AB001105	Hs.151413	glia maturation factor, beta	5.5
	444478	W07318	Hs.240	M-phase phosphoprotein 1	5.5
	427975	AJ536065	Hs.122460	ESTs	5.5
	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic; stratum comeum)	5.5
	442914	AW188551	Hs.99519	Homo sapiens cDNA FLJ14007 fis, clone Y79AA10	5.5
10	417995	AW974175	Hs.188761	ESTs	5.4
	418946	AJ798841	Hs.132103	ESTs	5.4
	419963	AA743276	Hs.301052	ESTs	5.4
	420362	U79734	Hs.97206	huntingtin interacting protein 1	5.4
	422670	AA371612	Hs.115351	ESTs	5.4
15	432837	AA310693	Hs.279512	HSPC072 protein	5.4
	447020	T27308	Hs.16986	hypothetical protein FLJ11046	5.4
	458027	L49054	Hs.85195	ESTs, Highly similar to [(3:5)(q25.1;p34)] fus	5.4
	425217	AJ076696	Hs.155174	CDC5 (cell division cycle 5, S. pombe, homolo	5.4
	422938	NM_001809	Hs.1594	centromeres protein A (17kD)	5.4
20	450434	AA166950	Hs.18645	ESTs, Weakly similar to partial CDS [C.elegan	5.4
	438279	AA805168	Hs.165165	ESTs, Moderately similar to ALLU8_HUMAN ALU SU	5.4
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	5.3
	420328	Y18082	Hs.96870	staufer (Drosophila, RNA-binding protein) hom	5.3
	436586	AJ308862	Hs.167028	ESTs	5.3
25	435783	AB037734	Hs.4993	ESTs	5.3
	422306	BE044325	Hs.227280	Homo sapiens mRNA for Lsm5 protein	5.3
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	5.2
	453293	AA382267	Hs.10653	ESTs	5.2
	429944	R13949	Hs.226440	Homo sapiens clone 24881 mRNA sequence	5.2
30	434891	AA814309	Hs.123583	ESTs	5.2
	415263	AA948033	Hs.130853	ESTs	5.2
	409508	NM_006153	Hs.54589	NCK adaptor protein 1	5.2
	412848	AA121514	Hs.70832	ESTs	5.2
	421246	AW582662	Hs.300961	ESTs, Highly similar to AF151805 1 CGI-47 pro	5.2
35	431548	AJ834273	Hs.9711	Homo sapiens cDNA FLJ13018 fis, clone NT2RP30	5.2
	412719	AW016610	Hs.129911	ESTs	5.2
	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncogene h	5.1
	424078	AB006625	Hs.139033	paternally expressed gene 3	5.1
	433558	AA833757	Hs.201769	ESTs	5.1
40	434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone LNG070	5.1
	453911	AW503857	Hs.4007	Sarcolemmal-associated protein	5.1
	415539	AJ733881	Hs.72472	BMPR-1b; bone morphogenetic protein receptor	5.1
	442717	R88362	Hs.180591	ESTs, Weakly similar to R06F6.5b [C.elegans]	5.1
	432358	AJ093491	Hs.72830	ESTs	5.0
45	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblastoma c	5.0
	419699	AA248998	Hs.31246	ESTs	5.0
	420313	AB023230	Hs.96427	KIAA1013 protein	5.0
	422505	AL120862	Hs.124165	ESTs; (HSA)PAP protein (programmed cell deat	5.0
	425733	F13287	Hs.159388	Homo sapiens clone 23578 mRNA sequence	5.0
50	434160	BE551196	Hs.114275	ESTs	5.0
	435094	AJ560129	Hs.277523	EST	5.0
	436812	AW298067		gb:U1-H-BW0-ajp-g-09-0-U1.s1 NCL_CGAP_Sub6 Ho	5.0
	432415	T16971	Hs.289014	ESTs	4.9
	406117			0	4.9
55	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	4.9
	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (from cl	4.9
	448621	AJ097144	Hs.5250	ESTs, Weakly similar to BACR37P7.g [D.melanog	4.9
	453001	AW131636	Hs.191260	ESTs	4.9
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone HEP091	4.9
60	418811	AK001407	Hs.88663	hypothetical protein FLJ10545	4.9
	436754	AJ061288	Hs.133437	ESTs, Moderately similar to gonadotropin indu	4.8
	437212	AJ765021	Hs.210775	ESTs	4.8
	447312	AJ434345	Hs.36908	activating transcription factor 1	4.8
	409732	NM_016122	Hs.56148	NY-REN-58 antigen	4.8
65	434690	AJ867679	Hs.148410	ESTs	4.8
	444172	BE147740	Hs.104558	ESTs	4.8
	424539	L02911	Hs.150402	activin A receptor, type I	4.8
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	4.8
	406076	AL390179	Hs.137011	Homo sapiens mRNA; cDNA DKFZp547P134 (from cl	4.8
70	420179	N74530	Hs.21168	ESTs	4.7
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain 12	4.7
	419247	S65791	Hs.89764	fragile X mental retardation 1	4.7
	420850	BE139590	Hs.122406	ESTs	4.7
	425420	BE536911	Hs.234545	ESTs	4.7
75	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	4.7
	419131	AA406293	Hs.301622	ESTs	4.7
	422278	AF072873	Hs.114218	ESTs	4.7
	451684	AF216751	Hs.26813	CDA14	4.6
	400296	AA305627	Hs.139336	ATP-binding cassette; sub-family C (CFTR/MRP)	4.6
80	408425	AW058674	Hs.44787	Homo sapiens mRNA; cDNA DKFZp434C0227 (from c	4.6
	417168	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (from c	4.6
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	4.6
	442917	AA314907	Hs.85950	ESTs	4.6
	432268	AJ800271	Hs.129445	hypothetical protein FLJ12496	4.6
	452795	AW392555	Hs.18878	hypothetical protein FLJ21620	4.6

	457300	AW297436	Hs.158849	Homo sapiens cDNA: FLJ21663 fis, clone COL088	4.6
	459551	AI472808		gb:U70e07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Hom	4.6
	421977	W94197	Hs.110165	ribosomal protein L26 homolog	4.6
5	429441	AJ224172	Hs.204096	lipophilin B (interglobin family member), pro	4.6
	449722	BE260074	Hs.23960	cyclin B1	4.6
	431689	AA305688	Hs.287695	UDP-GalbetaGlcNAc beta 1,3-galactosyltransfe	4.5
	425178	H16097	Hs.181027	ESTs	4.5
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain 9	4.5
10	436556	AI364997	Hs.7572	ESTs	4.5
	400534			0	4.5
	417845	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (from c	4.5
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE; Human selenium d	4.5
	448305	AA625207	Hs.264915	Homo sapiens cDNA FLJ12908 fis, clone NT2RP20	4.5
15	441006	AW605267	Hs.7627	CGI-60 protein	4.5
	414569	AF109298	Hs.118259	Prostate cancer associated protein 1	4.5
	447924	AI817226	Hs.170337	ESTs	4.5
	425508	NM_003666	Hs.158205	basic leucine zipper nuclear factor 1 (JEM-1)	4.5
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppressor	4.4
20	432842	AW674093	Hs.279525	hypothetical protein PR02605	4.4
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affinity	4.4
	414699	AI815523	Hs.76930	synuclein, alpha (non A4 component of amyloid	4.4
	412733	AA984472	Hs.74554	KIAA0080 protein	4.4
	419790	U79250	Hs.93201	glycerol-3-phosphate dehydrogenase 2 (mitocho	4.4
25	433377	AI752713	Hs.43845	ESTs	4.4
	449535	W15267	Hs.23672	low density lipoprotein receptor-related prot	4.4
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	4.4
	443881	R64512	Hs.237146	Homo sapiens cDNA FLJ14234 fis, clone NT2RP40	4.4
	423025	AA831267	Hs.12244	Homo sapiens cDNA: FLJ23581 fis, clone LNG136	4.4
30	408621	AI970672	Hs.46638	chromosome 11 open reading frame 8; fetal br	4.3
	416241	N52639	Hs.32683	ESTs	4.3
	432005	AA524190	Hs.120777	ESTs, Weakly similar to ELL2_HUMAN RNA POLYME	4.3
	435532	AW291488	Hs.117305	ESTs	4.3
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	4.3
35	454193	BE141183		gb:MR0-HT0071-191199-001-b04 HT0071 Homo sapi	4.3
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (melanom	4.3
	406069			0	4.3
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone LNG055	4.3
	418413	R95735	Hs.117753	ESTs, Weakly similar to antigen of the monod	4.3
40	452028	AK001859	Hs.27595	hypothetical protein FLJ10997	4.3
	418693	AI750878	Hs.87409	thrombospondin 1	4.3
	410361	BE391804	Hs.62661	guanylate binding protein 1, Interferon-induc	4.2
	409763	AL043212		gb:DKFZp434H0623_r1 434 (synonym: htes3) Homo	4.2
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2, partial	4.2
45	408908	BE296227	Hs.48915	serine/threonine kinase 15	4.2
	413582	AW295647	Hs.71331	Homo sapiens cDNA: FLJ21971 fis, clone HEP057	4.2
	423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	4.2
	425024	R39235	Hs.12407	ESTs	4.2
	447153	AA805202	Hs.173912	eukaryotic translation initiation factor 4A,	4.2
50	447406	BE618060	Hs.282862	ESTs	4.2
	449347	AV649748	Hs.295901	ESTs	4.2
	414279	AW021691	Hs.3804	DKFZP564C1940 protein	4.2
	428856	AA436735	Hs.183171	Homo sapiens cDNA: FLJ22002 fis, clone HEP066	4.2
	407872	AB039723	Hs.40735	frizzled (Drosophila) homolog 3	4.2
55	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phosphate),	4.2
	436406	AW105723	Hs.125346	ESTs	4.2
	438209	AL120659	Hs.6111	KIAA0307 gene product	4.2
	443653	AA137043	Hs.9663	programmed cell death 6-interacting protein	4.1
	454556	AW807073		gb:MR4-ST0062-031199-018-d06 ST0062 Homo sapi	4.1
60	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP20	4.1
	412593	Y07558	Hs.74088	early growth response 3	4.1
	416566	NM_003914	Hs.79378	cyclin A1	4.1
	426342	AF093419	Hs.169378	multiple PDZ domain protein	4.1
	428417	AK001699	Hs.184227	F-box only protein 21	4.1
65	429317	AA831552	Hs.268016	solute carrier family 5 (inositol transporter	4.1
	446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ12534 fis, clone NT2RM40	4.1
	422988	AW673847	Hs.97321	ESTs	4.0
	434657	AA641876	Hs.191840	ESTs	4.0
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1, 64k	4.0
70	443271	BE568568	Hs.195704	ESTs	4.0
	421437	AW821252	Hs.104336	ESTs	4.0
	401644			0	4.0
	405095			0	4.0
	418417	R77182		gb:U65e02r1 Soares placenta Nb2HP Homo sapi	4.0
75	420807	AA280627	Hs.57846	ESTs	4.0
	429529	AA454190	Hs.193811	ESTs, Moderately similar to reduced expressio	4.0
	457726	AI217477	Hs.194591	ESTs	4.0
	431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic protein type	4.0
	453403	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fis, clone PLACE10	4.0
80	442768	AL048534	Hs.48458	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	4.0
	413430	R22479	Hs.24650	Homo sapiens cDNA FLJ13047 fis, clone NT2RP30	4.0
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	4.0
	425692	D90041	Hs.155958	NAT1; arylamine N-acetyltransferase	4.0
	407792	AI077715	Hs.39384	putative secreted ligand homologous to ftx1	4.0
	408353	BE439838	Hs.44298	hypothetical protein	4.0

5	421175	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transcript	3.9
	420324	AF163474	Hs.96744	DKFZP586D0823 protein, Prostate androgen-regu	3.9
	417531	NM_003157	Hs.1087	serine/threonine kinase 2	3.9
	458924	BE242158	Hs.24427	DKFZP566O1646 protein	3.9
	400185			0	3.9
10	401480			0	3.9
	410360	AW663690		gb:bj21g03.x1 NCL_CGAP_L8 Homo sapiens cDNA	3.9
	410908	AA121686	Hs.10592	ESTs	3.9
	420159	AI572490	Hs.99785	ESTs	3.9
	422805	AA436989	Hs.121017	H2A histone family; member A	3.9
15	424639	AI917494	Hs.131329	ESTs	3.9
	428555	NM_002214	Hs.184908	Integrin, beta 8	3.9
	431699	NM_001173	Hs.267831	Homo sapiens cDNA FLJ12952 fis, clone NT2RP20	3.9
	433703	AA210863	Hs.3532	nemo-like kinase	3.9
	437144	AL049466	Hs.7859	ESTs	3.9
20	452728	AI915676	Hs.239708	ESTs	3.9
	430447	W17064	Hs.241451	SWI/SNF related, matrix associated, actin dep	3.9
	440594	AW445167	Hs.126036	ESTs	3.9
	408938	AA059013	Hs.22607	ESTs	3.9
	427051	BE178110	Hs.173374	ESTs	3.9
25	447568	AF155655	Hs.18885	CGI-116 protein	3.9
	457211	AW972565	Hs.32399	ESTs, Weakly similar to Similar to Ena-VASP 1	3.9
	443475	AI066470	Hs.134482	ESTs	3.9
	433447	U29195	Hs.3281	neuronal pentraxin II	3.9
	428093	AW594506	Hs.104830	ESTs	3.8
30	437938	AI950087		ESTs; Weakly similar to Gag-Pol polyprotein [3.8
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfotransf	3.8
	429250	H56585	Hs.198308	tryptophan rich basic protein	3.8
	441859	AW194364	Hs.128022	ESTs, Weakly similar to FIG1 MOUSE FIG-1 PROT	3.8
	437700	AA766060	Hs.122848	ESTs	3.8
35	439560	BE565647	Hs.74899	hypothetical protein FLJ12820	3.8
	409584	AA045857	Hs.54943	fracture callus 1 (rat) homolog	3.8
	428474	AA453441	Hs.31511	ESTs	3.8
	431965	BE175190		gb:QV2-HT0577-010500-165-g04 HT0577 Homo sapi	3.8
	454018	AW016892	Hs.241652	ESTs	3.8
40	426320	W47595	Hs.169300	transforming growth factor, beta 2	3.8
	439635	AA477288	Hs.94891	Homo sapiens cDNA: FLJ22729 fis, clone HSI156	3.8
	417517	AF001176	Hs.82238	POP4 (processing of precursor, S. cerevisiae)	3.8
	446402	AI681145	Hs.160724	ESTs	3.8
	450238	AW162998	Hs.24584	KIAA1376 protein	3.8
45	410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar ataxi	3.8
	400268			0	3.8
	418217	AI910647	Hs.13442	ESTs	3.8
	421928	AF013758	Hs.109643	polyadenylate binding protein-interacting pro	3.8
	417300	AI765227	Hs.55610	solute carrier family 30 (zinc transporter),	3.8
50	414136	AA812434	Hs.178227	ESTs	3.8
	453945	NM_005171	Hs.36908	activating transcription factor 1	3.7
	400240			0	3.7
	407877	AW016811	Hs.234478	Homo sapiens cDNA: FLJ22648 fis, clone HSI073	3.7
	450581	AF081513	Hs.25195	endometrial bleeding associated factor (left-	3.7
55	418223	NM_014733	Hs.83790	KIAA0305 gene product	3.7
	411704	AI499220	Hs.71573	hypothetical protein FLJ10074	3.7
	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta-5-de	3.7
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	3.7
	402820			0	3.7
60	408090	BE173621	Hs.292478	ESTs	3.7
	416421	AA134006	Hs.79306	eukaryotic translation initiation factor 4E	3.7
	418282	AA215535	Hs.98133	ESTs	3.7
	418454	AA315308		gb:EST187095 Colon carcinoma (HCC) cell line	3.7
	418668	AW407987	Hs.87150	Human clone A9A2BR11 (CAC)n(GTG)n repeat-con	3.7
65	422290	AA495854	Hs.48827	hypothetical protein FLJ12085	3.7
	432824	AK001783	Hs.279012	hypothetical protein FLJ10921	3.7
	439907	AA853978	Hs.124577	ESTs	3.7
	447479	AB037634	Hs.18685	Homo sapiens mRNA for KIAA1413 protein, parti	3.7
	451073	AI758905	Hs.206063	ESTs	3.7
70	450377	AB033091	Hs.24936	ESTs	3.7
	414343	AL036166	Hs.75914	coated vesicle membrane protein	3.7
	448807	AI571940	Hs.7549	ESTs	3.7
	442821	BE391929	Hs.8752	Putative type II membrane protein	3.7
	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	3.7
75	418068	AW971155	Hs.293902	ESTs, Weakly similar to prolyl 4-hydroxylase	3.7
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-associated	3.7
	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	3.7
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PLACE10	3.7
	411402	BE297855	Hs.69855	NRAS-related gene	3.7
80	450447	AF212223	Hs.25010	hypothetical protein P15-2	3.6
	414706	AW340125	Hs.76989	KIAA0097 gene product	3.6
	434228	Z42047	Hs.283978	ESTs; KIAA0738 gene product	3.6
	434164	AW207019	Hs.148135	ESTs	3.6
	409533	AW869543	Hs.21291	mitogen-activated protein kinase kinase kinas	3.6
	402222			0	3.6
	404915			0	3.6
	404996			0	3.6
	411560	AW851186		gb:JL3-CT0220-150200-071-H05 CT0220 Homo sapi	3.6

5	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT2RP40	3.6
	426010	AA136563	Hs.1975	Homo sapiens cDNA: FLJ21007 fis, clone CAE038	3.6
	427038	NM_014633	Hs.173288	KIAA0155 gene product	3.6
	439255	BE164500		gb:RC4-HT0469-230300-014-e10 HT0469 Homo sapi	3.6
	458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone HEP024	3.6
	415115	AA214228	Hs.127751	hypothetical protein	3.6
	453468	W00712	Hs.32990	DKFZP566F084 protein	3.6
	441205	AW137827	Hs.176904	ESTs	3.6
10	452693	T79153	Hs.48589	zinc finger protein 228	3.6
	417389	BE260964	Hs.82045	Midkine (neurite growth-promoting factor 2)	3.6
	448105	AW591433	Hs.170675	ESTs, Weakly similar to TMS2_HUMAN TRANSMEMBR	3.6
	451522	BE565817	Hs.26498	hypothetical protein FLJ21657	3.6
	440048	AA897461	Hs.158469	ESTs, Weakly similar to envelope protein [Hs	3.5
15	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)-like	3.5
	452030	AL137578	Hs.27607	Homo sapiens mRNA; cDNA DKFZp564N2464 (from c	3.5
	400666			0	3.5
	422646	H87863	Hs.151380	ESTs	3.5
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, with Glu	3.5
20	408730	AV660717	Hs.47144	DKFZP586N0819 protein	3.5
	401517			0	3.5
	413775	AW409934	Hs.75528	nucleolar GTPase	3.5
	417177	NM_004458	Hs.81452	fatty-acid-Coenzyme A ligase, long-chain 4	3.5
	427943	AW959075		gb:EST371145 MAGE resequences, MAGE Homo sapi	3.5
25	439107	AL046134	Hs.27895	ESTs	3.5
	447268	AI370413	Hs.36563	Homo sapiens cDNA: FLJ22418 fis, clone HRC085	3.5
	412604	AW978324	Hs.47144	DKFZP586N0819 protein	3.5
	427134	AA398409	Hs.173561	EST	3.5
	430273	AI311127	Hs.125522	ESTs	3.5
30	436671	AW137159	Hs.146151	ESTs	3.5
	433037	NM_014158	Hs.279938	HSPC067 protein	3.5
	453745	AA952989	Hs.63908	Homo sapiens HSPC316 mRNA, partial cds	3.5
	400531	AF151064	Hs.36069	hypothetical protein	3.5
	433345	AI681545	Hs.152982	EST cluster (not in UniGene)	3.4
35	406400	AA343629	Hs.104570	kallikrein 8 (neurokinin)	3.4
	407596	R86913		gb:yg30f05.r1 Soares fetal liver spleen 1NFLS	3.4
	453779	N35187	Hs.43388	ESTs	3.4
	444858	AI199738	Hs.208275	ESTs, Weakly similar to unnamed protein produ	3.4
	447688	N87079	Hs.19236	NADH dehydrogenase (ubiquinone) 1 beta subcom	3.4
40	424856	AA347746	Hs.9521	ESTs, Weakly similar to KIAA1015 protein [Hs	3.4
	407864	AF069291	Hs.40539	chromosome 8 open reading frame 1	3.4
	404108			0	3.4
	403729			0	3.4
	404232			0	3.4
45	423687	AA329633	Hs.133011	ESTs, Highly similar to Z117_HUMAN ZINC FINGE	3.4
	428372	AK000684	Hs.183887	hypothetical protein FLJ22104	3.4
	439741	BE379646	Hs.6904	Homo sapiens mRNA full length insert cDNA clo	3.4
	441447	AA934077	Hs.126980	ESTs	3.4
	448358	R44433	Hs.106614	Human DNA sequence from clone RP4-534K7 on ch	3.4
50	450926	AI744361	Hs.205591	ESTs, Weakly similar to zinc finger protein P	3.4
	458477	NM_000314	Hs.10712	phosphatase and tensin homolog (mutated in mu	3.4
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cys-X-C	3.4
	452822	X85689	Hs.288617	Homo sapiens cDNA: FLJ22621 fis, clone HSI056	3.4
	441111	AI806867	Hs.126594	ESTs	3.4
55	447519	U46258	Hs.23448	ESTs	3.4
	446913	AA430650	Hs.16529	transmembrane 4 superfamily member (tetraspan	3.4
	449581	AI989517	Hs.181605	ESTs	3.4
	456132	BE219771	Hs.237146	Homo sapiens cDNA FLJ14234 fis, clone NT2RP40	3.4
	448186	AA262105	Hs.4094	Homo sapiens cDNA FLJ14208 fis, clone NT2RP30	3.4
60	422611	AA158177	Hs.118722	fucosyltransferase 8 (alpha (1,6) fucosyltran	3.4
	441433	AA933809	Hs.42746	ESTs	3.4
	417837	AL079905	Hs.1103	transforming growth factor, beta 1	3.4
	450516	AA902658	Hs.21943	NIF3 (Ngg1 interacting factor 3, S.pombe homo	3.4
	407796	AA195509	Hs.272239	lymphocyte activation-associated protein	3.3
65	419200	AW966405	Hs.288856	prefoldin 5	3.3
	423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (from c	3.3
	445679	AI343868	Hs.58800	Homo sapiens cDNA FLJ12488 fis, clone NT2RM20	3.3
	435014	BE560898	Hs.10026	ribosomal protein L17 isolog	3.3
	446619	AL076643	Hs.313	secreted phosphoprotein 1 (osteopontin, bone	3.3
70	439170	AA332365	Hs.165539	ESTs	3.3
	429830	AI537278	Hs.225841	DKFZP434D193 protein	3.3
	428943	AW086180	Hs.37636	ESTs, Weakly similar to KIAA1392 protein [Hs	3.3
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	3.3
	408805	H69912	Hs.48269	vaccinia related kinase 1	3.3
75	441134	W29092	Hs.7678	cellular retinoic acid-binding protein 1	3.3
	408532	AJ453137	Hs.63176	ESTs	3.3
	409517	X90780	Hs.54668	troponin I, cardiac	3.3
	414304	AI621276	Hs.165998	DKFZP564M2423 protein	3.3
	436427	AI344378	Hs.143399	ESTs	3.3
80	436662	AI582393	Hs.126695	ESTs	3.3
	440304	BE159984	Hs.125395	ESTs	3.3
	447385	F12863		gb:HSC3FE081 normalized infant brain cDNA Hom	3.3
	451177	AI969716	Hs.13034	ESTs	3.3
	428949	AA442153	Hs.104744	ESTs, Weakly similar to AF208855 1 BM-013 [H	3.3
	451743	AW074266	Hs.23071	ESTs	3.3

	421515	Y11339	Hs.105352	GallNAc alpha-2, 6-sialyltransferase 1, long f	3.3
	446351	AW444551	Hs.258532	ESTs	3.3
	435102	AW899053	Hs.76917	F-box only protein 8	3.3
5	418216	AA662240	Hs.283099	AF15q14 protein	3.3
	401508			0	3.3
	437108	AA434054	Hs.80624	Homo sapiens cDNA: FLJ23442 fis, clone HSI009	3.3
	416530	U62801	Hs.79381	kalikrein 6 (neurosin, zyme)	3.3
	443171	BE281128	Hs.9030	TONDU	3.3
10	458627	AW088642	Hs.97984	ESTs; Weakly similar to WASP-family protein [3.3
	412078	X69699	Hs.73149	paired box gene 8	3.3
	414080	AA135257	Hs.47783	ESTs; Weakly similar to T12540 hypothetical p	3.3
	401197			0	3.3
	422134	AW179019	Hs.112110	ESTs	3.3
15	409044	AI129586	Hs.33033	ESTs	3.3
	416198	H27332	Hs.99598	ESTs	3.2
	438481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-conjugat	3.2
	436525	AA721428	Hs.26145	Homo sapiens cDNA FLJ14127 fis, clone MAMMA10	3.2
	409142	AL136877	Hs.50758	chromosome-associated polypeptide C	3.2
20	428819	AL135623	Hs.193914	KIAA0575 gene product	3.2
	428728	NM_016625	Hs.191381	ESTs; Weakly similar to hypothetical protein	3.2
	421261	AA600853	Hs.98133	ESTs	3.2
	446219	AI287344	Hs.149827	ESTs	3.2
	457574	H88717	Hs.27774	ESTs, Highly similar to AF161349 1 HSPC086 [H	3.2
25	409172	Z99399	Hs.118145	ESTs	3.2
	419388	T67012	Hs.75323	prohibitin	3.2
	434187	AA627098	Hs.99103	ESTs; Weakly similar to I38428 T-complex prot	3.2
	445060	AA830811	Hs.88808	ESTs	3.2
	448254	AI829900	Hs.22829	ESTs	3.2
30	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	3.2
	411393	AW797437	Hs.69771	B-factor, properdin	3.2
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37kD)	3.2
	408418	AW863897	Hs.44743	KIAA1435 protein	3.2
	442025	AW887434	Hs.11810	ESTs; Weakly similar to CD4.2 [C.elegans]	3.2
35	417006	AW673606	Hs.80758	aspartyl-tRNA synthetase	3.2
	407881	AW072003	Hs.40958	heparan sulfate (glucosamine) 3-O-sulfotransf	3.2
	444755	AA431791	Hs.183001	ESTs	3.2
	402829			0	3.2
	451593	AF151879	Hs.26706	CGI-121 protein	3.2
40	419926	AW900992	Hs.93796	DKFZP586D2223 protein	3.2
	434551	BE387162	Hs.280858	ESTs, Highly similar to XPB_HUMAN DNA-REPAIR	3.2
	445929	AI089660	Hs.7838	makorin, ring finger protein, 1	3.2
	409365	AA702376	Hs.226440	Homo sapiens clone 24881 mRNA sequence	3.2
	418836	AI655499	Hs.161712	ESTs	3.2
45	441020	W79283	Hs.35962	ESTs	3.1
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38kD)	3.1
	413010	AA393273	Hs.75133	transcription factor 6-like 1 (mitochondrial	3.1
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	3.1
	410486	AW235094	Hs.193424	ESTs; Weakly similar to KIAA1064 protein [H.s	3.1
50	434540	NM_016045	Hs.5184	TH1 drosophila homolog	3.1
	409178	BE393948	Hs.50915	kalikrein 5	3.1
	439480	AL038511	Hs.125316	ESTs	3.1
	417848	AA206581	Hs.39457	ESTs	3.1
	446293	AI420213	Hs.149722	ESTs	3.1
55	408108	AI580492	Hs.42743	hypothetical protein	3.1
	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer, nonpo	3.1
	410519	AW612264	Hs.131705	ESTs	3.1
	421587	AI133161	Hs.286131	CGI-101 protein	3.1
	440046	AW402306	Hs.6877	hypothetical protein FLJ10483	3.1
60	453931	AL121278	Hs.25144	ESTs	3.1
	454423	AW603985	Hs.179662	nucleosome assembly protein 1-like 1	3.1
	459089	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (from c	3.1
	418735	N48769	Hs.44609	ESTs	3.1
	414245	BE148072	Hs.75850	WAS protein family, member 1	3.1
65	410909	AW898161	Hs.53112	ESTs; Weakly similar to ALU8_HUMAN ALU SUBFAM	3.1
	434926	BE543269	Hs.50252	Homo sapiens HSPC283 mRNA, partial cds	3.1
	409239	AA740875	Hs.44307	ESTs	3.1
	429017	AA463605	Hs.238995	ESTs	3.1
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	3.1
70	426514	BE616533	Hs.301122	bone morphogenetic protein 7 (osteogenic prot	3.1
	448133	AA723157	Hs.73769	folate receptor 1 (adult)	3.1
	418792	AB037805	Hs.88442	KIAA1384 protein	3.1
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S. cere	3.1
	402077			0	3.1
75	440671	AW297920	Hs.130054	ESTs	3.1
	418890	X17360	Hs.278255	homeo box D4	3.1
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	3.1
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. cerevi	3.1
	431221	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B; yeast)	3.1
80	443584	AB07036	Hs.101619	ESTs	3.1
	445525	BE149866	Hs.14831	ESTs	3.1
	410441	BE288210		gls601118016F1 NIH_MGC_17 Homo sapiens cDNA c	3.1
	422634	NM_016010	Hs.118821	CGI-62 protein	3.0
	420022	AA256253	Hs.120817	ESTs	3.0
	453912	AL121031	Hs.32556	KIAA0379 protein	3.0

5	456844	AI284155	Hs.152981	CDP-diacylglycerol synthase (phosphatidate cy	3.0
	414941	C14865	Hs.182159	ESTs	3.0
	407807	AL031427	Hs.40094	Human DNA sequence from clone 167A19 on chrom	3.0
	414725	AA769791	Hs.120355	Homo sapiens cDNA FLJ13148 fs, clone NT2RP30	3.0
	444420	AI148157	Hs.146766	ESTs	3.0
	431742	NM_016652	Hs.268281	CGI-201 protein	3.0
	412519	AA196241	Hs.73980	troponin T1, skeletal, slow	3.0
	418348	AI537187	Hs.96322	Homo sapiens cDNA: FLJ23560 fs, clone LNG098	3.0
10	444261	AA298958	Hs.10724	MDS023 protein	3.0
	457465	AW301344	Hs.195969	ESTs	3.0
	443933	AI091631	Hs.135501	Homo sapiens two pore potassium channel KT3.3	3.0
	442150	AI368158	Hs.128864	ESTs	3.0
	414883	AA926960	Hs.77550	CDC28 protein kinase 1	3.0
15	442879	AF032922	Hs.8813	synactin binding protein 3	3.0
	437949	U78519	Hs.41654	ESTs	3.0
	403515			0	3.0
	403864			0	3.0
	407785	AW207285	Hs.98279	ESTs	3.0
20	426199	AA371865	Hs.97090	ESTs	3.0
	426324	AW291787	Hs.200933	ESTs	3.0
	427738	NM_000318	Hs.180612	peroxisomal membrane protein 3 (35kD, Zellweg	3.0
	427837	U87309	Hs.180941	vacuolar protein sorting 41 (yeast homolog)	3.0
	439430	AF124250	Hs.6564	breast cancer anti-estrogen resistance 3	3.0
25	442039	AW276240	Hs.128352	ESTs, Weakly similar to p80 [R.norvegicus]	3.0
	446978	NM_001938	Hs.16697	down-regulator of transcription 1, TBP-binding	3.0
	452431	U88879	Hs.29499	tail-like receptor 3	3.0
	452841	T17431	Hs.65412	DEADH (Asp-Glu-Ala-Asp/His) box polypeptide	3.0
	432114	AL036021	Hs.225597	ESTs	3.0
30	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapiens]	3.0
	442607	AA507576	Hs.288361	KIAA0741 gene product	3.0
	453920	AI133148	Hs.36602	I factor (complement)	3.0
	430000	AW205931	Hs.99598	ESTs	3.0
	429184	AI688663	Hs.116586	ESTs	3.0
35	453331	AI240655	Hs.8895	ESTs	3.0
	448663	BE614599	Hs.106823	H.sapiens gene from PAC 42616, similar to syn	3.0
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	3.0
	401714			0	3.0
	400903			0	3.0
40	428428	AL037544	Hs.184298	cyclin-dependent kinase 7 (homolog of Xenopus	3.0
	443761	AI525743	Hs.160603	ESTs	3.0
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on chrom	3.0
	442580	AI733682	Hs.130239	ESTs	3.0

TABLE 10B:

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

50	Pkey	CAT Number	Accession
	407596	1003489_1	R86913 R86901 H25352 R01370 H43764 AW044451 W21298
	409763	115392_1	AL043212 AA077575 AA077655 R19502 BE545457 AI638421 R14093
	410360	1197225_2	AW663690
	410441	120358_1	BE298210 AI672315 AW086489 BE298417 AA455921 AA902537 BE327124 R14963 AA085210 AW274273 AI333584 AI369742 AI039658
55	411560	1249443_1	AI885095 AI476470 AI287650 AI885299 AI965381 AW592624 AW340136 AI266556 AA456390 AI310815 AA484951
	414315	143512_1	AW851186 AW996967 BE143458
	418417	1750818_1	Z24878 AA494098 F13654 AA494040 AA143127
	418454	175699_1	R77182 R77197 R80484
	419348	184129_1	AA315308 AA233392 BE538098 BE087173
60	424770	243504_1	AI830417 AA236612
	427943	284802_1	AA425562 AI880208 AA346646 N22655 AW811775 AW811786
	431965	33959_2	AW959075 W06838 AA417863
	436812	427323_1	BE175190 BE003348
65	437838	44573_2	AW298057 AA731645 AA810101 AW194180 AI690673 AW978773
			AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598
			AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444
			N92578 F13493 AA927794 AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344
			AI741346 AI689062 AA282915 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA888777 AA488892 AI356394
			AW103813 AI539642 AA642789 AA856975 AW505512 AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209
70			AW856538 AA180009 AA337499 AW961101 AA251669 AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584
			AA908741 AW072629 AW513996 AA293273 AA969759 N75628 N23388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701
			AW613456 AI373032 AI564269 F00531 H83488 W37181 W78802 R66056 AI002839 R67840 AA300207 AW859581 T63226 F04005
	439255	470321_1	BE164500 AA832198 BE164502
	447385	719912_1	F12863 AI377223 T75099
75	454193	1050256_1	BE141183 AW178167 AW178162 AW178166 AW178172 AW845893 AW178159 AW178222 AW178213 AW178215 AW178090 AW178091
			AW178161 AW178207 AW178210 AW178214 AW178212 BE140918 BE140917 AW178135 AW178205 AW178209 AW178223 AW178220
			AW178206 AW178203 AW178165 AW178168 AW178160 AW178136 AW845878 AW178131 AW178138 AW178105 AW845894 AW178129
			AW845810 AW845828 AW178216 AW178112 AW178211 AW178224 BE140915 AW178221 AW178130 AW178134 AW178096 AW178108
			AW178133 AW178164 AW178218 AW178171 AW178157 AW178158 AW178103 BE141189 AW178170 AW845816 BE141586 AW178156
			AW178104 AW178163 AW178093 AW178208 AW178137 AW178140 AW178219 BE141592 AW845901 BE141580 AW178155 BE141598
80			BE140957
	454556	1223878_1	AW807073 AW807055 AW807067 AW807276 AW807030 AW807363 AW845892 AW807091 AW807275 AW807284 AW807287 AW845891
			AW807195 AW807271
	454933	1245515_1	BE141714 AW845993 AW845989

TABLE 10C:

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495

Strand: Indicates DNA strand from which exons were predicted

NL_position: Indicates nucleotide positions of predicted exons

Pkey	Ref	Strand	NL_position
400534	6981826	Minus	278637-279292
400666	8118498	Plus	17982-18115,20297-20458
400903	2911732	Plus	59112-59228
401197	9719705	Plus	176341-176452
401480	7321503	Plus	168120-166347,168451-166557,169651-169832
401508	7534110	Minus	110778-110983
401517	7677912	Plus	28278-29770
401644	8576138	Plus	82655-83959
401714	6715702	Plus	96484-96681
402077	8117414	Plus	65014-65195
402222	9958106	Plus	3261-3834,3939-4269
402408	9796239	Minus	110326-110491
402820	6456853	Minus	82274-82443
402829	8918414	Plus	101532-101852,102006-102263
403381	9438267	Minus	26009-26178
403515	7656757	Minus	173358-179553
403729	7543752	Minus	37662-37909
403864	7709019	Minus	51753-51890,79290-79445
404108	8247074	Minus	63603-64942
404232	8218045	Minus	71800-71956
404552	7243881	Plus	19854-20010
404567	7249169	Minus	101320-101501
404599	8705107	Plus	110443-110733
404915	7341768	Minus	100915-101087
404988	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
405095	8072599	Plus	138877-139066
406069	9117732	Plus	68880-69374
406117	9142932	Plus	54304-54584

Table 11A lists about 222 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 10A, except that the ratio was greater than or equal to 2.0, and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g., Ig, fn3, egf, 7tm domains, signal sequences, transmembrane domains). Predicted protein domains are noted.

TABLE 11A: ABOUT 222 UP-REGULATED GENES ENCODING EXTRACELLULAR/CELL SURFACE PROTEINS, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES

Pkey: Primekey

Ex. Accn: Exemplar Accession

UG ID: UniGene ID

Title: UniGene title

PFAM domains: predicted protein structural domains

ratio: ratio tumor vs normal tissue

Pkey	Ex. Accn	UG ID	Title	PFAM domains	ratio
400292	AA250737	Hs.72472	BMPR-Ib; bone morphogenetic pro	pkinase,Activin_rec	30.0
400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Strom	SS,hemopexin,Peptidas	25.2
427585	D31152	Hs.179729	collagen; type X; alpha 1 (Schmid m	C1q,Collagen	22.7
436982	AB018305	Hs.5378	spondin 1, (I-spondin) extracellular m	bsp_1	19.0
428579	NM_005756	Hs.184942	G protein-coupled receptor 64	TM	17.4
443646	AJ085198	Hs.298699	ESTs	TSPN,vwc,bsp_1,EGF	15.1
436209	AW850417	Hs.254020	ESTs, Moderately similar to unname	TM	14.1
418601	AA279490	Hs.86368	calmeglin	SS,calreticulin	13.8
428532	AF157326	Hs.184788	TBP-interacting protein	TM	13.6
427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) rec	TM,neur_chan	11.8
432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamin	TM,Glycos_transf_2,Ri	11.0
404567	NM_015902	Hs.278428	progesterone induced protein (DDG)	TM,HECT,z-UBR1	10.8
445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	SS,MAM,EGF	8.9
409928	AL137163	Hs.57549	hypothetical protein dJ47384	TM,MSP_domain	8.8
407001	U12471	Hs.247954	Human thrombospondin-1 gene, par	TSPN,vwc,bsp_1,EGF	8.5
453370	AJ470523	Hs.182356	ESTs, Moderately similar to translat	ABC_tran,ABC_membr	8.4
400288	AA032279	Hs.61635	STEAP1	TM	8.1
431725	X65724	Hs.2839	Nonie disease (pseudoglioma)	SS,Cys_knot	7.9
429609	AF002246	Hs.210863	cell adhesion molecule with homolo	TM,fn3,Ig	7.8
412170	D16532	Hs.73729	very low density lipoprotein recepto	TM,Igf1_recept_a,ldl_rec	7.4
428954	AF100781	Hs.194678	WNT1 inducible signaling pathway	SS,IGFBP,Cys_knot,bsp	7.4
418007	M13509	Hs.83169	Matrix metalloproteinase 1 (interstitia	SS,hemopexin,Peptidas	7.2
424001	W67883	Hs.137478	KIAA1051 protein	Pep_M12B_propep,Rep	7.2
456965	AW131888	Hs.172792	ESTs, Weakly similar to hypothetica	TM	7.1
446142	AJ754693	Hs.145968	ESTs	Cadherin_C_term,cadhe	7.0
415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 TFP	Kunitz_BPTLG-gamma	6.8
438167	R28363	Hs.24286	ESTs	7tm_1	6.6
452097	AB002364	Hs.27918	ADAM-TS3; a disintegrin-like and	Pep_M12B_propep,Rep	6.4
449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose in	SS	5.8
425371	D49441	Hs.155981	mesothelin	SS	5.7
407945	X69208	Hs.606	ATPase, Cu++ transporting, alpha p	TM,E1-E2_ATPase,Hy	5.6
424620	AA101043	Hs.151254	kalikrein 7 (chymotryptic; stratum c	SS,trypsin	5.5
420362	U79734	Hs.97206	huntingtin interacting protein 1	TM,ENTH1_LWEQ	5.4

5	413384	NM_000401	Hs.75334	exostoses (multiple) 2	TM	5.3
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	Collagen,TSPN	5.2
	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral	TGF-beta,TGFB_propep	5.1
	415539	A1733881	Hs.72472	BMP-1b; bone morphogenetic pro	kinase,Activin_rec	5.1
	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	TM	4.9
	424539	L02911	Hs.150402	activin A receptor, type I	Activin_rec,kinase	4.8
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase d	disintegrin,Reprolysin,P	4.7
	451684	AF216751	Hs.26813	CD414	TM	4.6
10	400296	AA305627	Hs.139336	ATP-binding cassette; sub-family C	TM,ABC_tran,ABC_m	4.6
	428597	NM_003816	Hs.2442	a disintegrin and metalloproteinase d	TM	4.5
	400534	AP000541		predicted exons	TM,KRAB,zf-C2H2	4.5
	425506	NM_003668	Hs.158205	basic leucine zipper nuclear factor 1	TM,Folate_carrier	4.5
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high aff	TM,SDF	4.4
	449535	W15267	Hs.23872	low density lipoprotein receptor-rela	SS,ldl_recept_b,ldl_rece	4.4
15	452028	AK001859	Hs.27595	hypothetical protein FLJ10997	Zn_carbOxep,Propep_M	4.3
	418693	A1750878	Hs.87409	thrombospondin 1	EGF,TSPN,isp_1,isp_3	4.3
	410361	BE391804	Hs.62661	guanylate binding protein 1, interfer	TM,GBP	4.2
	407872	AB039723	Hs.40735	frizzled (Drosophila) homolog 3	Frizzled,Fz,7tm_2	4.2
	421502	AF111858	Hs.105039	solute carrier family 34 (sodium pho	TM,Na_P1_cotrans	4.2
20	412494	AL133900	Hs.792	ADP-ribosylation factor domain pro	ar,zf-B_box,zf-C3HC4	4.0
	405095	NM_014479	Hs.145296	disintegrin protease	Reprolysin,disintegrin	4.0
	431130	NM_008103	Hs.2719	epididymis-specific; whey-acidic pro	SS,wap	4.0
	407792	A1077715	Hs.39384	putative secreted ligand homologous	SS	4.0
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-s	TM	3.8
25	450581	AF081513	Hs.25195	endometrial bleeding associated fact	SS,TGF-beta,TGFB_pro	3.7
	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3,	TM,Sterol_desat	3.7
	450447	AF212223	Hs.25010	hypothetical protein P15-2	TM,ANF_receptor,guan	3.6
	414706	AW340125	Hs.76989	KIAA0097 gene product	TM	3.6
	417389	BE260964	Hs.82045	Midkine (neurite growth-promoting	TM,PTN_MK	3.6
30	400666	X07820	Hs.2258	Matrix Metalloproteinase 10 (Strom	SS,hemopexin,Peptidas	3.5
	406400	AA343629	Hs.104570	kallikrein 8 (neurosin/ovasin)	SS,trypsin	3.4
	407864	AF069291	Hs.40539	chromosome 8 open reading frame 1	TM,FHA,BRCT	3.4
	452822	X85689	Hs.288617	Homo sapiens cDNA: FLJ22621 fis,	EGF,in3,kinase	3.4
	446913	AA430650	Hs.16529	transmembrane 4 superfamily memb	TM,transmembrane4	3.4
35	422611	AA158177	Hs.118722	fucosyltransferase 8 (alpha 1,6) fuc	SS	3.4
	423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZ	cadherin,Cadherin_C_1a	3.3
	435102	AW899053	Hs.76917	F-box only protein 8	TM,Sec7	3.3
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	SS,TM,trypsin	3.3
	401197			predicted exons	ar,Ets	3.3
40	436525	AA721428	Hs.26145	Homo sapiens cDNA FLJ14127 fis,	TM	3.2
	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	TM	3.2
	411393	AW797437	Hs.69771	B-factor, properdin	SS,sushi,trypsin,vwa,lib	3.2
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-s	SS	3.2
45	418836	A1655499	Hs.161712	ESTs	kinase,Activin_rec	3.2
	409178	BE393948	Hs.50915	kallikrein 5	SS,trypsin	3.1
	421987	A1133161	Hs.286131	CGI-101 protein	TM	3.1
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	SS	3.1
	426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteo	SS,TGFB_propeptide,T	3.1
50	448133	AA723157	Hs.73769	folate receptor 1 (adult)	TM	3.1
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprot	SS,Peptidase_M10,hem	3.1
	456844	A1264155	Hs.152981	CDP-diacylglycerol synthase (phosp	TM,Cydylyltrans	3.0
	414725	AA769791	Hs.120355	Homo sapiens cDNA FLJ13148 fis,	SPRY,7tm_1	3.0
	407785	AW207285	Hs.98279	ESTs	Sema,lg	3.0
55	427738	NM_000318	Hs.180612	peroxisomal membrane protein 3 (35	TM,zf-C3HC4	3.0
	452431	U88879	Hs.29499	ldl-like receptor 3	TM,TIR,LRCT	3.0
	453920	A1133148	Hs.36602	I factor (complement)	ldl_recept_a,trypsin,SRC	3.0
	453331	A1240685	Hs.8895	ESTs	disintegrin,Reprolysin,P	3.0
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	TM,7tm_2	3.0
60	428428	AL037544	Hs.184298	cyclin-dependent kinase 7 (homolog	TM,kinase	3.0
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembra	TM,LRCT,LRRT,LR	2.9
	408380	AF123050	Hs.44532	ubiquitin	TM,ubiquitin,7tm_3,AN	2.9
	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase d	disintegrin,Reprolysin	2.9
	420757	X78592	Hs.99915	androgen receptor (dihydrotestostero	TM,Androgen_recep,ho	2.9
65	424406	D54120	Hs.146409	wingless-type MMTV integration sit	cadherin,Cadherin_C_1a	2.9
	428549	AA430064	Hs.220929	ESTs, Moderately similar to ARF-fa	ar	2.9
	419452	U33635	Hs.90572	PTK protein tyrosine kinase 7	TM,kinase,lg	2.9
	452281	T93500	Hs.28792	ESTs	TGFB_propeptide,TGF-	2.9
	420440	NM_002407	Hs.97644	mammaglobin 2	SS,Uteroglobin	2.9
70	418848	A1820961	Hs.193465	ESTs	kinase,Activin_rec	2.9
	421991	NM_014918	Hs.110488	KIAA0990 protein	SS	2.9
	433190	M26901	Hs.3210	renin	SS,asp	2.9
	424538	NM_005095	Hs.150390	zinc finger protein 262	TM	2.8
	433002	AF048730	Hs.279906	cyclin T1	SS	2.8
75	444342	NM_014398	Hs.10887	similar to lysosome-associated mem	TM,Lamp	2.8
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	TM	2.8
	428450	NM_014791	Hs.184339	KIAA0175 gene product	TM,kinase,KA1	2.8
	450171	AL133661	Hs.24583	hypothetical protein DKFZp434C03	TM	2.8
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate tran	TM,GATase_2,SIS	2.8
80	430016	NM_004736	Hs.227656	xenotropic and polytropic retrovirus	TM	2.8
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	Collagen,COLFI,TSPN	2.8
	424894	H83520	Hs.153678	reproduction 8	SS,UBX	2.8
	430651	AA961694	Hs.105187	kinasin protein 9 gene	SS	2.7
	414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-	TM	2.7
	448595	AB014544	Hs.21572	KIAA0644 gene product	TM,LRCT,LR	2.7

5	452835	AK001269	Hs.30738	ESTs	TM	2.7
	403019	AA834626	Hs.66718	RAD54 (S.cerevisiae)-like	SS,Anti_proliferat	2.7
	420281	AI623693	Hs.191533	ESTs	Cation_efflux	2.7
	434815	AF155582	Hs.46744	core1 UDP-galactose:N-acetylgalact	SS	2.6
	432201	AI538613	Hs.135657	TMPPRSS3a mRNA for serine protea	trefoil,typsin	2.6
	430450	R23553	Hs.241489	hypothetical protein	SS	2.6
	448402	BE244226	Hs.21094	RAB18, member RAS oncogene fam	ras,arf	2.6
	421802	BE261458	Hs.108408	CGI-78 protein	TM	2.6
10	452355	N54926	Hs.29202	G protein-coupled receptor 34	TM,7tm_1	2.6
	417742	R64719		gb:EST22d11 WATM1 Homo sapie	ank,death,RHD,TIG	2.6
	451346	NM_008338	Hs.26312	glioma amplified on chromosome 1	TM,Ig,LRRLRRNT,LR	2.6
	433147	AF091434	Hs.43080	platelet derived growth factor C	TM,PDGF,CUB	2.6
	420079	NM_014051	Hs.94898	PTD011 protein	SS,TM	2.6
15	419918	X80700	Hs.93728	pre-B-cell leukemia transcription fac	homeobox,Ig,Acytransf	2.5
	432350	NM_005865	Hs.274407	protease, serine, 16 (thymus)	SS	2.5
	406671	AA129547	Hs.285754	mel proto-oncogene (hepatocyte gro	pkinase,Sema,Plexin_re	2.5
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	SS,TIR,Ig	2.5
	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	TM	2.5
20	433929	AI375499	Hs.27379	ESTs	EGF,Ig_recept_La,Ig_re	2.5
	443562	AF118838	Hs.9599	solute carrier family 25, member 13	TM,milo_carr	2.5
	414386	X00442	Hs.75990	haptoglobin	sushi,trypsin	2.5
	417578	AA339449	Hs.82285	phosphoribosylglycinamide formyltr	AIRS,tomyL_transf,GA	2.5
	449207	AL044222	Hs.23255	nucleoporin 155kD	TM	2.5
25	418107	AA173846	Hs.79015	antigen identified by monoclonal ant	TM,Ig	2.4
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	TM,PH	2.4
	414812	X72755	Hs.77367	monokine induced by gamma interfe	SS,Ig	2.4
	406137	R42764	Hs.3248	mutS (E. coli) homolog 6	TM,MutS_C,MutS_N,P	2.4
	450710	AW953381	Hs.18627	ESTs, Weakly similar to G01447 GP	TM	2.4
30	430291	AV660345	Hs.238126	CGI-49 protein	TM	2.4
	425184	BE278288	Hs.155048	Lutheran blood group (Aubergier b a	Ig	2.4
	451418	BE387790	Hs.26369	ESTs	TM	2.4
	412277	BE277592	Hs.73799	guanine nucleotide binding protein (TM,G-alpha	2.4
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A	SS,Ig	2.4
35	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphatase cyclase	TM,RCT	2.3
	418224	NM_002902	Hs.79088	reticulocalbin 2, EF-hand calcium bi	SS,efhand	2.3
	452268	NM_003512	Hs.28777	H2A histone family, member L	histone,Catc_CGRP_I44	2.3
	451668	Z43948	Hs.26789	ASPIC (acidic secreted protein in ca	SS,TM	2.3
	400880	M84349	Hs.119653	CD59 antigen	SS,UPAR_LY6	2.3
40	421340	F07783	Hs.1369	decay accelerating factor for comple	SS,sushi	2.3
	443986	AI381750	Hs.283437	HTGN29 protein	TM	2.3
	443037	AW500305	Hs.8906	syntaxin 7	TM,Syntaxin	2.3
	440516	S42303	Hs.161	cadherin 2, type 1, N-cadherin (neur	HNH,cadherin,Cadherin	2.3
	404877	AI394145	Hs.18048	melanoma antigen MAGE-10	TM,MAGE	2.3
45	440704	M69241	Hs.162	insulin-like growth factor binding pr	SS,thyroglobulin_1,IgF	2.3
	437852	D63209	Hs.5944	solute carrier family 11 (proton-coup	TM	2.3
	418624	AI734080	Hs.104211	ESTs	Sema,Ig	2.2
	410434	AF051152	Hs.63668	tol-like receptor 2	SS,TIR,LRRCCT,LR	2.2
50	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatina	SS,ln2,hemopexin,Pepti	2.2
	431457	NM_012211	Hs.256297	Integrin, alpha 11	TM,FG-GAP,vwa	2.2
	407907	AI752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5	SS,Lysyl_hydro	2.2
	400898	AF220030	Hs.125300	Homo sapiens tripartite motif protein	SPRY,7tm_1	2.2
	400303	AA242758	Hs.79136	Human breast cancer, estrogen regul	SS,TM	2.2
	411789	AF245505	Hs.72157	Homo sapiens mRNA; cDNA DKFZ	Ig,LRRCCT	2.2
55	414809	AI434699	Hs.77356	transferrin receptor (p90, CD71)	TM,PA,Ribosomal_S2	2.2
	401131	NM_011651	Hs.298023	Homo sapiens aquaporin 5 (AQP5),	TM,MIP	2.2
	400277	Y00281	Hs.2280	Human mRNA for ribophorin I	TM	2.1
	409317	U20165	Hs.53250	bone morphogenetic protein recepto	TM,pkinase	2.1
	409956	AW103364	Hs.727	H.sapiens activin beta-A subunit (ex	TGF-beta,TGFb_propep	2.1
60	451253	H48299	Hs.26126	claudin 10	TM,PMP22_Claudin	2.1
	429638	AI916662	Hs.211577	Kinectin 1 (kinesin receptor)	TM	2.1
	409267	NM_012453	Hs.52515	transducin (beta)-like 2	TM,WD40	2.1
	418414	J04977	Hs.84981	X-ray repair complementing defectiv	SS	2.1
	449057	AB037784	Hs.22941	ESTs	TM	2.1
65	417666	AI345001	Hs.82380	menage a trois 1 (CAK assembly fac	zf-C3HC4	2.1
	428485	NM_002950	Hs.2280	ribophorin I	TM	2.1
	445798	NM_012421	Hs.13321	rearranged L-myc fusion sequence	TM,zf-C2H2	2.1
	430057	AW450303	Hs.2534	bone morphogenetic protein recepto	TM,Activin_recpt,pkina	2.1
70	425189	H16622		gb:ym25c07.r1 Soares Infant brain 1	RasGEF,PH,fibrinogen	2.1
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycopro	SS,Glyco_hydro_18	2.1
	421343	BE246444	Hs.283685	hypothetical protein FLJ20396	TM	2.1
	425627	AF019512	Hs.297007	ESTs	TM,Peptidase_M50	2.1
	426261	AW242243	Hs.168670	peroxisomal farnesylated protein	E1-E2_ATPase,Cation	2.1
	431638	NM_000916	Hs.2820	oxytocin receptor	TM,7tm_1	2.1
75	455546	AI690321	Hs.203845	ESTs, Weakly similar to TWIK-rela	TM	2.1
	421685	AF189723	Hs.106778	calcium transport ATPase ATP2C1	TM,E1-E2_ATPase,H	2.1
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C	TM,ABC_tran,ABC_m	2.1
	424800	AL035588	Hs.153203	MyoD family inhibitor	TM	2.1
	410007	AW950887	Hs.57813	zinc ribbon domain containing, 1	TFIS	2.1
80	436135	D85390	Hs.5057	carboxypeptidase D	SS,Zn_carbOpept	2.1
	420633	NM_014581	Hs.99526	odorant-binding protein 2B	TM,Iipocalin	2.1
	420162	BE378432	Hs.95577	cyclin-dependent kinase 4	pkinase,ank,ArtGap,PH	2.1
	426156	BE244537	Hs.167382	natriuretic peptide receptor A/guany	TM,ANF_receptor,guan	2.0
	442711	AF151073	Hs.8645	hypothetical protein	TM	2.0
	411872	AW327356	Hs.90918	chromosome 11 open reading frame	TM	2.0

5	427801	AW979155	Hs.234433	hypothetical protein PRO1068	TM,Aa_trans	2.0
	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	TM	2.0
	431183	NM_005855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplas	TM,ER_lumen_recept,I	2.0
	431846	BE018924	Hs.271580	Uroplakin 1B	TM,transmembrana4	2.0
	404210	U02478	Hs.100469	Human AF-6 mRNA	TM,RA,DIL,PDZ,FHA	2.0
	435640	AF220053	Hs.54960	uncharacterized hematopoietic stem/	TM,SET,zf-CXXC,PHD	2.0
	447906	AL050062	Hs.19999	DKFZP566K023 protein	SS	2.0
	412666	AL080116	Hs.74420	origin recognition complex, subunit	TM	2.0
10	417181	L10123	Hs.1071	surfactant protein A binding protein	TM	2.0
	423945	AA410943	Hs.72472	BMPR-Ib; bone morphogenetic pro	TM,kinase,Activin_rec	2.0
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	SS,trypsin	2.0
	448350	L14561	Hs.78546	Homo sapiens clone 24411 mRNA s	TM,E1-E2,ATPase,H	2.0
	401093	AI955244	Hs.121520	HYPOTHETICAL 16.4 kDa PROTE	TM,LRRCCT	2.0
15	415664	NM_004939	Hs.78580	DEAD/H (Asp-Glu-Ala-Asp/His) ho	DEAD,helicase_C,SPRY	2.0
	448165	NM_005591	Hs.202379	meiotic recombination (S. cerevisiae	DNA_repair,Glyco_tran	2.0
	416391	AI878927	Hs.79284	mesoderm specific transcript (mouse	TM,abhydrolase	2.0
	422926	NM_016102	Hs.121748	ring finger protein 16	SPRY,zf-C3HC4,zf-B	2.0
	446849	AL076617	Hs.16251	cleavage and polyadenylation specif	TM	2.0
20	427617	D42063	Hs.179825	RAN binding protein 2-like 1	TM,Ran_BP1,zf-RanBP	2.0
	411678	AI807114	Hs.71465	squalene epoxidase	TM,Monooxygenase	2.0
	432554	AA79813	Hs.278411	NCK-associated protein 1	TM	2.0

TABLE 11B:

Pkey: Unique Eos probasel identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

25	Pkey	CAT Number	Accession
	417742	1696282_1	R64719 Z44680 R12451
30	425189	247825_1	H16622 R17322 AA351959

TABLE 11C:

Pkey: Unique number corresponding to an Eos probasel

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosomes 22" Dunham, et al. (1999) *Nature* 402:489-495

Strand: Indicates DNA strand from which exons were predicted

Nt_position: Indicates nucleotide positions of predicted exons

35	Pkey	Ref	Strand	Nt_position
	400534	6981826	Minus	278637-279292
40	401197	9719705	Plus	176341-176452

Table 12A lists about 57 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode either enzymes or proteins amenable to modulation by small molecules. These were selected as for Table 10A, except that the ratio was greater than or equal to 2.0, and the predicted protein contained a structural domain that is indicative of enzymatic function or of being modulated by small molecules (e.g., kinase, peptidase, isomerase, transporters). Predicted protein domains are noted.

TABLE 12A: ABOUT 57 UP-REGULATED GENES ENCODING EXTRACELLULAR/CELL SURFACE PROTEINS, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES

Pkey: Primekey

Ex, Accn: Exemplar Accession

UG ID: UniGene ID

Title: UniGene title

PFAM domains: predicted structural domains

ratio: ratio tumor vs. normal

55	Pkey	Ex, Accn	UG ID	Title	PFAM domains	ratio
	400292	AA250737	Hs.72472	BMPR-Ib; bone morphogenetic pro	kinase,Activin_rec	30.0
	400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Strom	SS,Peptidase_M10	25.2
60	426427	M86699	Hs.169840	TTK protein kinase	kinase	18.7
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-rela	kinase	16.2
	433159	AB035898	Hs.150587	kinesin-like protein 2	kinesin	11.5
	453370	AF470523	Hs.182358	ESTs, Moderately similar to tranlat	ABC_tran	8.4
	418007	M13509	Hs.83169	Matrix metalloprotease 1 (interstitia	SS,Peptidase_M10	7.2
65	425465	L18954	Hs.1904	protein kinase C; iota	Ski_Sno,kinase_C	6.1
	409506	NM_006153	Hs.54589	NCK adaptor protein 1	SH2,SH3	5.2
	415539	AI733881	Hs.72472	BMPR-Ib; bone morphogenetic pro	kinase,Activin_rec	5.1
	424539	L02911	Hs.150402	activin A receptor, type I	Activin_rec,kinase	4.8
	400298	AA305627	Hs.139336	ATP-binding cassette; sub-family C	TM,ABC_tran	4.6
70	431699	NM_001173	Hs.267831	Homo sapiens cDNA FLJ12952 fis,	RhoGAP,FF,ras	3.9
	439560	BE565647	Hs.74899	hypothetical protein FLJ12820	C2,PI-PLC-Y,PI-PLC-X	3.8
	450447	AF212223	Hs.25010	hypothetical protein P15-2	ANF_receptor,kinase	3.6
	400666	X07820	Hs.2258	Matrix Metalloproteinase 10 (Strom	SS,Peptidase_M10	3.5
	452822	X85689	Hs.288617	Homo sapiens cDNA: FLJ22621 fis,	EGF,fn3,kinase	3.4
75	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	SS,TM,trypsin	3.3
	411393	AW797437	Hs.69771	B-factor, properdin	SS,sushi,trypsin,vwa,fn3,	3.2
	444755	AA431791	Hs.183001	ESTs	AAA	3.2
	418836	AI655499	Hs.161712	ESTs	kinase,Activin_rec	3.2
	409178	BE393948	Hs.50915	kallikrein 5	SS,trypsin	3.1
80	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprot	SS,Peptidase_M10,Jg	3.1
	453920	AI133148	Hs.36602	I factor (complement)	kl_recept_a,trypsin,SRCR	3.0
	404653	AA923729	Hs.26322	0	kinase	2.9
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	TM,kinase,Jg	2.9
	418848	AB20961	Hs.193465	ESTs	kinase,Activin_rec	2.9
	428450	NM_014791	Hs.184339	JQAA0175 gene product	TM,kinase,KA1	2.8

401323	AL158037		predicted exon	lactamase_B	2.7
444798	BE242144	Hs.12013	ATP-binding cassette, sub-family E	SH3, pkinase, ABC_tran	2.7
432201	AI538613	Hs.135657	TM6SS3a mRNA for serine protea	trypsin	2.6
448402	BE244226	Hs.21094	RAB18, member RAS oncogene fam	ras, raf	2.6
406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte gro	kinase, Sema	2.5
453448	AL036710	Hs.209527	ESTs	CNH, pkinase	2.5
414388	X00442	Hs.75990	haptoglobin	sushi, trypsin	2.5
421270	H56037	Hs.108146	ESTs	RhoGAP	2.4
414695	BE439915	Hs.76913	proteasome (prosome, macropain) su	proteasome	2.4
431341	AA307211	Hs.251531	proteasome (prosome, macropain) su	proteasome	2.4
424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (4	AAA, Viral_helicase1	2.2
424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatina	SS, m2, Peptidase_M10	2.2
416517	AA775987	Hs.79357	proteasome (prosome, macropain) 26	AAA	2.2
417601	NM_014735	Hs.82292	KIAA0215 gene product	PHD	2.1
400509	M97639	Hs.155585	receptor tyrosine kinase-like orphan	pro_isomerase	2.1
430057	AW450303	Hs.2534	bone morphogenetic protein recepto	Activin_recp, pkinase	2.1
421841	AA908197	Hs.108850	KIAA0935 protein	TPR, pkinase	2.1
453078	AF053551	Hs.31584	metaxin 2	pro_isomerase	2.1
424099	AF071202	Hs.139338	ATP-binding cassette, sub-family C	TMABC, tran	2.1
411190	AA306342	Hs.69171	protein kinase C-like 2	kinase, pkinase_C, HR1	2.1
407740	AA295547	Hs.62666	ESTs	p450	2.1
420162	BE378432	Hs.95577	cyclin-dependent kinase 4	kinase, ank, ArfGap, ras	2.1
420490	H69894	Hs.193041	ESTs	PI3Ka, PI3, PI4_kinase	2.1
426156	BE244537	Hs.167382	natruretic peptide receptor Aiguany	TM, ANF_receptor, pkinase	2.0
423945	AA410943	Hs.72472	BMFR-Itx, bone morphogenetic pro	TM, pkinase, Activin_recp	2.0
411773	NM_006799	Hs.72028	protease, serine, 21 (testisin)	SS, trypsin	2.0
447258	BE617527	Hs.180450	ribosomal protein S24	PI3Ka, PI4_kinase	2.0
427617	D42063	Hs.179825	RAN binding protein 2-like 1	TPR, pro_isomerase	2.0
453546	AF042385	Hs.33251	peptidylprolyl isomerase E (cycloph	pro_isomerase, rm	2.0

TABLE 12C:

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495

Strand: Indicates DNA strand from which exons were predicted

NL_position: Indicates nucleotide positions of predicted exons

Pkey	Ref	Strand	NL_position
401323	9212516	Plus	213509-214450

Table 13A lists about 1086 genes up-regulated in ovarian cancer compared to normal ovaries. These were selected as for Table 10A, except that the ratio was greater than or equal to 10, and the denominator was the median value for various non-malignant ovary specimens.

TABLE 13A: About 1086 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY

Pkey: Primekey

Ex. Accn: Exemplar Accession

UG ID: UniGene ID

Title: UniGene title

ratio: ration tumor vs. normal ovary

Pkey	Ex. Accn	UG ID	Title	ratio
439708	AW872527	Hs.59761	ESTs	109.2
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin, bone	107.8
422095	AI868872	Hs.289966	centropasmin (ferroxidase)	104.4
447111	AI017574	Hs.17409	cysteine-rich protein 1 (intestinal)	88.3
431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic protein type	82.8
431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (anti	81.9
413859	AW992356	Hs.8364	ESTs	73.9
446291	BE397753	Hs.14623	Interferon, gamma-inducible protein 30	72.7
426050	AF017307	Hs.166096	E74-like factor 3 (ets domain transcription f	68.1
411469	T09997	Hs.70327	cysteine-rich protein 2	66.6
429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	65.7
416971	R34657	Hs.80658	uncoupling protein 2 (mitochondrial, proton c	64.9
450273	AW298454	Hs.24743	hypothetical protein FLJ20171	62.5
446441	AK001782	Hs.15093	hypothetical protein	60.7
428758	AA433988	Hs.98502	Homo sapiens cDNA FLJ14303 fis, clone PLACE20	59.7
441406	Z45957	Hs.7837	Homo sapiens cDNA FLJ10457 fis, clone NT2RP10	57.8
441859	AW194364	Hs.128022	ESTs, Weakly similar to FIG1 MOUSE FIG-1 PROT	56.7
448406	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076	55.7
414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264	55.2
418068	AW971155	Hs.293902	ESTs, Weakly similar to prolyl 4-hydroxylase	54.8
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin, uteri	53.4
412636	NM_004415	Hs.74316	desmoplakin (DPI, DPII)	51.4
430634	AI860651	Hs.26685	ESTs	50.7
439318	AW837048	Hs.6527	G protein-coupled receptor 56	50.7
417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (versican)	50.6
407786	AA687538	Hs.38972	tetraspan 1	50.4
426836	N41720	Hs.172684	vesicle-associated membrane protein 8 (endobr	49.7
417308	H60720	Hs.81892	KIAA0101 gene product	48.9
436876	AI124756	Hs.5337	isocitrate dehydrogenase 2 (NADP+), mitochond	48.4
439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia viral	47.1
428289	M26301	Hs.2253	complement component 2	46.3
405484		0		46.1

	425371	D49441	Hs.155981	mesothelin	45.7
	403912			0	45.0
	443021	AA368546	Hs.8904	Ig superfamily protein	44.6
	427697	T18997	Hs.180372	BCL2-like 1	44.3
5	428227	AA321649	Hs.2248	INTERFERON-GAMMA INDUCED PROTEIN	44.0
	404678			0	43.9
	400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin 2)	43.8
	451035	AU076785	Hs.430	plastin 1 (I isoform)	43.8
10	440848	BE314650	Hs.7476	ATPase, H ⁺ transporting, lysosomal (vacuolar	42.8
	436278	BE386290	Hs.5097	synaptogyrin 2	42.4
	413936	AF113678	Hs.75621	serine (or cysteine) proteinase inhibitor, cl	42.1
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgranulin	42.1
	428411	AW291464	Hs.10338	ESTs	41.8
15	422168	W72424	Hs.112405	S100 calcium-binding protein A9 (calgranulin	41.5
	412477	AA150864	Hs.790	microsomal glutathione S-transferase 1	40.7
	417130	AW276858	Hs.81256	S100 calcium-binding protein A4 (calcium prot	40.1
	424673	AA345051	Hs.294092	ESTs	39.8
	416530	U62801	Hs.79361	kalikrein 8 (neurosin, zyma)	39.7
20	443162	T49551	Hs.9029	ESTs; Highly similar to KERATIN; TYPE I CYTO	39.5
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cys-Cys	39.3
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B, 92k	38.9
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprotein-39	38.5
	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member), pro	38.1
25	418526	BE018020	Hs.85838	soluble carrier family 16 (monocarboxylic acid	37.9
	415511	AJ732817	Hs.182362	ESTs	37.7
	409453	AI885516	Hs.95612	ESTs	37.7
	445537	AJ245671	Hs.12844	EGF-like domain; multiple 6	37.3
	442432	BE093589	Hs.38178	Homo sapiens cDNA: FLJ23468 fis, clone HSI118	37.3
30	408243	Y00787	Hs.624	Interleukin 8	37.3
	419092	J05581	Hs.89603	mucin 1, transmembrane	36.7
	444172	BE147740	Hs.104558	ESTs	36.0
	412115	AK001763	Hs.73239	hypothetical protein FLJ10901	35.8
	420440	NM_002407	Hs.97644	mammaglobin 2	35.7
35	414386	X00442	Hs.75990	haploglobin	35.3
	423225	AA852604	Hs.125359	Thy-1 cell surface antigen	35.1
	440598	H13032	Hs.103378	ESTs, Weakly similar to DRR1 [Hsapiens]	35.0
	413278	BE563085	Hs.833	Interferon-stimulated protein, 15 kDa	34.9
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	34.8
40	445919	T53519	Hs.290357	ESTs	34.7
	416854	H40164	Hs.80296	Purkinje cell protein 4	34.4
	414188	U33446	Hs.75799	protease, serine, 8 (prolactin)	34.2
	434371	AA631362		gbnp86b01.s1 NCI_CGAP_Thy1 Homo sapiens cDNA	33.9
	421937	AJ878857	Hs.109706	HN1 protein	33.9
45	449722	BE280074	Hs.23960	cyclin B1	33.8
	400965			0	33.7
	452203	X57522	Hs.158164	ATP-binding cassette, sub-family B (MDR/TAP),	33.5
	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncogene h	33.5
50	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, importin a	33.4
	408901	AK001330	Hs.48855	hypothetical protein FLJ10468	33.3
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	33.3
	422963	M79141	Hs.13234	ESTs	33.3
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia viral	33.2
55	431836	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	32.8
	421502	AF111858	Hs.105039	soluble carrier family 34 (sodium phosphate),	32.5
	431211	M86849	Hs.5556	Homo sapiens connexin 26 (GJB2) mRNA, complet	32.5
	436552	NM_014038	Hs.5216	HSPC028 protein	32.5
	442533	AA161224	Hs.8372	ubiquinol-cytochrome c reductase (6.4kD) subu	32.5
60	406400	AA343629	Hs.104570	kalikrein 8 (neurosin/ovasin)	32.4
	450353	AI244661	Hs.103296	ESTs	32.4
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKALP)	32.4
	433412	AV653729	Hs.8185	CGI-44 protein; sulfide dehydrogenase like (y	32.3
	441020	W79283	Hs.35962	ESTs	32.2
	432201	AJ538613	Hs.135657	TMPS33a mRNA for serine protease (ECHOS1) (T	32.0
65	424125	M31669	Hs.1735	inhibin, beta B (activin AB beta polypeptide)	31.9
	453309	AI791809	Hs.32949	defensin, beta 1	31.8
	408380	AF123050	Hs.44532	dibuliquitin	31.7
	419329	AY007220	Hs.288998	S100-type calcium binding protein A14	31.6
70	409231	AA446644	Hs.692	GA733-2; epithelial glycoprotein (EGP) (KSA)	31.6
	423961	D13668	Hs.136348	Homo sapiens mRNA for osteoblast specific fac	31.2
	413840	AI301558	Hs.290801	ESTs	30.8
	440943	AW082298	Hs.146161	ESTs, Weakly similar to KIAA0859 protein [Hs	30.8
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone COL013	30.4
	410132	NM_003480	Hs.58882	Microfibril-associated glycoprotein-2	30.2
75	418203	X54942	Hs.83758	CDC28 protein kinase 2	30.1
	412719	AW016610	Hs.129911	ESTs	30.0
	407862	BE548267	Hs.50724	Homo sapiens cDNA FLJ10934 fis, clone OVARC10	30.0
	431563	AI027643	Hs.120912	ESTs	29.9
	431743	AW972642	Hs.293055	ESTs	29.8
80	443295	AI049783	Hs.241284	ESTs	29.7
	413745	AW247252	Hs.75514	nucleoside phosphorylase	29.7
	441028	AI333660	Hs.17558	ESTs	29.6
	442315	AA173392	Hs.7956	ESTs	29.6
	452838	U65011	Hs.30743	Preferentially expressed antigen in melanoma	29.5
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to M	29.5

	432280	BE440142	Hs.2943	signal recognition particle 19kD	29.4
	420158	AJ791905	Hs.95549	hypothetical protein	29.3
	445033	AV652402	Hs.155145	ESTs	29.2
5	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	29.1
	432706	NM_013230	Hs.286124	CD24	29.0
	422163	AF027208	Hs.297332	prominin (mouse)-like 1	28.7
	447035	NM_004753	Hs.17144	short-chain dehydrogenase/reductase 1	28.6
	443958	BE241880	Hs.10029	cathepsin C	28.2
10	422956	BE545072	Hs.122579	ESTs	28.1
	450377	AB033091	Hs.24936	ESTs	28.0
	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	28.0
	444725	AW952022	Hs.234174	Homo sapiens cDNA FLJ13819 fis, clone THYR010	27.8
	430250	NM_016929	Hs.283021	chloride intracellular channel 5	27.7
	416305	AJ076628	Hs.79187	coxsackie virus and adenovirus receptor	27.6
15	418174	L20688	Hs.83656	Rho GDP dissociation inhibitor (GDI) beta	27.5
	417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cys-X-C	27.4
	417856	AW067903	Hs.82772	collagen, type XI, alpha 1	27.3
	427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3A	27.2
	442993	BE018682	Hs.44343	ESTs	27.2
20	407137	T97307	Hs.199067	v-erb-b2 avian erythroblastic leukemia viral	27.0
	419356	AJ656166	Hs.7331	ESTs	27.0
	433662	W07162	Hs.150826	CATX-8 protein	26.7
	422576	BE548555	Hs.118554	CGI-83 protein	26.4
25	423271	W47225	Hs.126256	interleukin 1, beta	26.3
	443715	AJ583187	Hs.9700	cyclin E1	26.1
	420186	NM_016925	Hs.95697	liver-specific bHLH-Zip transcription factor	26.0
	419551	AW582256	Hs.91011	anterior gradient 2 (Xenopus laevis) homolog	25.9
	443672	AA323362	Hs.9567	butyrobetaine (gamma), 2-oxoglutarate dioxyge	25.8
	416889	AW250318	Hs.80395	mal, T-cell differentiation protein	25.3
30	408474	AA188823	Hs.83196	Homo sapiens cDNA: FLJ23597 fis, clone LNG152	25.3
	411825	AK000334	Hs.72289	hypothetical protein FLJ20327	25.3
	400881			0	25.2
	440594	AW445167	Hs.126036	ESTs	25.1
35	414586	AA306160	Hs.76506	lymphocyte cytosolic protein 1 (L-plastin)	25.1
	411925	AW014588	Hs.72925	chromosome 11 open reading frame 13	25.1
	417869	BE076254	Hs.82793	proteasome (prosome, macropain) subunit, beta	25.0
	433447	U29195	Hs.3281	neuronal pentraxin II	25.0
	450858	C18458	Hs.25597	elongation of very long chain fatty acids (FE	24.8
40	410619	BE512730	Hs.65114	keratin 18	24.8
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	24.6
	421924	BE514514	Hs.109606	coronin, actin-binding protein, 1A	24.6
	446859	AJ494289	Hs.16297	COX17 (yeast) homolog, cytochrome c oxidase a	24.5
	421451	AA291377	Hs.50831	ESTs	24.3
45	433929	AJ375499	Hs.27379	ESTs	24.3
	438930	AW843633	Hs.81256	S100 calcium-binding protein A4 (calcium prot	24.2
	444212	AW503976	Hs.10649	basement membrane-induced gene	24.2
	441633	AW958544	Hs.112242	ESTs	24.2
	441134	W29092	Hs.7678	cellular retinoic acid-binding protein 1	24.2
50	417715	AW969587	Hs.86366	ESTs	24.1
	409361	NM_005982	Hs.54418	sine oculis homeobox (Drosophila) homolog 1	24.1
	416984	H38765	Hs.80706	diaphorase (NADH/NADPH) (cytochrome b-5 reduc	24.1
	430125	U46418	Hs.233950	serine protease inhibitor, Kunitz type 1	23.9
	434078	AW880709	Hs.283683	EST	23.8
55	408669	AJ493591	Hs.78146	platelet/endothelial cell adhesion molecule (23.8
	439413	AJ598252	Hs.37810	ESTs	23.7
	448034	AJ624049	Hs.277523	gbbs41a09.x1 NCL CGAP_Ut1 Homo sapiens cDNA	23.7
	420344	BE463721	Hs.97101	Putative G protein-coupled receptor GPCR150	23.6
	431243	U46455	Hs.252189	syndecan 4 (amphiglycan, ryudocan)	23.6
60	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated prot	23.5
	451267	AJ033894	Hs.117865	solute carrier family 17 (anion/sugar transpo	23.4
	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	23.4
	419693	AA133749	Hs.92323	FXFD domain-containing ion transport regulato	23.4
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth factor 8	23.4
65	451110	AJ955040	Hs.301584	ESTs	23.3
	426295	AW367283	Hs.75839	zinc finger protein 6 (CMPX1)	23.2
	448517	AA082750	Hs.42194	hypothetical protein FLJ22649 similar to sign	23.1
	424670	W61215	Hs.116651	epithelial V-like antigen 1	23.1
70	417847	AJ521558	Hs.288312	Homo sapiens cDNA: FLJ22316 fis, clone HRC052	23.1
	449027	AJ271216	Hs.22880	dipeptidylpeptidase III	23.1
	424969	AW950928	Hs.153998	creatine kinase, mitochondrial 1 (ubiquitous)	23.1
	433169	AB035698	Hs.150587	kinesin-like protein 2	23.0
	411393	AW797437	Hs.69771	B-factor, properdin	23.0
	434815	AF155582	Hs.46744	core1 UDP-galactose-4-epimerase	22.8
75	427585	D31162	Hs.179729	collagen, type X, alpha 1 (Schmid metaphyseal	22.7
	445721	H92136	Hs.13144	HSPC160 protein	22.6
	448258	BE586983	Hs.85015	ESTs, Weakly similar to A4P_HUMAN INTESTINAL	22.6
	456844	AJ264155	Hs.152981	CDP-diacylglycerol synthase (phosphatidate cy	22.6
	452698	NM_001295	Hs.301921	ESTs	22.5
80	418693	AJ750878	Hs.87409	thrombospondin 1	22.4
	414880	AW247305	Hs.119140	eukaryotic translation initiation factor 5A	22.4
	401519			0	22.3
	402496			0	22.3
	420324	AF163474	Hs.96744	DKFZP586D0823 protein, Prostate androgen-regu	22.3
	403022			0	22.2

	434042	AJ589941	Hs.8254	hypothetical protein PRO0899	22.1
	419080	AW150835	Hs.18878	hypothetical protein FLJ21620	22.1
	406545	AB018249	Hs.10458	small inducible cytokine subfamily A (Cys-Cys	22.1
	447362	AW176120	Hs.9061	ESTs	22.0
5	429547	AW009166	Hs.99376	ESTs	22.0
	427954	J03060	Hs.247551	metaxin 1	22.0
	423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (from c	22.0
	428392	H10233	Hs.2265	secretory granule, neuroendocrine protein 1 (21.9
10	444107	T46839	Hs.10319	UDP glycosyltransferase 2 family, polypeptide	21.7
	414421-	AJ521130	Hs.55567	ESTs, Weakly similar to LAK-4p [H.sapiens]	21.5
	412589	R28660	Hs.24305	ESTs	21.5
	446525	AW867069	Hs.211556	Homo sapiens cDNA: FLJ23378 fis, clone HEP162	21.5
	416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like docking	21.5
15	436972	AA284679	Hs.25640	claudin 3	21.5
	428698	AA852773	Hs.297839	ESTs; Weakly similar to neogenin [H.sapiens]	21.5
	421340	F07783	Hs.1369	decay accelerating factor for complement (CD5	21.4
	413966	AA133935	Hs.173704	ESTs	21.4
	448243	AW369771	Hs.77496	ESTs	21.3
20	421928	AF013758	Hs.109643	polyadenylate binding protein-interacting pro	21.3
	403399			0	21.3
	435793	AB037734	Hs.4993	ESTs	21.3
	432829	AW860548	Hs.280658	ESTs	21.2
	448057	AB037784	Hs.22941	ESTs	21.2
25	437575	AW954355	Hs.36529	ESTs	21.2
	401131			0	21.0
	407207	T03651	Hs.179661	tubulin, beta polypeptide	20.8
	444783	AJ001468	Hs.62180	ESTs	20.8
	426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	20.8
30	447343	AA256641	Hs.236894	ESTs; Highly similar to LOW-DENSITY LIPOPROTE	20.7
	409041	AB033025	Hs.50081	KIAA1199 protein	20.6
	421305	BE397354	Hs.289721	diphtheria toxin resistance protein required f	20.6
	411704	AJ499220	Hs.71573	hypothetical protein FLJ10074	20.5
	417018	M16038	Hs.80887	v-src-1 Yamaguchi sarcoma viral related oncog	20.5
35	432827	Z68128	Hs.3109	Rho GTPase activating protein 4	20.4
	410174	AA306007	Hs.59461	DKFZP434C245 protein	20.4
	425184	BE278288	Hs.155048	Lutheran blood group (Auberger b antigen incl	20.4
	452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	20.3
40	447526	AL048753	Hs.340	small inducible cytokine A2 (monocyte chemota	20.2
	447335	BE617695	Hs.286192	protein phosphatase 1, regulatory (inhibitor)	20.2
	424867	AJ024860	Hs.153591	Not56 (D. melanogaster)-like protein	20.1
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activating e	20.1
	429083	Y09397	Hs.227817	BCL2-related protein A1	20.0
	410173	AA706017	Hs.119944	ESTs	19.8
45	433047	M86135	Hs.279946	methionine-tRNA synthetase	19.8
	419088	AJ538323	Hs.77496	ESTs	19.7
	403381			0	19.6
	409162	H25530	Hs.50868	solute carrier family 22 (organic cation tran	19.5
	426150	NM_003658	Hs.167218	BarH-like homeobox 2	19.4
50	449292	AJ990292	Hs.225457	ESTs	19.4
	425207	AB014551	Hs.155120	rhoGTP guanine nucleotide exchange factor (G	19.4
	419950	AK001645	Hs.93871	hypothetical protein FLJ10783	19.3
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-conjugat	19.3
	445930	AF055009	Hs.13456	Homo sapiens clone 24747 mRNA sequence	19.2
55	446608	N75217	Hs.257846	ESTs	19.1
	425222	M85430	Hs.155191	villin 2 (ezrin)	19.1
	428309	M97815	Hs.183650	cellular retinoic acid-binding protein 2	19.1
	420005	AW271106	Hs.133294	ESTs	19.1
	436982	AB018305	Hs.5378	spondin 1, (I-spondin) extracellular matrix p	19.0
60	407142	AA412535	Hs.55235	sphingomyelin phosphodiesterase 2, neutral me	19.0
	430122	NM_013342	Hs.233765	TCF3 (E2A) fusion partner (in childhood Leuke	18.9
	446293	AA20213	Hs.149722	ESTs	18.9
	444825	AW167613	Hs.248	mitogen-activated protein kinase kinase kinas	18.9
	407634	AW016569	Hs.301280	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosam	18.9
65	445200	AA084460	Hs.12409	somatostatin	18.9
	418917	X02994	Hs.1217	adenosine deaminase	18.8
	435777	AW419202	Hs.288192	protein phosphatase 1, regulatory (inhibitor)	18.8
	431049	AA846576	Hs.103267	hypothetical protein FLJ22548 similar to gene	18.7
	426427	M86599	Hs.169840	TTK protein kinase	18.7
70	436281	AW411194	Hs.120051	ESTs	18.6
	425907	AA365752	Hs.155965	ESTs	18.6
	459720			ESTs	18.6
	421242	AW161386	Hs.13561	ESTs, Weakly similar to dJ37E16.5 [H.sapiens]	18.5
	457715	AA642402	Hs.59142	ESTs	18.5
75	451668	Z43948	Hs.26789	ASPC (acidic secreted protein in cartilage)A	18.4
	437142	AJ791617	Hs.145068	ESTs	18.4
	418588	BE387040	Hs.182476	ESTs, Weakly similar to similar to alpha/beta	18.3
	433068	NM_006456	Hs.288215	slatyltransferase	18.3
	419854	AW664873	Hs.87836	Homo sapiens PAC clone RP5-1087M19 from 7q11.	18.3
80	444726	NM_006147	Hs.11801	interferon regulatory factor 6	18.3
	423011	NM_000683	Hs.299847	ESTs, Highly similar to A2AD_HUMAN ALPHA-2C-2	18.2
	451428	AW083384	Hs.11067	ESTs, Weakly similar to K02E10.2 [C.elegans]	18.2
	424865	AF011333	Hs.153563	lymphocyte antigen 75	18.2
	418742	AW451197	Hs.113418	ESTs	18.1
	446627	AJ973016	Hs.15725	ESTs; hypothetical protein SBB148	18.1

	424885	AI333771	Hs.82204	ESTs	18.1
	402926			0	18.0
	405452			0	18.0
5	428641	AA431367	Hs.234546	GMFR2 for guanosine monophosphate reductase I	18.0
	454390	AB020713	Hs.56966	KIAA0906 protein	18.0
	441784	AI522132	Hs.28700	ESTs	18.0
	418758	AW959311	Hs.87019	ESTs	17.9
	408621	AI970872	Hs.46638	chromosome 11 open reading frame 8; fetal br	17.9
10	426201	AW182614	Hs.128499	ESTs	17.8
	410442	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta polype	17.8
	456423	AW748920		gb:CM2-BT0306-171199-034-g02 BT0306 Homo sapi	17.8
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein	17.8
	448110	AA626937	Hs.181551	ESTs	17.7
15	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	17.7
	405224			0	17.7
	447630	AI660149	Hs.44865	lymphoid enhancer-binding factor 1	17.7
	407653	NM_016429	Hs.37482	COP22 for nonclathrin coat protein zeta-COP	17.7
	427490	Z95152	Hs.178695	mitogen-activated protein kinase 13	17.6
20	414812	X72755	Hs.77367	monokine induced by gamma interferon	17.6
	427691	AW194426	Hs.20726	ESTs	17.6
	420650	AA455706	Hs.44581	heat shock protein hsp70-related protein	17.5
	439841	AF038961	Hs.6710	mannose-6-phosphate utilization defect 1	17.5
	425810	AI923627	Hs.31903	ESTs	17.5
25	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kd)	17.5
	456098	AW747800	Hs.55016	hypothetical protein FLJ21935	17.4
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	17.4
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-induc	17.4
	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kd, brain)	17.4
30	411734	AW374954	Hs.71779	Homo sapiens DNA from chromosome 19, cosmid F	17.3
	405295			0	17.3
	408340	AB037762	Hs.44268	myelin gene expression factor 2	17.3
	456068	AI677897	Hs.76640	RGC32 protein	17.3
35	448571	AA486794	Hs.66915	ESTs, Weakly similar to 16.7Kd protein [H.sap	17.2
	418829	AL117482	Hs.7978	DKFZP434C131 protein	17.2
	418004	U37519	Hs.87539	aldehyde dehydrogenase 8	17.2
	412078	X69699	Hs.73149	paired box gene 8	17.2
	414658	X58528	Hs.76781	ATP-binding cassette, sub-family D (ALD), mem	17.1
40	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (melanom	17.0
	426805	AB032945	Hs.172508	myosin VB	17.0
	410247	AF181721	Hs.61345	RU2S	17.0
	434516	AA807814	Hs.70582	ESTs, Moderately similar to AF144056 1 apopto	16.9
	428153	AW513143	Hs.98367	hypothetical protein FLJ22252 similar to SRY-	16.9
	417793	AW405434	Hs.82575	small nuclear ribonucleoprotein polypeptide B	16.9
45	454163	AW175997		gb:QV0-BT0078-190899-005-E02 BT0078 Homo sapi	16.9
	415402	AA164687	Hs.297889	ESTs	16.9
	420309	AW043637	Hs.21766	ESTs	16.9
	419201	M22324	Hs.1239	akanyl (membrane) aminopeptidase (aminopeptid	16.9
	444391	AL137697	Hs.11114	hypothetical protein dJ1181N3.1	16.9
50	457705	AW974668		gb:EST386757 MAGE resequences, MAGM Homo sapi	16.8
	412723	AA648459	Hs.179912	ESTs	16.8
	435774	R88066	Hs.4992	tumor suppressing subtransferable candidate 1	16.8
	408753	AI337192	Hs.47438	SH3 domain binding glutamic acid-rich protein	16.8
	447783	AF054178	Hs.18561	NADH dehydrogenase (ubiquinone) 1 alpha subco	16.8
55	418085	RA0328	Hs.258822	ESTs	16.7
	452472	AW957300	Hs.294142	ESTs, Weakly similar to SP49_HUMAN SPLICEOSOM	16.7
	409112	BE243971	Hs.50649	quinone oxidoreductase homolog	16.7
	410250	AI082777	Hs.61384	KIAA1445 protein	16.7
	446219	AI287344	Hs.149827	ESTs	16.6
60	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epithelial)	16.6
	425812	AA364128	Hs.245633	ESTs	16.6
	411742	AW247593	Hs.71819	eukaryotic translation initiation factor 4E b	16.6
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	16.6
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolo	16.6
65	440667	BE076969	Hs.7337	hypothetical protein FLJ10936	16.6
	430375	AW371048	Hs.93758	H4 histone family, member H	16.6
	419607	RS2557	Hs.91579	Homo sapiens clone 23783 mRNA sequence	16.6
	410328	BE080190	Hs.62275	CGI-141 protein	16.5
	405426			0	16.5
70	432636	AA340864	Hs.278562	claudin 7	16.5
	434725	AK000796	Hs.4104	hypothetical protein	16.5
	414683	S78296	Hs.76888	intermedin neuronal intermediate filament pro	16.5
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	16.5
	449944	AF290512	Hs.58215	Homo sapiens rholectin mRNA, partial cds	16.4
75	400666			0	16.4
	421536	BE250690	Hs.105509	CTL2 gene	16.4
	436032	AA150797	Hs.109276	latexin protein	16.4
	418196	AI745649	Hs.26549	ESTs, Weakly similar to T00066 hypothetical p	16.4
	452323	W44356	Hs.292812	ESTs, Weakly similar to C43H8.1 [C.elegans]	16.4
80	407699	AA825974	Hs.32646	Homo sapiens cDNA: FLJ21901 fis, clone HEP034	16.4
	414617	AI339520	Hs.20524	ESTs, Moderately similar to hexokinase I [H.s	16.3
	408204	AA454501	Hs.43666	protein tyrosine phosphatase type IVA, member	16.3
	452650	AW270150	Hs.254516	ESTs	16.3
	432906	BE265489	Hs.3123	lethal giant larvae (Drosophila) homolog 2	16.3
	402408			0	16.3

	408805	H69912	Hs.48269	vaccinia related kinase 1	16.3
	447155	AA100605	Hs.121557	ESTs, Weakly similar to AF251041 1 SGC32445 p	16.3
	405699			0	16.2
5	406893	M22406		gb:Human Intestinal mucin mRNA, partial cds,	16.2
	418629	BE247550	Hs.86859	growth factor receptor-bound protein 7 (GRB7)	16.2
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related kinase	16.2
	424243	AI949359	Hs.301837	ESTs, Highly similar to cis Golgi-localized c	16.2
	418462	BE001596	Hs.85266	integrin, beta 4	16.1
10	457205	AI905780	Hs.198272	NADH dehydrogenase (ubiquinone) 1 beta subcom	16.1
	428188	M98447	Hs.22	transglutaminase 1 (K polypeptide epidermal t	16.1
	449845	AW971183	Hs.60054	ESTs	16.1
	405429			0	16.1
	407375	AA091354		gb:J0815.seq.F Human fetal heart, Lambda ZAP	16.1
15	448377	AI494514	Hs.171380	ESTs	16.1
	431156	NM_002220	Hs.2722	inositol 1,4,5-bisphosphate 3-kinase A	16.0
	450043	AA885699	Hs.24332	CGI-26 protein	16.0
	403121			0	16.0
	400214			0	15.9
20	453252	R02436	Hs.215725	ESTs	15.9
	451734	NM_008176	Hs.26944	neurogranin (protein kinase C substrate, RC3)	15.9
	416855	AA188763	Hs.36793	Homo sapiens cDNA: FLJ23188 fs, clone LNG120	15.9
	424474	AA308883	Hs.148680	calcyon; D1 dopamine receptor-interacting pro	15.9
	423685	BE350494	Hs.49753	Homo sapiens mRNA for KIAA1561 protein, parti	15.9
25	428187	AI687303	Hs.285529	ESTs	15.9
	438817	AI023799	Hs.163242	ESTs	15.9
	425692	D90041	Hs.155955	NAT1; arylamine N-acetyltransferase	15.9
	421674	T10707	Hs.296355	neuronal PAS domain protein 2	15.9
	439999	AA115811	Hs.6838	ras homolog gene family, member E	15.9
30	411351	W02919	Hs.283476	peroxisomal acyl-CoA thioesterase	15.9
	413027	NM_002885	Hs.75151	RAP1, GTPase activating protein 1	15.9
	453684	AA355925	Hs.36232	KIAA0186 gene product	15.8
	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase C-beta	15.8
	422748	AA316266	Hs.129349	ESTs	15.8
35	414591	AI888490	Hs.55902	ESTs	15.8
	421877	AW250380	Hs.109059	mitochondrial ribosomal protein L12	15.8
	404780			0	15.8
	401192			0	15.8
	447519	U46258	Hs.23448	ESTs	15.8
40	434252	AF121858	Hs.12169	sorting nexin 8	15.7
	451253	H48299	Hs.26126	claudin 10	15.7
	435499	R89344	Hs.14148	ESTs	15.7
	422424	AI186431	Hs.116577	prostate differentiation factor; placental bo	15.7
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fs, clone NT2RP20	15.7
45	424562	AI420859	Hs.150557	basic transcription element binding protein 1	15.7
	443247	BE614387	Hs.47378	ESTs	15.7
	430696	AA531276	Hs.59509	ESTs	15.6
	437044	AL035864	Hs.69517	ESTs, highly similar to differentially expres	15.6
	428237	AF175206	Hs.183125	killer cell lectin-like receptor F1	15.6
50	440048	AA897461	Hs.158469	ESTs, Weakly similar to envelope protein JHs	15.6
	414922	D00723	Hs.77631	glycine cleavage system protein H (aminomethyl	15.6
	422030	X51416	Hs.110849	estrogen-related receptor alpha	15.6
	408716	AI567839	Hs.151714	ESTs	15.5
	410258	X52638	Hs.739	6-phosphofructo-2-kinase/fructose-2,6-bisphosp	15.5
55	410530	M25809	Hs.64173	ESTs, Highly similar to VAB1_HUMAN VACUOLAR A	15.5
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	15.5
	409015	BE389387	Hs.49767	NADH dehydrogenase (ubiquinone) Fe-S protein	15.5
	447549	AI871120	Hs.231265	ESTs	15.5
	449704	AK000733	Hs.23900	GTPase activating protein	15.4
60	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIb, recept	15.4
	421630	NM_001956	Hs.1407	endothelin 2	15.4
	433018	AI669760	Hs.188881	ESTs	15.4
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	15.3
	407014	U88268		gb:Human cytochrome b pseudogene, partial cds	15.2
65	429311	AF080157	Hs.198998	conserved helix-loop-helix ubiquitous kinase	15.2
	431842	NM_005764	Hs.271473	epithelial protein up-regulated in carcinoma,	15.2
	406907	Z25427		gb:Human protein-serine/threonine kinase	15.2
	458495	AI202029	Hs.148593	ESTs	15.2
	420551	AL137692	Hs.98780	Homo sapiens mRNA; cDNA DKFZp434P182 (from cl	15.1
70	448443	AW167128	Hs.231934	ESTs	15.1
	443848	AI085198	Hs.298699	ESTs	15.1
	431538	AL137547	Hs.259519	Homo sapiens mRNA; cDNA DKFZp434B1120 (from c	15.1
	436687	AA868643	Hs.120461	ESTs	15.1
	420917	AW135716	Hs.117330	ESTs	15.0
75	428575	M19684	Hs.184929	serine (or cysteine) proteinase inhibitor, cl	15.0
	403482			0	15.0
	421499	AI271438	Hs.105022	Homo sapiens PAC clone RP4-701016 from 7q33-q	15.0
	401047			0	14.9
	417749	U09196	Hs.82520	polymerase (DNA-directed), delta 4	14.9
80	416693	AJ373204	Hs.79531	Homo sapiens TTF-I interacting peptide 20 mRN	14.9
	428474	AB023182	Hs.184523	KIAA0965 protein	14.9
	428862	NM_000346	Hs.2316	SRY (sex-determining region Y)-box 9 (campome	14.9
	430271	T06199	Hs.237506	heat shock cognate 40	14.9
	414328	Z21666	Hs.75900	aconitase 2, mitochondrial	14.9
	415314	N88802	Hs.5422	glycoprotein M6B	14.8

	453735	AI066629	Hs.125073	ESTs	14.8
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fs, clone NT2RP20	14.8
	423575	C18863	Hs.163443	ESTs	14.8
	438081	H49548	Hs.298964	ESTs	14.8
5	403485			0	14.8
	452114	N22687	Hs.8238	ESTs	14.8
	426559	AB001914	Hs.170414	paired basic amino acid cleaving system 4	14.8
	412869	AA290712	Hs.82407	Homo sapiens HSPC296 mRNA, partial cds	14.8
10	452101	T60298		gb:gb87112.1 Stragene liver (937224) Homo	14.7
	420505	AW967984	Hs.291612	ESTs	14.7
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolog	14.7
	433336	AF017988	Hs.31388	ESTs; Highly similar to FRIZZLED PROTEIN PRE	14.7
	428977	AK001404	Hs.194698	cyclin B2	14.7
	429785	H82114	Hs.301769	ESTs	14.7
15	402424			0	14.7
	424971	AA479005	Hs.154036	tumor suppressing subtransferable candidate 3	14.7
	433037	NM_014158	Hs.279938	HSPC067 protein	14.6
	421670	BE207318	Hs.106874	BRCA1 associated protein-1 (ubiquitin carboxy	14.6
20	438598	AI805943	Hs.5723	Homo sapiens cDNA: FLJ23439 fs, clone HSI001	14.6
	453370	AI470523	Hs.182358	ESTs, Moderately similar to translation init	14.6
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fs, clone HEP091	14.6
	402287			0	14.6
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	14.6
25	442047	AA974598	Hs.150324	ESTs	14.5
	428582	BE336699	Hs.185055	BENE protein	14.5
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	14.5
	406851	AA609784	Hs.180255	major histocompatibility complex, class II, D	14.5
	457318	AI123657	Hs.127264	ESTs	14.5
30	420453	AL157500	Hs.97840	Homo sapiens mRNA: cDNA DKFZp434G015 (from cl	14.5
	436406	AW105723	Hs.125346	ESTs	14.5
	420738	AI263022	Hs.82204	ESTs	14.5
	419743	AW408762	Hs.127478	ESTs	14.5
	429113	D28235	Hs.196384	Prostaglandin-endoperoxide synthase 2 (COX-2)	14.5
35	450256	AA286887	Hs.24724	MFH-amplified sequences with leucine-rich tan	14.5
	424906	AI566086	Hs.153718	Homo sapiens mRNA for Hmcb33 protein, 3' untr	14.5
	427414	F11750	Hs.6647	Homo sapiens cDNA FLJ13088 fs, clone NT2RP30	14.4
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-activat	14.4
	418738	AW388633	Hs.6682	solute carrier family 7, member 11	14.3
40	429414	AI783658	Hs.202095	empty spiracles (Drosophila) homolog 2	14.3
	424669	AA417181	Hs.120858	Homo sapiens cDNA FLJ13945 fs, clone Y78AA10	14.3
	408989	AW361666	Hs.49500	KIAA0746 protein	14.3
	406788	AI911841	Hs.5184	TH1 drosophila homolog	14.3
	417861	AA334551	Hs.82767	sperm specific antigen 2	14.3
45	402104			0	14.3
	416368	R88849		gb:ym96a06.r1 Soares adult brain N2b4HB55Y Ho	14.2
	405802			0	14.2
	448357	N20169	Hs.108923	ESTs	14.2
	444261	AA298958	Hs.10724	MDS023 protein	14.2
50	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, with Glu	14.2
	425163	D10040	Hs.154890	fatty-acid-Coenzyme A ligase, long-chain 2	14.1
	402520			0	14.1
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain 9	14.1
	430044	AA464510	Hs.152812	EST cluster (not in UniGene)	14.1
55	429663	M68874	Hs.211587	Human phosphatidylcholine 2-acylhydrolase (cP	14.1
	427036	AA397625	Hs.163913	ESTs	14.1
	444381	BE387335	Hs.283713	ESTs	14.1
	432090	AW972855	Hs.292853	ESTs	14.0
	406778	H06273	Hs.101651	Homo sapiens mRNA: cDNA DKFZp434C107 (from cl	14.0
60	404961	AW972195	Hs.284236	aldo-keto reductase family 7, member A3 (alfa	14.0
	452313	Y00486	Hs.28914	adenine phosphoribosyltransferase	14.0
	452355	N54926	Hs.29202	G protein-coupled receptor 34	14.0
	429942	AI338993	Hs.134535	ESTs	14.0
	403165			0	13.9
65	442150	AI368158	Hs.128864	ESTs	13.9
	439709	AW401433	Hs.6649	hypothetical protein FLJ20128	13.9
	456799	AC004923	Hs.135187	Homo sapiens clone CDABP0025 mRNA sequence	13.9
	427358	AW023482	Hs.97849	ESTs	13.9
	448982	AI638164	Hs.225520	ESTs	13.9
70	432025	BE407132	Hs.111286	hypothetical protein FLJ22512	13.8
	427505	AA361562	Hs.178761	26S proteasome-associated pad1 homolog	13.8
	402965			0	13.8
	418601	AA279490	Hs.88368	calmeglin	13.8
	436954	AA740151	Hs.130426	ESTs	13.8
	405024			0	13.8
75	453976	BE463830	Hs.163714	ESTs	13.8
	431921	N46466	Hs.58879	ESTs	13.8
	401735			0	13.8
	445496	AB007860	Hs.12802	development and differentiation enhancing fac	13.8
80	425007	AA456483	Hs.172081	phosphodiesterase 4D, cAMP-specific (dunce (D	13.7
	409463	AI458165	Hs.17296	ESTs	13.7
	430193	AI826653	Hs.102928	Homo sapiens cDNA FLJ13479 fs, clone PLACE10	13.7
	458869	AI637934	Hs.224978	ESTs	13.7
	426769	AA075596	Hs.172153	glutathione peroxidase 3 (plasma)	13.7
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	13.7

	439901	N73885	Hs.124169	ESTs	13.7
	431374	BE258532	Hs.251871	CTP synthase	13.7
	432861	AA339526	Hs.279593	HSPC171 protein	13.7
5	441172	AI279652	Hs.132879	ESTs	13.7
	410001	AB041038	Hs.57771	kallikrein 11; serine protease (TLSP)	13.7
	430315	NM_004293	Hs.239147	guanine deaminase	13.6
	422769	AA938905	Hs.289112	CGI-43 protein	13.6
	402389			0	13.6
10	448977	X91809	Hs.22698	regulator of G-protein signalling 19	13.6
	459648			gbdL3-CT0220-150200-070-B02 CT0220 Homo sapi	13.6
	452972	M31732	Hs.31210	B-cell CLL/lymphoma 3	13.6
	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	13.6
	448585	AB020676	Hs.21543	KIAA0869 protein	13.6
15	428385	AF112213	Hs.184062	putative Rab5-interacting protein	13.6
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HEMBB10	13.6
	447238	AW451676	Hs.158564	ESTs	13.6
	437108	AA434054	Hs.80624	Homo sapiens cDNA: FLJ23442 fis, clone HSI009	13.6
	425749	AW328587	Hs.159448	surfeit 2	13.5
20	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	13.5
	413753	U17760	Hs.301103	Laminin, beta 3 (nicein (125kD), kalinin (140	13.5
	419034	NM_002110	Hs.89555	hemopoietic cell kinase	13.5
	448361	H82028	Hs.238707	Homo sapiens cDNA: FLJ22457 fis, clone HRC099	13.5
	412754	AW160375	Hs.74565	amyloid beta (A4) precursor-like protein 1	13.5
25	419081	A1798863	Hs.87191	ESTs	13.5
	407732	AW138839	Hs.24210	ESTs	13.5
	423329	AF054910	Hs.127111	teklin 2 (testicular)	13.5
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced, 68k	13.4
	439636	AF086467		gbdHomo sapiens full length insert cDNA clone	13.4
30	417605	AF006609	Hs.82294	regulator of G-protein signalling 3	13.4
	445861	BE293423	Hs.11809	single Ig IL-1R-related molecule	13.4
	447350	AI375572	Hs.172634	ESTs; HER4 (c-erb-B4)	13.4
	451807	W52854	Hs.27099	DKFZP564J0863 protein	13.4
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, long f	13.4
35	422443	NM_014707	Hs.116753	histone deacetylase 7B	13.4
	412504	Z44496	Hs.26039	Homo sapiens cDNA FLJ13937 fis, clone Y79AA10	13.4
	453344	BE349075	Hs.44571	ESTs	13.4
	402885			0	13.4
	438712	AW978161	Hs.169877	ESTs	13.4
40	421774	AL050374	Hs.108169	DKFZP586C1619 protein	13.3
	425638	NM_012337	Hs.158450	nasopharyngeal epithelium specific protein 1	13.3
	401897			0	13.3
	425601	AW629485	Hs.293352	ESTs	13.3
	450779	AW204145	Hs.156044	ESTs	13.3
45	444858	AI199738	Hs.208275	ESTs, Weakly similar to unnamed protein produ	13.3
	442619	AA447492	Hs.20183	ESTs, Weakly similar to AF164793 1 protein x	13.3
	434263	N34895	Hs.44848	ESTs	13.3
	426059	BE292842	Hs.166120	Interferon regulatory factor 7	13.3
	407467	D55638		gbdHuman B-cell PABL (pseudoautosomal boundar	13.3
50	412560	R24601	Hs.108300	CCR4-NOT transcription complex, subunit 3	13.2
	442986	AI025990	Hs.285520	ESTs	13.2
	420317	AB006628	Hs.96485	KIAA0290 protein	13.2
	443211	AI128388	Hs.143655	ESTs	13.2
	434361	AF129755	Hs.117772	ESTs	13.2
55	423493	AI815965	Hs.129683	ubiquitin-conjugating enzyme E2D 1 (homologou	13.2
	414183	AW957446	Hs.301711	ESTs	13.2
	447778	BE620592	Hs.71190	ESTs	13.2
	435106	AA100847	Hs.193380	ESTs, Highly similar to AF174600 1 F-box prot	13.1
	439490	AW249197	Hs.100043	ESTs, Weakly similar to PSF_HUMAN PTB-ASSOCIA	13.1
60	409606	AW444594	Hs.2387	transglutaminase 4 (prostate)	13.1
	421308	AA687322	Hs.192843	ESTs	13.1
	414950	C15407		gbdC15407 Clontech human aorta polyA+ mRNA (6	13.1
	416783	AA206186	Hs.79889	monocyte to macrophage differentiation-associ	13.1
	415927	AL120168	Hs.78919	Kell blood group precursor (McLeod phenotype)	13.1
65	422605	H16646	Hs.118666	Human clone 23759 mRNA, partial cds	13.0
	430427	AA296701	Hs.241413	opticin	13.0
	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic; stratum corneum)	13.0
	421693	X71490	Hs.106876	ATPase, H+ transporting, lysosomal (vacuolar	13.0
	407727	AW411148	Hs.38044	DKFZP584M082 protein	13.0
70	427706	AW971225	Hs.293800	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	13.0
	406709	AI355761	Hs.242463	keratin 8	13.0
	405353			0	13.0
	453060	AW294092	Hs.21594	ESTs	13.0
	459299	BE094291	Hs.155651	hepatocyte nuclear factor 3, beta	13.0
75	447843	AW337186	Hs.224891	ESTs	13.0
	446576	AI659477	Hs.51820	ESTs, Moderately similar to ALU7_HUMAN ALU SU	13.0
	449700	L02867	Hs.78358	ESTs	13.0
	436476	AA326108	Hs.53631	ESTs	13.0
	432532	AW058459	Hs.162246	ESTs	13.0
80	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	13.0
	432673	AB028859	Hs.278605	ER-associated DNAJ; ER-associated Hsp40 co-ch	12.9
	414684	AW630023	Hs.76893	3-hydroxybutyrate dehydrogenase (heart, mito	12.9
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipase A1a	12.9
	427923	AW274357	Hs.268384	Fzr1 protein	12.9
	437395	AL365408	Hs.10632	hypothetical protein DKFZp762M136	12.9

	441627	AA947552	Hs.58086	ESTs	12.9
	419084	AA496539	Hs.179902	transporter-like protein	12.9
	423087	AA321355	Hs.285401	ESTs	12.9
5	423070	R55677	Hs.155569	ESTs	12.8
	441344	BE250144	Hs.41514	ESTs	12.8
	423527	AJ206965	Hs.105861	Homo sapiens cDNA FLJ13824 fis, clone THYRO10	12.8
	417006	AW673606	Hs.80758	aspartyl-tRNA synthetase	12.8
	453552	AL041941	Hs.154729	3-phosphoinositide dependent protein kinase-1	12.8
10	453657	W23237	Hs.286162	ESTs	12.8
	434414	AJ798376		gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens cDNA	12.7
	456051	T85626	Hs.76239	hypothetical protein FLJ20608	12.7
	451659	BE379761	Hs.14248	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	12.7
	418216	AA662240	Hs.283099	AF15q14 protein	12.7
	423281	AJ271684	Hs.126355	C-type (calcium dependent, carbohydrate-recog	12.7
15	424275	AW673173	Hs.144505	DKFZP566F0546 protein	12.7
	440062	AJ350518	Hs.129692	ESTs	12.7
	444371	BE540274	Hs.239	Forkhead box M1	12.7
	412520	AA442324	Hs.795	H2A histone family, member O	12.7
	413349	BE086692		gb:QV1-BT0678-130400-156-g07 BT0678 Homo sapi	12.7
20	414500	W24087	Hs.76285	DKFZP566B167 protein	12.6
	428261	AW176254	Hs.143475	ESTs	12.6
	402238			0	12.6
	400280			0	12.6
25	421248	AW582962	Hs.300961	ESTs, Highly similar to AF151805 1 CGI-47 pro	12.6
	442028	AW956698	Hs.14456	neural precursor cell expressed, developmenta	12.6
	435502	L13266	Hs.105	glutamate receptor, ionotropic, N-methyl D-as	12.6
	409964	AW368228	Hs.67928	ESTs	12.6
	418783	AW382887	Hs.88474	prostaglandin-endoperoxide synthase 1 (prosta	12.5
	452117	AJ421760	Hs.77870	Homo sapiens cDNA FLJ12750 fis, clone NT2RP20	12.5
30	448074	BE521355	Hs.27160	ESTs	12.5
	442655	AW027457	Hs.30323	ESTs	12.5
	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	12.5
	400240			0	12.5
35	413048	M93221	Hs.75182	mannose receptor, C type 1	12.5
	426215	AW953419	Hs.155223	ESTs	12.5
	430024	AJ808780	Hs.227730	integrin, alpha 6	12.5
	445655	AA873830	Hs.167746	B cell linker protein	12.5
	419941	X98654	Hs.93837	phosphatidylinositol transfer protein, membra	12.5
40	425280	U31519	Hs.1872	phosphoenolpyruvate carboxykinase 1 (soluble)	12.5
	427767	AJ879283	Hs.180714	cytochrome c oxidase subunit VIa polypeptide	12.4
	450243	AW119084	Hs.201037	ESTs	12.4
	408930	AA146721	Hs.49005	hypothetical protein	12.4
	418783	T41368		gb:ph1d1_19/1TV Outward Alu-primed hncDNA lib	12.4
45	452096	BE394901	Hs.226785	ESTs	12.4
	424513	BE385864	Hs.149894	mitochondrial translational initiation factor	12.4
	422306	BE044325	Hs.227280	Homo sapiens mRNA for Lsm5 protein	12.4
	409031	AA376836	Hs.76728	ESTs	12.4
	435515	N40080	Hs.6879	DC13 protein	12.4
50	429583	NM_006412	Hs.209119	1-acylglycerol-3-phosphate O-acyltransferase	12.3
	449643	R05989	Hs.19603	ESTs	12.3
	440313	AL050060	Hs.7158	DKFZP566H073 protein	12.3
	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	12.3
	447357	AJ375922	Hs.159367	ESTs	12.3
55	405089			0	12.3
	414972	BE263782	Hs.77695	KIAA0008 gene product	12.3
	435039	AW043921	Hs.130526	ESTs	12.3
	447033	AJ357412	Hs.157601	EST - not in UniGene	12.3
	427521	AW973352	Hs.299056	ESTs	12.3
60	409377	AA300274	Hs.115659	Homo sapiens cDNA: FLJ23461 fis, clone HSI077	12.3
	400116			0	12.3
	445808	AL137516	Hs.13323	hypothetical protein FLJ22059	12.2
	457817	AA247751	Hs.79572	cathepsin D (lysosomal aspartyl protease)	12.2
	442410	AW996503	Hs.197680	ESTs	12.2
65	445404	AJ261687	Hs.145541	ESTs, Weakly similar to JC4974 sodium iodide	12.2
	403372	AW249152	Hs.44017	SIR2 (silent mating type information regulati	12.2
	427082	AB037858	Hs.173484	hypothetical protein FLJ10337	12.2
	433764	AW753676	Hs.39982	ESTs	12.2
	400268			0	12.2
70	433190	M26901	Hs.3210	renin	12.2
	444863	AW384082	Hs.301323	ESTs	12.2
	434779	AF153815	Hs.50151	potassium inwardly-rectifying channel, subfam	12.2
	451346	NM_006338	Hs.26312	glioma amplified on chromosome 1 protein (leu	12.2
	430262	AA218780	Hs.237323	N-acetylglucosamine-phosphate mutase	12.2
	421071	AJ311238	Hs.104476	ESTs	12.2
75	426773	NM_015556	Hs.172180	KIAA0440 protein	12.1
	409178	BE393948	Hs.50915	kalikrein 5	12.1
	400250			0	12.1
	428450	NM_014791	Hs.184339	KIAA0175 gene product	12.1
80	414531	T69387	Hs.76364	allograft inflammatory factor 1	12.1
	448210	AW247775	Hs.7393	hypothetical protein from EUROIMAGE 1987170	12.1
	440081	AA853389	Hs.135643	ESTs	12.1
	413179	N99692	Hs.75227	NADH dehydrogenase (ubiquinone) 1 alpha subco	12.1
	447551	BE066634	Hs.929	myosin, heavy polypeptide 7, cardiac muscle,	12.1
	400517	AF242388	Hs.149585	lensin	12.1

	401610		0	12.0
	454381	AI935093	Hs.193428	ESTs
	443997	AW081465	Hs.299644	ESTs
	402944		0	12.0
5	430537	BE160081	Hs.256290	S100 calcium-binding protein A11 (calgizarin)
	415099	AA92170	Hs.77917	ubiquitin carboxyl-terminal esterase L3 (ubiq
	445422	AV653731	Hs.282829	ESTs
	416667	AK000526	Hs.79457	hypothetical protein FLJ20519
	442611	BE077165	Hs.177537	ESTs
10	443271	BE568568	Hs.195704	ESTs
	415120	N64464	Hs.34950	ESTs
	439574	AA69788	Hs.165190	ESTs
	405804		0	12.0
	412519	AA196241	Hs.73980	troponin T1, skeletal, slow
15	414135	NM_004419	Hs.2128	dual specificity phosphatase 5
	447075	AV662037	Hs.124740	ESTs
	416841	N33878	Hs.249495	heterogeneous nuclear ribonucleoprotein A1
	402943		0	11.9
	416933	BE561850	Hs.80506	small nuclear ribonucleoprotein polypeptide A
20	439744	AL389994	Hs.301272	ESTs, Weakly similar to homologue of Drosophila
	405762		0	11.9
	408983	NM_000492	Hs.663	cystic fibrosis transmembrane conductance reg
	455102	BE005496		gb:CM1-BN0117-110400-183-b09 BN0117 Homo sapi
	402840		0	11.9
25	449183	AA445022	Hs.196985	Homo sapiens cDNA: FLJ21135 fis, clone CAS072
	439273	AW139099	Hs.269701	ESTs
	450484	BE220675		gb:U98111.x1 NCL CGAP_Lu24 Homo sapiens cDNA
	445431	AF137386	Hs.12701	plasmolipin
	401888		0	11.9
30	426037	AW160780	Hs.166071	cyclin-dependent kinase 5
	416742	R38644	Hs.248420	ESTs
	418324	AW246273	Hs.84131	threonyl-tRNA synthetase
	412870	N22788	Hs.82407	Homo sapiens HSPC296 mRNA, partial cds
	432680	T47364	Hs.278613	interferon, alpha-inducible protein 27
35	421478	AI683243	Hs.97258	ESTs
	426635	BE395109	Hs.129327	ESTs
	420523	AA262999	Hs.42788	ESTs
	426227	U87058	Hs.168102	Human proteinase activated receptor-2 mRNA; 3
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractual arachnod
40	441816	AA01807	Hs.149997	ESTs
	424596	AB020639	Hs.151017	estrogen-related receptor gamma
	400640		0	11.8
	448133	AA723157	Hs.73769	folate receptor 1 (adult)
	401532		0	11.8
45	400161		0	11.8
	442556	AL137761	Hs.8379	Homo sapiens mRNA; cDNA DKFZp586L2424 (from c
	451002	AA013299	Hs.8018	ESTs, Weakly similar to ALU3_HUMAN ALU SUBFAM
	401879		0	11.7
	415989	AI267700	Hs.111128	ESTs
50	416434	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated
	410816	AW873401	Hs.273599	ESTs
	449239	T24653	Hs.23360	likely ortholog of yeast ARV1
	447669	AL049985	Hs.19180	Homo sapiens mRNA; cDNA DKFZp564E122 (from cl
	436877	AA931484	Hs.121255	ESTs, Weakly similar to cDNA EST EMBL:D67419
55	434580	R13052	Hs.3964	Homo sapiens clone 24877 mRNA sequence
	448105	AW591433	Hs.170675	ESTs, Weakly similar to TMS2_HUMAN TRANSMEMBR
	400279		0	11.7
	440497	AA887266	Hs.144979	ESTs
	451260	AW750773		gb:CM0-CN0044-260100-164-h03 CN0044 Homo sapi
60	429175	AI953040	Hs.127714	ESTs, Moderately similar to SOX30 protein [H]
	408209	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule)
	428856	AA436735	Hs.183171	Homo sapiens cDNA: FLJ22002 fis, clone HEP066
	420153	N22120	Hs.75277	hypothetical protein FLJ13910
	428760	AI351459	Hs.192398	ESTs
65	421401	AW410478	Hs.104019	transforming, acidic coiled-coil containing p
	404502		0	11.6
	430423	AI190548	Hs.143479	ESTs, Weakly similar to hypothetical protein
	405192		0	11.6
	439092	AA830149		gb:acc44f08.s1 NCL CGAP_GCB1 Homo sapiens cDNA
70	401714		0	11.5
	439335	AA742697	Hs.62492	ESTs, Weakly similar to S59856 collagen alpha
	406082	S47833	Hs.82927	adenosine monophosphate deaminase 2 (isoform
	401010		0	11.5
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkinesin6)
75	409339	AB020686	Hs.54037	ectonucleotide pyrophosphatase/phosphodiester
	459684			gb:aa086a08.x1 Schiller meningioma Homo sapien
	451051	BE254309	Hs.125262	DKFZP586G1624 protein
	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chronic
	412153	R87934		gb:yo47b10.r1 Soares adult brain N2b4HB55Y Ho
80	427256	AL042436	Hs.97723	ESTs
	406708	AI282759	Hs.242463	keratin 8
	457644	AA770080	Hs.144962	ESTs, Moderately similar to I59365 ubiquitin
	422848	Z25884	Hs.121483	chloride channel 1, skeletal muscle (Thomsen
	424134	AF070637	Hs.140950	hypothetical protein

5	451931	AK000208	Hs.27267	Homo sapiens cDNA FLJ20201 fis, clone COLF121	11.4
	400438	AF185611	Hs.115352	growth hormone 1	11.4
	412994	D32257	Hs.75113	general transcription factor IIA	11.4
	408124	U89337	Hs.42853	cAMP responsive element binding protein-like	11.4
	452249	BE394412	Hs.61252	ESTs	11.4
10	424627	AA344555		gbr:EST50715 Gall bladder ! Homo sapiens cDNA	11.4
	405626			0	11.4
	436690	AA373970	Hs.183096	ESTs	11.4
	415862	R51034	Hs.144513	ESTs	11.4
	405755	N80129	Hs.94360	metallothionein 1L	11.4
15	433657	A1244368	Hs.8124	PH domain containing protein in retina 1	11.4
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	11.4
	423334	AK000906	Hs.127273	hypothetical protein FLJ10044	11.4
	433053	BE301909	Hs.278952	glutathione S-transferase subunit 13 homolog	11.4
	428423	AU076517	Hs.184276	solute carrier family 9 (sodium/hydrogen exch	11.3
20	442353	BE379594	Hs.49136	ESTs	11.3
	447700	A1420183	Hs.171077	ESTs, Weakly similar to similar to serine/thr	11.3
	402077			0	11.3
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypeptide 1	11.3
	405145			0	11.3
25	428248	AJ126772	Hs.40479	ESTs	11.3
	425508	AA991551	Hs.97013	ESTs	11.3
	428340	AF261088	Hs.154721	aconitase 1, soluble	11.3
	431452	AJ073841	Hs.152372	ESTs	11.3
	446651	AA393907	Hs.97179	ESTs	11.3
30	443755	C18397	Hs.9730	tachykinin 3 (neuromedin K, neurokinin beta)	11.3
	436209	AW850417	Hs.254020	ESTs, Moderately similar to unnamed protein p	11.3
	401020			0	11.3
	456724	AW247388	Hs.301423	calcium binding protein 1 (calbrain)	11.2
	407227	H94949	Hs.171955	trophinin associated protein (lastin)	11.2
35	402066			0	11.2
	442721	AJ015892	Hs.101282	Homo sapiens mRNA; cDNA DKFZp434B102 (from cl	11.2
	401025			0	11.2
	452423	AA991724	Hs.180535	Homo sapiens cDNA: FLJ22711 fis, clone HSI133	11.2
	431685	AW296135	Hs.267659	vav 3 oncogene	11.2
40	425176	AW015644	Hs.301430	ESTs, Moderately similar to TEF1_HUMAN TRANSC	11.2
	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-relate	11.2
	409079	W87707	Hs.82065	Interleukin 6 signal transducer (gp130; oncos	11.2
	456995	T89832	Hs.170278	ESTs	11.2
	419223	X60111	Hs.1244	CD9 antigen (p24)	11.2
45	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	11.2
	407604	AW191962	Hs.288061	actin, beta	11.2
	437829	T08353	Hs.106642	ESTs, Weakly similar to hypothetical protein	11.1
	415789	H01581		gb:yj33108.r1 Soares placenta Nb2HP Homo sapi	11.1
	424447	AL137376	Hs.147368	Homo sapiens mRNA; cDNA DKFZp434J0226 (from c	11.1
50	436034	AF282693	Hs.150185	inflammation-related G protein-coupled recept	11.1
	404931			0	11.1
	445979	AJ695047	Hs.202395	ESTs	11.1
	446733	AA863360	Hs.26040	ESTs; Highly similar to CYTOCHROME P450 IVA2	11.1
	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated protein	11.1
55	445258	AJ635931	Hs.147613	ESTs	11.1
	417251	AW015242	Hs.99488	ESTs; Weakly similar to ORF YKR074w [S.cerevi	11.1
	421041	N36914	Hs.14691	ESTs	11.1
	425537	AB007913	Hs.158291	KIAA0444 protein	11.1
	435763	AJ243929	Hs.190419	ESTs	11.1
60	444790	AB030506	Hs.118955	B9 protein	11.1
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	11.1
	433882	U90441	Hs.3622	procollagen-proline, 2-oxoglutarate 4-dioxyge	11.1
	405358			0	11.1
	435814	AW615179	Hs.152870	ESTs	11.0
65	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	11.0
	446772	AW294404	Hs.144515	Homo sapiens cDNA FLJ11672 fis, clone HEMBA10	11.0
	456694	AW016382	Hs.105642	Homo sapiens cDNA: FLJ23271 fis, clone HEP001	11.0
	441128	AA570256	Hs.54628	ESTs	11.0
	432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polypeptid	11.0
70	412576	AA447718	Hs.107057	ESTs	11.0
	411122	F00809	Hs.143696	coactivator-associated arginine methyltransfe	11.0
	427225	AA432391	Hs.258903	Homo sapiens mRNA for KIAA1640 protein, parti	11.0
	426260	NM_002541	Hs.168669	oxoglutarate dehydrogenase (lipoamide)	11.0
	444652	BE513613	Hs.11538	actin related protein 2/3 complex, subunit 1A	11.0
75	431947	AL359613	Hs.49933	hypothetical protein DKFZp762D1011	11.0
	414432	BE378174	Hs.26506	Homo sapiens clone CDABP0005 mRNA sequence	11.0
	458627	AW088642	Hs.97984	ESTs; Weakly similar to WASP-family protein [10.9
	409142	AL136877	Hs.50758	chromosome-associated polypeptide C	10.9
	447627	AF090922	Hs.285902	CGI-113 protein	10.9
80	447656	NM_003726	Hs.19126	src kinase-associated phosphoprotein of 55 kD	10.9
	454227	AW963897	Hs.44743	KIAA1435 protein	10.9
	402927			0	10.9
	422380	AA309881	Hs.136246	ESTs	10.9
	455986	BE177736		gbr:RC1-HT0598-140300-021-g06 HT0598 Homo sapi	10.9
	410962	BE273749	Hs.752	FK506-binding protein 1A (12kD)	10.9
	450361	BE327108	Hs.202512	ESTs	10.9
	457484	H57645		gbr:y21e01.r1 Soares fetal liver spleen 1NFS	10.9
	407903	A1287341	Hs.154029	bHLH factor Hes4	10.9

	403398		0	10.9
	401405		0	10.9
	405570		0	10.9
5	421240	R72730	Hs.29283	ESTs, Weakly similar to PLK_HUMAN PROTEOGLYCA
	403649		0	10.9
	447824	BE620800		gb:601483379T1 NIH_MGC_69 Homo sapiens cDNA c
	450935	BE514743	Hs.25684	tumor suppressor deleted in oral cancer-relat
	439853	AL119566	Hs.6721	lysophospholipase-like
10	451852	R51928		gb:7171c05.r1 Soares breast 2NbhBst Homo sapi
	431218	NM_002145	Hs.2733	homeo box B2
	457794	AA589292	Hs.246850	ESTs
	444374	AA009841	Hs.11039	Homo sapiens cDNA FLJ12798 fis, clone NT2RP20
	456566	AW235317	Hs.259214	ESTs
15	405552		0	10.8
	439436	BE140845	Hs.57868	ESTs
	435310	AA705075	Hs.169536	Rhesus blood group-associated glycoprotein
	411125	AA151647	Hs.68877	cytochrome b-245, alpha polypeptide
	415807	H03139	Hs.24683	ESTs
20	409430	R21945	Hs.166975	splicing factor, arginine/serine-rich 5
	417033	H83784	Hs.40532	ESTs, Weakly similar to PEBP MOUSE PHOSPHATID
	418484	R87580		gb:ym89h07.r1 Soares adult brain N2b4HB55Y Ho
	404567		0	10.8
	418384	AW149266	Hs.25130	ESTs
25	421971	U83127	Hs.110121	SEC7 homolog
	428769	AW207175	Hs.106771	ESTs
	459104	R19238	Hs.282057	ESTs
	410898	AW809637		gb:MR4-ST0124-261099-015-b07 ST0124 Homo sapi
	416969	A815443	Hs.283404	organic cation transporter
30	408786	AA688292	Hs.118553	ESTs
	426298	AW965058	Hs.111583	ESTs
	421595	AB014520	Hs.105958	Homo sapiens cDNA: FLJ22735 fis, clone HUV001
	408007	AW135865	Hs.246783	ESTs
	400167		0	10.7
35	445243	AL217439	Hs.109854	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM
	421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (achondro
	412241	AW948343		gb:RC0-MT0015-130400-031-c01 MT0015 Homo sapi
	425827	W28316		gb:45b6 Human retina cDNA randomly primed sub
	420255	NM_007289	Hs.1298	membrane metallo-endopeptidase (neutral endop
40	430891	U22492	Hs.248118	G protein-coupled receptor 8
	402883		0	10.7
	423811	AW299598	Hs.50895	homeo box C4
	447078	AW885727	Hs.301570	ESTs
45	414343	AL036166	Hs.75914	coated vesicle membrane protein
	446913	AA430650	Hs.16529	transmembrane 4 superfamily member (tetraspan
	452279	AA266844	Hs.61260	hypothetical protein FLJ13164
	401220		0	10.7
	459259	AJ003294		gb:AJ003294 Selected chromosome 21 cDNA libra
50	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family
	448449	BE314567	Hs.211440	ESTs
	429670	LD1087	Hs.211593	protein kinase C, theta
	446759	R61463	Hs.16165	expressed in activated T/LAK lymphocytes
	400776		0	10.7
55	428093	AW594506	Hs.104830	ESTs
	412801	AA121055		gb:zm22b01.r1 Stratagene pancreas (937208) Ho
	440545	AW183201	Hs.190559	ESTs
	434540	NM_016045	Hs.5184	TH1 drosophila homolog
	414273	BE269057		gb:601184231F1 NIH_MGC_8 Homo sapiens cDNA d
	401817		0	10.6
60	410423	AW402432	Hs.63489	protein tyrosine phosphatase, non-receptor ty
	430590	AW383947	Hs.246381	CD68 antigen
	426680	AA320160	Hs.171811	adenylate kinase 2
	445413	AA151342	Hs.12577	CGI-147 protein
	402947		0	10.6
65	457426	AW971119		gb:EST383206 MAGE resequences, MAGL Homo sapi
	424148	BE242274	Hs.1741	Integrin, beta 7
	404944		0	10.6
	405421		0	10.6
	416772	A1733872	Hs.79769	protocadherin 1 (cadherin-like 1)
70	414191	AW250089	Hs.75807	POZ and LIM domain 1 (elfin)
	457588	AI571225	Hs.284171	KIAA1535 protein
	406038	Y14443	Hs.88219	zinc finger protein 200
	404790		0	10.6
	418922	AW956580	Hs.42699	Thrombospondin-1 (Hs.87409)
75	425940	AB023184	Hs.163990	KIAA0967 protein
	448749	AW859679	Hs.21902	Homo sapiens clone 25237 mRNA sequence
	418870	AF147204	Hs.89414	CKCR4; chemokine CXC receptor 4 (fusin)
	417933	X02308	Hs.82962	thymidylate synthetase
	450538	AW297396	Hs.227052	ESTs
80	427928	AA417682	Hs.119217	ESTs
	432721	AL121478	Hs.3132	steroidogenic acute regulatory protein
	429267	AA299290	Hs.246857	ESTs, Highly similar to S71100 protein kinase
	439190	AW978693	Hs.293811	ESTs
	408975	AW958693	Hs.49391	hypothetical protein LOC54149
	415130	W85893	Hs.249867	ESTs

5	425738	H29630	Hs.159408	Homo sapiens clone 24420 mRNA sequence	10.5
	440232	AJ766925	Hs.112554	ESTs	10.5
	425055	AA371906	Hs.294151	ESTs, Moderately similar to KIAA0544 protein	10.5
	420829	AW665612	Hs.221969	ESTs	10.5
	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	10.5
10	407771	AL138272	Hs.82713	ESTs	10.5
	444611	AK002180	Hs.11449	DKFZP564O123 protein	10.5
	444665	BE613126	Hs.47783	ESTs, Weakly similar to T12540 hypothetical p	10.5
	448030	N30714	Hs.20181	HDCME31P protein	10.5
	438982	AW979101	Hs.291980	ESTs	10.5
15	446224	AW450551	Hs.13308	ESTs	10.5
	405108			0	10.5
	438233	W52448	Hs.56147	ESTs	10.5
	401799			0	10.5
	454038	X06374	Hs.37040	platelet-derived growth factor alpha polypept	10.5
20	414222	AL135173	Hs.878	sorbitol dehydrogenase	10.5
	421828	AW891865	Hs.289109	dimethylarginine dimethylaminohydrolase 1	10.5
	422626	AA344932	Hs.118786	metallothionein 2A	10.5
	449261	AJ637592	Hs.224958	ESTs	10.4
	416218	R21499	Hs.23213	ESTs	10.4
25	457848	W26524	Hs.125682	ESTs; Weakly similar to D2092.2 [C.elegans]	10.4
	442577	AA292998	Hs.163900	ESTs	10.4
	406505	AF016272	Hs.115418	cadherin 16, KSP-cadherin	10.4
	412258	AA376768	Hs.288977	Homo sapiens cDNA: FLJ22622 fis, clone HSI056	10.4
	422224	AI905780	Hs.198272	NADH dehydrogenase (ubiquinone) 1 beta subcom	10.4
30	447774	BE018118	Hs.19554	chromosome 1 open reading frame 2	10.4
	403914			0	10.4
	406329			0	10.4
	402423			0	10.4
	431986	AA536130	Hs.149018	ESTs	10.4
35	423145	BE264548	Hs.222190	ESTs, Weakly similar to secretory carrier mem	10.4
	414402	BE294186		gbc601172959F1 NIH_MGC_17 Homo sapiens cDNA c	10.4
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	10.4
	426095	AJ278023	Hs.89986	ESTs	10.4
	434577	R37316	Hs.179769	Homo sapiens cDNA: FLJ22487 fis, clone HRC109	10.4
40	442415	AJ005101	Hs.129550	ESTs	10.3
	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	10.3
	435084	D17516	Hs.301607	adenylate cyclase activating polypeptide 1 (p	10.3
	431724	AA514535	Hs.283704	ESTs	10.3
	456798	AJ006422	Hs.135183	centaurin-alpha	10.3
45	417370	T28651	Hs.82030	tryptophanyl-tRNA synthetase	10.3
	422598	AF063611	Hs.118633	2'-5'-oligoadenylate synthetase-like	10.3
	435226	AI248938	Hs.270106	ESTs	10.3
	433192	AB040880	Hs.225594	ESTs, Moderately similar to KIAA1447 protein	10.3
	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	10.3
50	416228	AW505190	Hs.79089	sema domain, immunoglobulin domain (Ig), tran	10.3
	453403	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fis, clone PLACE10	10.3
	447906	AL050062	Hs.19999	DKFZP566K023 protein	10.3
	401782	NM_012434	Hs.117865	solute carrier family 17 (anion/sugar transpo	10.3
	453927	AA082465	Hs.301751	ESTs, Weakly similar to /prediction	10.3
55	450737	AW007152	Hs.203330	ESTs	10.3
	421633	AF121860	Hs.106260	sorting nexin 10	10.3
	409881	AF139799	Hs.202830	ESTs	10.3
	432883	U48936	Hs.3112	sodium channel, nonvoltage-gated 1, gamma	10.3
	440099	AL080058	Hs.6909	DKFZP564G202 protein	10.3
60	419024	X56411	Hs.1219	alcohol dehydrogenase 4 (class II), pi polype	10.3
	401835			0	10.3
	408896	AJ610447	Hs.48778	riban protein	10.3
	443120	AW402677	Hs.290801	ESTs	10.3
	400208			0	10.2
65	416908	AA333990	Hs.80424	coagulation factor XIII, A1 polypeptide	10.2
	400166			0	10.2
	434642	W25739	Hs.135287	ESTs	10.2
	424837	BE276113	Hs.153436	N-acetyltransferase, homolog of S. cerevisiae	10.2
	435075	R51094	Hs.12400	ESTs	10.2
70	425912	AL137629	Hs.162189	serine/threonine kinase with Dbl- and pleckst	10.2
	435080	AI831760	Hs.155111	ESTs	10.2
	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin-like	10.2
	410020	T86315	Hs.728	ribonuclease, RNase A family, 2 (liver, eosin	10.2
	411410	R20693	Hs.69954	laminin, gamma 3	10.2
75	450294	H42587	Hs.238730	ESTs	10.2
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PLACE10	10.2
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	10.2
	400812			0	10.2
	425843	BE313280	Hs.159827	death associated protein 3	10.2
80	449392	Z41698	Hs.26039	Homo sapiens cDNA FLJ13937 fis, clone Y79AA10	10.2
	409089	NM_014781	Hs.50421	KIAA0203 gene product	10.2
	401383			0	10.2
	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Drosoph	10.2
	442912	AJ088060	Hs.131450	ESTs	10.2
	400854	D25969	Hs.76325	Homo sapiens cDNA: FLJ23125 fis, clone LNG082	10.2
	401029	BE382701	Hs.25960	v-myc avian myelocytomatosis viral related on	10.2
	416602	NM_006159	Hs.79389	net (chicken)-like 2	10.2
	421805	AI660247	Hs.32699	ESTs, Weakly similar to LIV-1 protein [H.sapi	10.2

	405094			0	10.2
	450832	AW970602	Hs.105421	ESTs	10.2
	440076	R32052	Hs.178617	ESTs, Weakly similar to AF151840 1 CGI-82 pro	10.2
5	447563	BE536115	Hs.160983	ESTs	10.2
	421238	AB033101	Hs.102796	KIAA1275 protein	10.2
	400882			0	10.2
	415738	BE539367	Hs.295953	ESTs, Weakly similar to AF220049 1 uncharacter	10.1
	445464	AW172389	Hs.249999	ESTs	10.1
10	459042	AW272058	Hs.210338	ESTs	10.1
	414469	R51952	Hs.32587	steroid receptor RNA activator 1 (complexes w	10.1
	434732	AJ078443		gb:oz05g05.x1 Soares_fetal_liver_spleen_1NFLS	10.1
	441030	AW204139	Hs.174424	ESTs, Weakly similar to p140mDia [M.musculus]	10.1
	446855	BE616767	Hs.16269	B-cell CLL/lymphoma 7B	10.1
15	456785	AF151074	Hs.132744	hypothetical protein	10.1
	404182			0	10.1
	410358	AW975168	Hs.13337	ESTs, Weakly similar to unnamed protein produ	10.1
	430355	NM_006219	Hs.239818	phosphoinositide-3-kinase, catalytic, beta po	10.1
	442152	R39246	Hs.239666	Homo sapiens cDNA FLJ13495 fis, clone PLACE10	10.1
20	436354	AB79252	Hs.5151	Homo sapiens mRNA; cDNA DKFZp564C2163 (from c	10.1
	426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	10.1
	450599	AA460865	Hs.48516	ESTs	10.1
	454393	BE153288		gb:PMO-HT0335-180400-008-c08 HT0335 Homo sapi	10.1
	403383			0	10.1
25	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer, nonpo	10.1
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	10.1
	412116	AW402166	Hs.784	Epstein-Barr virus induced gene 2 (lymphocyte	10.1
	413808	J00287	Hs.182183	caldesmon 1	10.0
	458572	AJ223423	Hs.292794	ESTs	10.0
30	403295			0	10.0
	403910			0	10.0
	453400	AI991901	Hs.82590	ESTs, Moderately similar to ALU7_HUMAN ALU SU	10.0
	406502			0	10.0
	404743			0	10.0
35	412517	BE271584		gb:601141065F1 NIH_MGC_9 Homo sapiens cDNA cl	10.0
	402679			0	10.0
	455864	BE148970		gb:CMO-HT0245-031199-085-h05 HT0245 Homo sapi	10.0
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxygenase	10.0
	419280	W07506	Hs.283725	Homo sapiens cDNA FLJ12627 fis, clone NT2RM40	10.0
40	443503	AV645438	Hs.282927	ESTs	10.0
	423165	AI937547	Hs.124915	Human DNA sequence from clone 380A1 on chromo	10.0
	450206	AI796450	Hs.201600	ESTs	10.0
	459052	AA298812	Hs.98539	ESTs	10.0
	456248	AL035786	Hs.82425	actin related protein 2/3 complex, subunit 5	10.0
45	428438	NM_001955	Hs.2271	Endothelin 1	10.0
	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgranulin	10.0
	426127	L36983	Hs.167013	dynamitin 2	10.0

TABLE 13B:

Pkey: Unique Eos probeset Identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

50	Pkey	CAT Number	Accession
	410896	1226053_1	AW809637 AW809697 AW810554 AW809707 AW809885 AW810000 AW810088 AW809742 AW809816 AW809749 AW809639 AW809722
55			AW809835 AW809774 AW810023 AW810013 AW809813 AW809660 AW809728 AW809768 AW809951 AW809657 AW809954
	412153	1279701_1	R87934 AW898205 AW896020 AW896035
	412241	1284681_1	AW948343 AW948341 AW902855 AW984737
	412517	130281_1	BE271584 AA112511
60			AA121055 AA330917
	412801	132825_1	BE086692 BE087077 BE087072
	413349	1363558_1	BE269057 BE513434 BE396654
	414273	1431911_1	BE294186 BE298975
	414402	1443240_1	C15407 D81769 D61133
	414950	1509777_1	H01581 H12850 R65905 H13053
65			R88849 R84573 H50890
	415789	1555357_1	R87580
	416368	1591066_1	T41368 T41369 T41294
	418464	1759038_2	AA344555 AA344312 AW963070
	418783	1789791_1	W28316 W26507 AA364334
70			AA631362 AA631438
	424627	241724_1	AI798376 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231
	425827	256834_1	AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174
	434371	384839_1	T61139 AA149776 AA699829 AW879188 AW813567 AW813538 AI267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705
75			AA157730 AA157715 AA053524 AW849581 AW854566 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824
	434414	38585_1	AI829309 AW991957 N66951 AA527374 H66215 AA045564 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662
			AW817705 AW817703 AW817659 BE081531 H59570
	434732	392447_1	AJ078443 AA648102 AJ765577 AW974381
	439092	468554_1	AA830149 AW978407 MB5983 AW503637
80			AF086467 W81444 W81445
	439636	47467_1	BE620800
	447824	73861_1	BE220675 AA345621 AA009992
	450484	83645_1	AW750773 AJ768154
	451260	863912_1	R51928 AI820698 R48360 AI820694
	451852	888359_1	T60298 AI858257 T69667 T67634 T61224 T71537 T68933
	452101	898742_1	

	454163	1048369_1	AW175997 AW176000 AW175999 AW175994 AW176004 AW175989
	454393	115888_1	BE153288 BE153151 BE152925 AA078302
	455102	1253524_1	BE005496 BE005494 AW856324 AW900199
5	455864	1377038_1	BE148970 BE148975 BE148957 BE148937
	455986	1397521_1	BE177736 BE177735 BE177734
	456423	187241_1	AW748920 AA487506 AA248914 AA780494
	457426	336189_1	AW971119 AA574265 AA513268
	457484	342113_1	H57645 T19302 AA527038 Z24851 H93171
10	457705	389383_1	AW974668 AA661959 AA649572 AA640401 AA640402
	459259	966269_1	AJ003294 AJ003315 AJ003293

TABLE 13C:

Pkey: Unique number corresponding to an Eos probe set

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495

Strand: Indicates DNA strand from which exons were predicted

NL_position: Indicates nucleotide positions of predicted exons

20	Pkey	Ref	Strand	NL_position
	400640	8117686	Plus	144324-144429
	400666	8118496	Plus	17982-18115,20297-20456
	400776	8131651	Plus	103576-103720
	400812	8568711	Plus	71708-72153
25	400881	2842777	Minus	91446-91603,92123-92265
	400882	2842777	Minus	110431-110709
	400965	7770576	Minus	173043-173564
	401010	8117391	Minus	83967-84180
	401020	8117458	Minus	59085-60227
30	401025	8117518	Minus	179287-179483,181044-181166,181844-182039
	401047	6705887	Minus	4804-5035,5133-5314
	401131	8699812	Minus	94802-94987,95804-95987,96323-96487,97596-97826
	401192	9719502	Minus	69559-70101
	401220	9929324	Minus	48079-48279
35	401383	6721135	Minus	155543-157381
	401405	7768126	Minus	69276-69452,69548-69958
	401519	6649315	Plus	157315-157950
	401532	7798785	Plus	124414-124950,125050-125418
	401610	7705041	Minus	18921-19505
40	401714	6715702	Plus	96484-96681
	401735	3252819	Plus	217235-217356,217621-217873
	401799	7331447	Plus	147802-148251
	401817	7417850	Minus	45888-46535
	401835	7139700	Plus	142257-142742
45	401879	8099914	Minus	101064-102827
	401888	8516069	Minus	189498-190514
	401897	8569218	Plus	604-767
	402066	6649269	Plus	135543-136031
	402077	8117414	Plus	65014-65195
50	402104	8119072	Plus	122409-122600
	402238	7690126	Plus	24726-24880,26791-27021
	402287	4559317	Plus	40811-42447
	402389	9885999	Minus	771-972,1571-1683
	402408	9796239	Minus	110326-110491
55	402423	9796344	Minus	62487-62664
	402424	9796344	Minus	64925-65073
	402486	9797769	Minus	8615-9103
	402520	7596899	Minus	171761-171996
	402679	8113438	Plus	132079-132216
60	402840	9369121	Minus	57118-57306
	402883	9926562	Plus	38666-38803,38885-39019,39097-39231,39308-39445
	402885	9926751	Plus	71919-72049
	402926	8217647	Minus	41261-41443
	402927	8217647	Minus	47247-47396
	402943	6456831	Plus	38467-39068
65	402944	9368423	Plus	110411-110716,111173-111640
	402947	9368458	Minus	101629-101991
	402965	9581599	Minus	46865-46941,47032-47148
	403022	3132351	Plus	92097-92864
70	403121	9180223	Plus	4059-4258
	403165	9838098	Minus	90595-91848
	403295	8096528	Plus	22386-22708
	403381	9438267	Minus	26009-26178
	403383	9438267	Minus	119837-121197
	403398	6862689	Minus	13685-14699
75	403399	6684178	Plus	61841-62145,62367-62756
	403482	9966050	Plus	196964-197135
	403485	9966528	Plus	2888-3001,3198-3532,3655-4117
	403649	8705159	Minus	27141-27247
80	403910	7710710	Minus	5761-6188
	403912	7710730	Minus	72000-72290,72431-72700,72929-73199
	403914	7417588	Minus	7431-8472
	404182	4775644	Plus	18163-18444
	404502	7229863	Minus	56277-56819
	404567	7249169	Minus	101320-101501

	404678	9797204	Plus	115196-115448
	404743	8894169	Minus	120556-120999
	404780	9887810	Minus	175708-175871
5	404790	7230958	Plus	38611-38761
	404931	7342203	Plus	44226-44382
	404944	6899705	Plus	4256-4581
	405024	7107727	Plus	88500-88697
	405089	8072523	Plus	103182-103973
10	405094	8072579	Plus	135587-135758
	405108	7107890	Minus	135020-135472
	405145	9438278	Plus	37883-38052,38138-38332
	405192	7230070	Plus	115629-116071
	405224	6731245	Minus	14413-15979
15	405295	3818412	Plus	56933-57099
	405353	2811095	Plus	118525-118892
	405358	2341017	Minus	18016-18315
	405421	7243869	Minus	97411-97687
	405428	7243900	Minus	37640-37817
20	405452	7656638	Minus	93876-94275
	405484	5922025	Plus	199214-199579,199672-199920,200262-200495
	405552	1552506	Plus	45199-45647
	405570	2808656	Plus	98208-98331
	405626	4508116	Minus	89275-89384,92450-92629,97091-97279,98546-98666
25	405699	4165331	Plus	100727-100859
	405762	5931935	Plus	160502-161110
	405802	5924004	Minus	27743-28264
	405804	7274891	Minus	122557-123551
	406329	6982072	Minus	607903-608271
30	406429	9256476	Minus	83206-83365,94051-94193
	406502	7711350	Minus	63430-63602

Table 14A lists about 695 genes up-regulated in ovarian cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 4.0. The "average" ovarian cancer level was set to the 90th percentile amongst various ovarian cancers. The "average" normal adult tissue level was set to the 90th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 14A: ABOUT 695 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES

Key: Primekey

Ex. Accn: Exemplar Accession

UG ID: UniGene ID

Title: UniGene title

ratio: ratio of tumor vs. normal tissues

	Pkey	Ex. Accn	UG ID	Title	ratio
	452838	U85011	Hs.30743	Preferentially expressed antigen in melanoma	70.4
	438817	AI023799	Hs.163242	ESTs	62.8
	432938	T27013	Hs.3132	steroidogenic acute regulatory protein	57.8
50	421478	AI683243	Hs.97258	ESTs	45.7
	415989	AI267700	Hs.111128	ESTs	42.7
	418179	X51630	Hs.1145	Wilms tumor 1	36.0
	449034	AI624049		gbt541a09.x1 NCL CGAP_U11 Homo sapiens cDNA clone	34.0
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	30.5
55	428153	AW513143	Hs.98367	hypothetical protein FLJ22252 similar to SRY-box c	30.1
	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular matrix protei	29.4
	427585	D31152	Hs.179729	collagen; type X; alpha 1 (Schmid metaphyseal chon	27.0
	435094	AI560129	Hs.277523	EST	26.2
	430691	C14187	Hs.103538	ESTs	26.2
60	430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDNA clone EU	26.1
	415511	AI732617	Hs.182362	ESTs	24.8
	448243	AW369771	Hs.77496	ESTs	24.7
	428187	AI687303	Hs.285529	ESTs	23.9
	408081	AW451597	Hs.167409	ESTs	21.9
65	418007	M13509	Hs.83169	Matrix metalloproteinase 1 (interstitial collagenase	20.6
	400292	AA250737	Hs.72472	BMPLR-1b; bone morphogenetic protein receptor; typ	20.6
	422956	BE545072	Hs.122579	ESTs	20.0
	413335	AI613318	Hs.48442	ESTs	19.9
	423739	AA398155	Hs.97600	ESTs	18.9
70	410929	H47233	Hs.30643	ESTs	18.5
	424086	AI351010	Hs.102267	lysyl oxidase	17.7
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related kinase 2	17.4
	427356	AW023482	Hs.97849	ESTs	17.4
	407168	R45175		gbryg40f01.s1 Soares infant brain 1N1B Homo sapien	17.1
75	407638	AJ404672	Hs.288693	EST	17.1
	427469	AA403084	Hs.269347	ESTs	17.0
	438993	AA828995		integrin; beta 8	16.7
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	16.5
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDNA clone EU	16.5
80	421155	H87879	Hs.102267	lysyl oxidase	16.1
	426635	BE395109	Hs.129327	ESTs	15.9
	431989	AW972870	Hs.291069	ESTs	15.9
	422805	AA436989	Hs.121017	H2A histone family; member A	15.9
	444783	AK001468	Hs.62180	ESTs	15.8

	424581	M62062	Hs.150917	catenin (cadherin-associated protein), alpha 2	15.7
	453197	AF916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMIL	15.7
	459325	AW088369	Hs.282184	ESTs	15.6
5	428976	AL037824	Hs.194695	ras homolog gene family, member 1	15.1
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolog)-II	15.0
	408660	AA525775	Hs.292523	ESTs	15.0
	410247	AF181721	Hs.61345	RU2S	15.0
	418738	AW388633	Hs.6682	solute carrier family 7, member 11	15.0
10	459583	AI907673		gb:IL-BT152-080399-004 BT152 Homo sapiens cDNA, mR	14.8
	413623	AA825721	Hs.246973	ESTs	14.8
	439706	AW872527	Hs.59761	ESTs	14.7
	409041	AB033025	Hs.50081	KIAA1199 protein	14.6
	451110	AI955040	Hs.301584	ESTs	14.5
	436775	AA731111	Hs.291891	ESTs	14.3
15	443211	AI128388	Hs.143655	ESTs	14.3
	445258	AI635931	Hs.147613	ESTs	14.2
	447350	AI375572	Hs.172634	ESTs; HER4 (c-erb-B4)	14.2
	428227	AA321649	Hs.2248	INTERFERON-GAMMA INDUCED PROTEIN PRECURS	14.1
20	453392	U23752	Hs.32984	SRY (sex determining region Y)-box 11	13.9
	447033	AI357412	Hs.157601	EST - not in UniGene	13.7
	423811	AW299598	Hs.50895	homeo box C4	13.7
	452481	N78223	Hs.108106	transcription factor	13.7
	451106	BE382701	Hs.25960	N-myc	13.6
25	416208	AW291168	Hs.41295	ESTs	13.5
	452249	BE394412	Hs.61252	ESTs	13.4
	452055	AI377431	Hs.293772	ESTs	13.2
	439243	AA593254	Hs.191349	ESTs	13.1
	420149	AA255920	Hs.88085	ESTs	12.9
30	429125	AA446854	Hs.271004	ESTs	12.9
	413597	AW302885	Hs.117183	ESTs	12.8
	416566	NM_003914	Hs.79378	cyclin A1	12.8
	442438	AA959598		gb:os26b003.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clon	12.7
	407710	AW022727	Hs.23616	ESTs	12.6
35	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	12.6
	428392	H10233	Hs.2265	secretory granule, neuroendocrine protein 1 (7B2 p	12.4
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	12.3
	447700	AA420183	Hs.171077	ESTs, Weakly similar to similar to serine/threonin	12.2
	458027	L49054	Hs.85195	ESTs, Highly similar to (3:5)(q25.1;p34) fusion g	12.2
40	408460	AA054726	Hs.285574	ESTs	12.2
	424735	U31875	Hs.152677	short-chain alcohol dehydrogenase family member	12.0
	415263	AA948033	Hs.130853	ESTs	11.9
	400298	AA032278	Hs.61635	STEAP1	11.8
	452096	BE394901	Hs.226785	ESTs	11.7
45	421451	AA291377	Hs.50831	ESTs	11.6
	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-related pro	11.6
	443715	AI583187	Hs.9700	cyclin E1	11.5
	402606	#(NOCAT)			11.5
	436954	AA740151	Hs.130425	ESTs	11.5
50	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affinity gluta	11.5
	410102	AW248508	Hs.279727	ESTs;	11.4
	408562	AA436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein, partial cd	11.4
	452030	AL137578	Hs.27607	Homo sapiens mRNA; cDNA DKFZp564N2464 (from clon	11.4
	442353	BE379594	Hs.49136	ESTs	11.3
55	427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3A	11.2
	453160	AI263307	Hs.146228	ESTs	11.2
	426427	M86699	Hs.169840	TTK protein kinase	11.1
	449433	AI672096	Hs.9012	ESTs	11.1
	412723	AA648459	Hs.179912	ESTs	11.1
60	400250			0	11.1
	419752	AA249573	Hs.152618	ESTs	11.1
	438167	R28363	Hs.24286	ESTs	11.1
	434539	AW748078	Hs.214410	ESTs	10.9
	429918	AW873986	Hs.119383	ESTs	10.8
65	450375	AA009547	Hs.8850	a disintegrin and metalloproteinase domain 12 (mel	10.8
	400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin 2)	10.8
	420900	AL045633	Hs.44269	ESTs	10.8
	428758	AA433988	Hs.98502	Homo sapiens cDNA FLJ14303 fs, clone PLACE2000132	10.7
	446142	AI754693	Hs.145968	ESTs	10.7
70	421285	NM_000102	Hs.1363	cytochrome P450, subfamily XVII (steroid 17-alpha-	10.6
	433496	AF064254	Hs.49765	VERY-LONG-CHAIN ACYL-COA SYNTHETASE	10.6
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	10.5
	433447	U29195	Hs.3281	neuronal pentraxin II	10.4
	424188	AW954552	Hs.142634	zinc finger protein	10.4
75	414245	BE148072	Hs.75850	WAS protein family, member 1	10.3
	426462	U59111	Hs.169993	dermatan sulphate proteoglycan 3	10.3
	418601	AA279490	Hs.86368	calmeglin	10.3
	444170	AW613879	Hs.102408	ESTs	10.3
80	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate polypeptide	10.3
	407378	AA299264		gb:EST11752 Ularus Homo sapiens cDNA 5' end simila	10.2
	440901	AA909358	Hs.128612	ESTs	10.2
	407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequence.	10.2
	415227	AW821113	Hs.72402	ESTs	10.2
	409269	AA576953	Hs.22972	Homo sapiens cDNA FLJ13352 fs, clone OVARC1002165	10.1
	450480	X82125	Hs.25040	zinc finger protein 239	10.1

	418088	AI538323	Hs.77496	ESTs	10.0
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1 (yeast hom	9.9
	428253	AL133640	Hs.183357	Homo sapiens mRNA; cDNA DKFZp586C1021 (from clone	9.8
5	426471	M22440	Hs.170009	transforming growth factor, alpha	9.8
	407881	AW072003	Hs.40868	heparan sulfate (glucosamine) 3-O-sulfotransferase	9.7
	452291	AF015592	Hs.28853	CDK7 (cell division cycle 7, S. cerevisiae, homolog	9.7
	445537	AJ245571	Hs.12844	EGF-like domain; multiple 6	9.7
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequence	9.6
10	423992	AW898292	Hs.137206	Homo sapiens mRNA; cDNA DKFZp564H1663 (from clone	9.6
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rakinesin6)	9.6
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphorylation regu	9.6
	438209	AL120659	Hs.6111	KIAA0307 gene product	9.5
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain-binding p	9.5
	424945	AI221919	Hs.173438	hypothetical protein FLJ10582	9.5
15	414972	BE263782	Hs.77695	KIAA0008 gene product	9.4
	439262	AA832333	Hs.124399	ESTs	9.4
	403381	#(NOCAT)		0	9.3
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP2003117	9.3
20	435509	AI458879	Hs.181915	ESTs	9.3
	445413	AA151342	Hs.12677	CGI-147 protein	9.2
	414083	AL121282	Hs.257786	ESTs	9.2
	421373	AA808229	Hs.167771	ESTs	9.2
	430510	AW162916	Hs.241576	hypothetical protein PRO2577	9.1
25	446999	AA151520	Hs.278525	hypothetical protein PRO2605	9.1
	459587	AA031956		gb:z15e04.s1 Soares_pregnanL_uterus_NbHPU Homo sa	9.1
	414569	AF109298	Hs.118258	Prostate cancer associated protein 1	9.1
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	9.0
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to M	9.0
30	408908	BE296227	Hs.48915	serine/threonine kinase 15	9.0
	431548	AI834273	Hs.9711	Homo sapiens cDNA FLJ13018 fis, clone NT2RP3000685	9.0
	433764	AW753676	Hs.39982	ESTs	9.0
	434636	AA083764	Hs.241334	ESTs	8.9
	451807	W52854	Hs.27099	DKFZP564J0863 protein	8.8
35	437872	AK002015	Hs.5887	RNA binding motif protein 7	8.8
	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	8.8
	420092	AA814043	Hs.88045	ESTs	8.8
	420159	AI572490	Hs.99785	ESTs	8.8
	447184	AF026941	Hs.17518	Homo sapiens c1g5 mRNA, partial sequence	8.8
40	451254	AI571016	Hs.172967	ESTs	8.8
	432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-a	8.7
	450434	AA166950	Hs.18645	ESTs, Weakly similar to partial CDS [C.elegans]	8.7
	400301	X03635	Hs.1657	Estrogen receptor 1	8.7
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfotransferase	8.7
45	434891	AA814309	Hs.123583	ESTs	8.7
	436812	AW298067		gb:U1-H-BWO-ajp-g-09-0-ULs1 NCI_CGAP_Sub6 Homo s	8.7
	438885	AI886558	Hs.184987	ESTs	8.7
	449765	N92293	Hs.206832	EST, Moderately similar to ALU8_HUMAN ALU SUBFAM	8.7
	447342	AI199268	Hs.19322	ESTs; Weakly similar to IIII ALU SUBFAMILY J WARNI	8.6
50	434424	AI811202	Hs.125365	Homo sapiens cDNA: FLJ23523 fis, clone LNG05548	8.6
	438078	AI016377	Hs.131693	ESTs	8.6
	437212	AI765021	Hs.210775	ESTs	8.5
	417728	AW138437	Hs.24790	KIAA1573 protein	8.5
	438081	H49548	Hs.298964	ESTs	8.5
55	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	8.4
	435663	AI023707	Hs.134273	ESTs	8.4
	424717	H03754	Hs.152213	wingless-type MMTV integration site family, member	8.4
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxygenase COOH	8.4
	450505	NM_004572	Hs.25051	plakophilin 2	8.4
60	436211	AK001581	Hs.80961	polymerase (DNA directed), gamma	8.3
	436396	AI683487	Hs.299112	Homo sapiens cDNA FLJ11441 fis, clone HEMBA1001323	8.3
	425695	NM_005401	Hs.159238	protein tyrosine phosphatase, non-receptor type 14	8.3
	438180	AA808189	Hs.272151	ESTs	8.2
	447268	AI370413	Hs.36563	Homo sapiens cDNA: FLJ22418 fis, clone HRC08590	8.2
65	433159	AB035898	Hs.150587	kinesin-like protein 2	8.1
	400195			0	8.1
	424908	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3' untransla	8.1
	438202	AW169287	Hs.22588	ESTs	8.1
	438915	AA280174	Hs.23282	ESTs	8.1
70	448776	BE302464	Hs.30057	transporter similar to yeast MRS2	8.1
	453884	AA355925	Hs.36232	KIAA0186 gene product	8.0
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone receptor; t	8.0
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDNA clone EU	8.0
	453102	NM_007197	Hs.31664	fizzled (Drosophila) homolog 10	8.0
75	424001	W67883	Hs.137476	KIAA1051 protein	8.0
	434415	BE177494		gb:RC6-HT0596-270300-011-C05 HT0596 Homo sapiens c	8.0
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransferase, phosph	7.9
	438956	AW978074		gb:EST391184 MAGE resequences, MAGP Homo sapiens c	7.9
	415245	N59650	Hs.27252	ESTs	7.9
80	422352	AA766296	Hs.99200	ESTs	7.9
	425492	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	7.8
	442655	AW027457	Hs.30323	ESTs	7.8
	445657	AW612141	Hs.279575	ESTs	7.8
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	7.8
	426320	W47595	Hs.169300	transforming growth factor, beta 2	7.8

	414142	AW368397	Hs.150042	ESTs	7.7
	412170	D16532	Hs.73729	very low density lipoprotein receptor	7.6
	410011	AB020641	Hs.57856	PFTAIKE protein kinase 1	7.6
5	436476	AA326108	Hs.53631	ESTs	7.6
	414132	AI801235	Hs.48480	ESTs	7.6
	437789	AI581344	Hs.127812	ESTs, Weakly similar to AF141326 1 RNA helicase HD	7.6
	450192	AA263143	Hs.24596	RAD51-interacting protein	7.6
	449328	AI962493	Hs.197647	ESTs	7.5
10	440238	AW451870	Hs.155644	paired box gene 2	7.5
	403657	#(NOCAT)		0	7.5
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	7.5
	418735	N48769	Hs.44609	ESTs	7.5
	413627	BE182082	Hs.246973	ESTs	7.4
	446293	AI420213	Hs.149722	ESTs	7.4
15	441627	AA947552	Hs.58086	ESTs	7.4
	425465	L18964	Hs.1904	protein kinase C; iota	7.3
	409242	AL080170	Hs.51692	DNFZP434C091 protein	7.3
	450262	AW409872	Hs.271166	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFA	7.3
20	440250	AA876179	Hs.134650	ESTs	7.3
	451659	BE379761	Hs.14248	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMIL	7.3
	458861	AI530223		gb:ad06g08.r1 Proliferating Erythroid Cells (LCB-a	7.3
	436032	AA150797	Hs.109276	latadin protein	7.2
	407771	AL138272	Hs.62713	ESTs	7.2
25	435039	AW043921	Hs.130526	ESTs	7.2
	444342	NM_014338	Hs.10887	similar to lysosome-associated membrane glycoprote	7.2
	407829	AA045084	Hs.29725	Homo sapiens cDNA FLJ13197 fis, clone NT2RP3004451	7.2
	409731	AA125985	Hs.56145	thymosin, beta, Identified in neuroblastoma cells	7.2
	404253	#(NOCAT)		0	7.1
30	424120	T80579	Hs.290270	ESTs	7.1
	429126	AW172356	Hs.95083	ESTs	7.1
	413573	AI733859	Hs.149089	ESTs	7.1
	421464	AA291553	Hs.180088	ESTs	7.0
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 20kD	7.0
35	437938	AI960087		ESTs, Weakly similar to Gag-Pol polyprotein [M.mus	7.0
	420362	U79734	Hs.97206	huntingtin interacting protein 1	7.0
	444743	AA045548	Hs.11817	nudix (nucleoside diphosphate linked moiety X)-typ	7.0
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 TFPI2	6.9
	410568	AW162948	Hs.64542	pre-mRNA cleavage factor Im (68kD)	6.9
40	429418	AI381026	Hs.99283	ESTs	6.9
	409178	BE393948	Hs.50915	kallikrein 5	6.9
	446608	N75217	Hs.257846	ESTs	6.9
	425905	AB032959	Hs.161700	KIAA1133 protein	6.9
	428532	AF157326	Hs.184786	TBP-interacting protein	6.9
45	433426	H69125	Hs.133525	ESTs	6.9
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo sapiens	6.8
	437960	AI669586	Hs.222194	ESTs	6.8
	423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR motif, Y is	6.8
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40kD)	6.8
50	448674	W31178	Hs.154140	ESTs	6.8
	438122	AI620270	Hs.129837	ESTs	6.8
	440048	AA897461	Hs.158469	ESTs, Weakly similar to envelope protein [H.sapien	6.7
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (melanoma, p1	6.7
	407162	N63855	Hs.142634	zinc finger protein	6.7
55	410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar ataxia 3,	6.7
	424639	AI917494	Hs.131329	ESTs	6.7
	432415	T16971	Hs.289014	ESTs	6.7
	421470	R27496	Hs.1378	annexin A3	6.7
	445459	AI478629	Hs.158465	ESTs	6.7
60	418203	X54942	Hs.83758	CDC28 protein Kinase 2	6.6
	432809	AA565509	Hs.131703	ESTs	6.6
	409234	AI879419	Hs.27206	ESTs	6.6
	438394	BE379623	Hs.27693	CGI-124 protein	6.6
	452097	AB002364	Hs.27916	ADAM-TS3; a disintegrin-like and metalloproteas	6.6
65	453745	AA952989	Hs.63908	Homo sapiens HSPC316 mRNA, partial cds	6.6
	414136	AA812434	Hs.178227	ESTs	6.6
	423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	6.6
	454018	AW016892	Hs.241652	ESTs	6.6
	452281	T93500	Hs.28792	ESTs	6.5
70	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic; stratum corneum)	6.5
	452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transporter), me	6.5
	434149	Z43829	Hs.19574	ESTs, Weakly similar to katanin p80 subunit [H.sap	6.5
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	6.4
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	6.4
75	409517	X90780	Hs.54668	tropoin I, cardiac	6.4
	432666	AW204069	Hs.129250	ESTs, Weakly similar to unnamed protein product [H	6.4
	448706	AW291095	Hs.21814	class II cytokine receptor ZCYTOR7	6.4
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDN	6.4
	413582	AW295647	Hs.71331	Homo sapiens cDNA: FLJ21971 fis, clone HEP05790	6.4
80	419917	AA320068	Hs.93701	Homo sapiens mRNA; cDNA DKFZp434E232 (from clone	6.4
	424153	AA451737	Hs.141496	MAGE-like 2	6.4
	434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone LNG07061	6.4
	435082	AA664273	Hs.186104	Homo sapiens cDNA FLJ13803 fis, clone THYR01000187	6.4
	441081	AI584019	Hs.169006	ESTs, Moderately similar to plakophilin 2b [H.sapi	6.4
	443539	AI076182	Hs.134074	ESTs	6.4

	443830	AI142095	Hs.143273	ESTs	6.4
	452606	N45202	Hs.90012	Homo sapiens cDNA: FLJ23441 fis, clone HSI00612	6.4
	418384	AW149266	Hs.25130	ESTs	6.3
5	425371	D49441	Hs.155981	mesothelin	6.3
	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member), prostate	6.3
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induced gene	6.3
	437117	ALD49256	Hs.122593	ESTs	6.3
	449579	AW207260	Hs.134014	prostate cancer associated protein 6	6.3
10	453370	AI470523	Hs.182356	ESTs, Moderately similar to translation initiation	6.3
	426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteogenic protein 1	6.3
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	6.3
	408155	AB014528	Hs.43133	KIAA0628 gene product	6.2
	452904	AL157581	Hs.30957	Homo sapiens mRNA; cDNA DKFZp434E0626 (from clone	6.2
	439138	AI742605	Hs.193696	ESTs	6.2
15	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	6.2
	436281	AW411194	Hs.120051	ESTs	6.1
	407385	AA610150	Hs.272072	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFA	6.1
	406815	AA833930	Hs.288036	RNA isopentenylpyrophosphate transferase	6.1
20	430437	AI768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PLACE1008369	6.1
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (from clone	6.1
	415139	AW975942	Hs.48524	ESTs	6.1
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family A, member	6.1
	433527	AW235613	Hs.133020	ESTs	6.1
	449448	D60730	Hs.57471	ESTs	6.1
25	457733	AW974812	Hs.291971	ESTs	6.1
	457979	AA776655	Hs.270942	ESTs	6.1
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein	6.0
	423554	M90518	Hs.1674	glutamine-fructose-6-phosphate transaminase 1	6.0
30	421502	AF111858	Hs.105039	solute carrier family 34 (sodium phosphate), membe	6.0
	412733	AA984472	Hs.74554	KIAA0080 protein	6.0
	422095	AI868872	Hs.288968	ceruloplasmin (ferroxidase)	6.0
	449347	AV649748	Hs.295901	ESTs	6.0
	440870	AI687284	Hs.150539	Homo sapiens cDNA FLJ13793 fis, clone THYRO1000085	6.0
35	437478	AL390172	Hs.118811	ESTs	6.0
	411598	BE336654	Hs.70937	H3 histone family, member K	6.0
	418134	AA397769	Hs.86617	ESTs	6.0
	418845	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alpha)	6.0
	452039	AI922988	Hs.172510	ESTs	6.0
40	410555	U92649	Hs.64311	a disintegrin and metalloproteinase domain 17 (tum	5.9
	412719	AW016610	Hs.129911	ESTs	5.9
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PLACE1009150	5.9
	437099	N77793	Hs.48659	ESTs, Highly similar to LMA1_HUMAN LAMININ ALPH	5.9
	453431	AF094754	Hs.32973	glycine receptor, beta	5.9
45	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane protein 2	5.9
	417866	AW067903	Hs.82772	"collagen, type XI, alpha 1"	5.9
	420440	NM_002407	Hs.97644	mammaglobin 2	5.9
	430291	AV660345	Hs.238126	CGI-49 protein	5.9
	405547	#(NOCAT)		0	5.9
50	427510	Z47542	Hs.179312	small nuclear RNA activating complex, polypeptide	5.9
	435793	AB037734	Hs.4993	ESTs	5.8
	427975	AI536065	Hs.122460	ESTs	5.8
	428949	AA442153	Hs.104744	ESTs, Weakly similar to AF208855 1 BM-013 [H.sapie	5.8
	452693	T79153	Hs.48589	zinc finger protein 228	5.8
55	440138	AB033023	Hs.6982	hypothetical protein FLJ10201	5.8
	421246	AW582962	Hs.300961	ESTs, Highly similar to AF151805 1 CGI-47 protein	5.8
	445424	AB028945	Hs.12696	contactin SH3 domain-binding protein	5.8
	448186	AA262105	Hs.4094	Homo sapiens cDNA FLJ14208 fis, clone NT2RP3003264	5.8
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	5.7
60	419335	AW950146	Hs.284137	Homo sapiens cDNA FLJ12888 fis, clone NT2RP2004081	5.7
	420637	AW976153		gb:EST388262 MAGE resequences, MAGN Homo sapiens	5.7
	431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AOKA01954	5.7
	446868	AV660737	Hs.135100	ESTs	5.7
	452971	AI873878	Hs.91789	ESTs	5.7
65	428927	AA441837	Hs.90250	ESTs	5.7
	425282	AW163518	Hs.155485	huntingtin interacting protein 2	5.7
	419247	S65791	Hs.89764	fragile X mental retardation 1	5.7
	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapiens]	5.7
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	5.6
70	447078	AW885727	Hs.301570	ESTs	5.6
	421247	BE391727	Hs.102910	general transcription factor IIF, polypeptide 4 [5	5.6
	407896	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophila homolog	5.6
	436558	AI364997	Hs.7572	ESTs	5.6
	417830	AW504786	Hs.132808	epithelial cell transforming sequence 2 oncogene	5.6
75	429826	N93266	Hs.40747	ESTs	5.6
	432030	AI908400	Hs.143789	ESTs	5.6
	443270	NM_004272	Hs.9192	Homer, neuronal immediate early gene, 1B	5.5
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMIL	5.5
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	5.5
80	419558	AW953679	Hs.278394	ESTs	5.5
	427388	AW836261	Hs.177486	amyloid beta (A4) precursor protein (protease nex	5.5
	427961	AW293165	Hs.143134	ESTs	5.5
	404561	#(NOCAT)		0	5.5
	429582	NM_006308	Hs.211602	SMC1 (structural maintenance of chromosomes 1, yea	5.5
	407216	N91773	Hs.102267	lysyl oxidase	5.5

	410658	AW105231	Hs.192035	ESTs	5.5
	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	5.5
	414315	Z24878		gb:HSB65D052 STRATAGENE Human skeletal muscle cD	5.5
5	427878	C05766	Hs.181022	CGI-07 protein	5.5
	431041	AA490967	Hs.105276	ESTs	5.5
	441645	AJ222279	Hs.201555	ESTs	5.5
	428071	AF212848	Hs.182339	transcription factor ESE-38	5.4
	436406	AW105723	Hs.125346	ESTs	5.4
10	429181	AW979104	Hs.294009	ESTs	5.4
	410909	AW898161	Hs.53112	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMIL	5.4
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT2RP2000814	5.4
	451996	AW514021	Hs.245510	ESTs	5.4
	448318	AW236021	Hs.108788	ESTs, Weakly similar to zesta [D.melanogaster]	5.4
15	441433	AA933809	Hs.42746	ESTs	5.4
	445495	BE622641	Hs.38489	ESTs	5.4
	410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone NT2RM4002571	5.4
	442611	BE077155	Hs.177537	ESTs	5.4
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced protein 6	5.4
20	453161	AA626608	Hs.61656	ESTs	5.4
	419948	AB041035	Hs.93847	NADPH oxidase 4	5.3
	427718	AJ798680	Hs.25933	ESTs	5.3
	453867	AJ929383	Hs.108196	HSPC037 protein	5.3
	422634	NM_016010	Hs.118821	CGI-62 protein	5.3
25	444478	W07318	Hs.240	M-phase phosphoprotein 1	5.3
	428002	AA418703		gb:zv98cd3.s1 Soares_NhHMPu_S1 Homo sapiens cDNA c	5.3
	443486	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)	5.3
	451177	AJ969716	Hs.13034	ESTs	5.3
	408298	AJ745325	Hs.271923	ESTs; Moderately similar to IIII ALU SUBFAMILY SB2	5.3
30	435867	AA954229	Hs.114052	ESTs	5.3
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	5.3
	448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P1124 (from clone	5.3
	427660	AJ741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone CAE06654	5.3
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	5.3
35	433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMAN ALU SUBFA	5.3
	449532	W74653	Hs.271593	ESTs	5.3
	452822	X85689	Hs.288617	Homo sapiens cDNA: FLJ22621 fis, clone HSI05658	5.3
	437641	AA811452	Hs.291911	ESTs	5.2
40	418379	AA218940	Hs.137516	fiddletin-like 1	5.2
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	5.2
	433589	AA886530	Hs.188912	ESTs	5.2
	409143	AW025980	Hs.138965	ESTs	5.2
	410303	AA324597	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT2RP2004321	5.2
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	5.2
45	424698	AA164366	Hs.151973	hypothetical protein FLJ10378	5.2
	431229	AA496479		gb:zv37h05.r1 Soares ovary tumor NbHOT Homo sapien	5.2
	433377	AJ752713	Hs.43845	ESTs	5.2
	445236	AK001676	Hs.12457	hypothetical protein FLJ10814	5.2
	406367	#(NOCAT)		0	5.2
50	442500	AJ819068	Hs.209122	ESTs	5.2
	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	5.2
	419140	AJ982647	Hs.215725	ESTs	5.2
	411078	AJ222020	Hs.182364	ESTs, Weakly similar to 25 kDa trypsin inhibitor [5.2
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	5.2
55	427061	AB032971	Hs.173392	KIAA1145 protein	5.2
	439042	AW979172		gb:EST391282 MAGE resequences, MAGP Homo sapiens c	5.2
	452930	AW195285	Hs.194097	ESTs	5.2
	417791	AW965339	Hs.111471	ESTs	5.1
	433277	W27266	Hs.151010	ESTs	5.1
60	447835	AW591623	Hs.164129	ESTs	5.1
	434401	AJ864131	Hs.71119	Putative prostate cancer tumor suppressor	5.1
	437496	AA452378	Hs.170144	Homo sapiens mRNA; cDNA DKFZp547J125 (from clone D	5.1
	418849	AW474547	Hs.53565	ESTs, Weakly similar to B0491.1 [C.elegans]	5.1
	428093	AW594506	Hs.104830	ESTs	5.1
65	408621	AJ970672	Hs.46538	chromosome 11 open reading frame 8; fetal brain (5.1
	453096	AW294631	Hs.11325	ESTs	5.1
	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	5.1
	436787	AA908554	Hs.192756	ESTs	5.1
	446577	AB040933	Hs.15420	KIAA1500 protein	5.1
70	437267	AW511443	Hs.258110	ESTs	5.0
	419423	D26488	Hs.90315	KIAA0007 protein	5.0
	404939			0	5.0
	439052	AF085917	Hs.37921	ESTs	5.0
	447020	T27308	Hs.16986	hypothetical protein FLJ11046	5.0
75	453878	AW964440	Hs.19025	ESTs	5.0
	410824	AW994813	Hs.33264	ESTs	5.0
	427701	AA411101	Hs.221750	ESTs	5.0
	424602	AK002055	Hs.301129	Homo sapiens clone 23859 mRNA sequence	5.0
	430044	AA464510	Hs.152812	EST cluster (not in UniGene)	5.0
80	417423	AA197341	Hs.111164	ESTs	5.0
	421477	AJ904743	Hs.104650	hypothetical protein FLJ10292	5.0
	433384	AJ021992	Hs.124244	ESTs	5.0
	434160	BE551196	Hs.114275	ESTs	5.0
	443555	N71710	Hs.21398	ESTs, Moderately similar to GNPI_HUMAN GLUCOSAM	5.0
	416198	H27332	Hs.99598	ESTs	4.9

	424539	L02911	Hs.150402	activin A receptor, type I	4.9
	436645	AW023424	Hs.156520	ESTs	4.9
	417251	AW015242	Hs.99488	ESTs; Weakly similar to ORF YKR074w [S.cerevisiae]	4.9
5	447207	AA442233	Hs.17731	hypothetical protein FLJ12892	4.9
	416565	AW000960	Hs.44970	ESTs	4.9
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	4.9
	435420	AJ928513	Hs.59203	ESTs	4.9
	435532	AW291488	Hs.117305	ESTs	4.9
10	443268	AJ800271	Hs.129445	hypothetical protein FLJ12496	4.9
	446140	AA356170	Hs.26750	Homo sapiens cDNA: FLJ21908 fis, clone HEP03830	4.9
	452891	N75582	Hs.212875	ESTs; Weakly similar to KIAA0357 [H.sapiens]	4.9
	431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic protein type; fou	4.9
	408938	AA059013	Hs.22607	ESTs	4.9
	432842	AW674093	Hs.279525	hypothetical protein PRO2605	4.9
15	436754	AJ061288	Hs.133437	ESTs; Moderately similar to gonadotropin inducible	4.9
	442573	H93366	Hs.7567	Branched chain aminotransferase 1, cytosolic, U215	4.9
	409049	AA423132	Hs.146343	ESTs	4.9
	422475	AL359938	Hs.117313	Meis (mouse) homolog 3	4.9
	447112	H17800	Hs.7154	ESTs	4.9
20	458627	AW088642	Hs.97984	ESTs; Weakly similar to WASP-family protein [H.sap	4.8
	431689	AA305588	Hs.267695	UDP-GalbetaGlcNAc beta 1,3-galactosyltransferase,	4.8
	410530	M25809	Hs.64173	ESTs; Highly similar to VAB1_HUMAN VACUOLAR AT	4.8
	429414	AJ783656	Hs.202095	empty spiracles (Drosophila) homolog 2	4.8
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR/MRP), mem	4.8
25	422505	AL120862	Hs.124165	ESTs; (HSA)PAP protein (programmed cell death 9;	4.8
	425977	R15138	Hs.165570	Homo sapiens clone 25052 mRNA sequence	4.8
	428555	NM_002214	Hs.184908	Integrin, beta 8	4.8
	452909	NM_015368	Hs.30985	parmaxin 1	4.8
	449535	W15267	Hs.23672	low density lipoprotein receptor-related protein 6	4.8
30	452232	AW020603	Hs.271698	ESTs	4.8
	409732	NM_016122	Hs.58148	NY-REN-58 antigen	4.8
	415115	AA214228	Hs.127751	hypothetical protein	4.7
	423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (from clon	4.7
	411085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT2RM4000200	4.7
35	423575	C18863	Hs.163443	ESTs	4.7
	415211	R64730.comp	Hs.155986	ESTs; Highly similar to SPERM SURFACE PROTEIN SP1	4.7
	418804	AA809632		gbnz17h04.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clo	4.7
	428405	Y00762	Hs.2268	cholinergic receptor, nicotinic, alpha polypeptide	4.7
40	432885	AJ753709	Hs.152484	ESTs	4.7
	433330	AW207084	Hs.132816	ESTs	4.7
	453047	AW023798	Hs.286025	ESTs	4.7
	421308	AA687322	Hs.192843	ESTs	4.7
	456273	AF154846	Hs.1148	zinc finger protein	4.7
45	443933	AJ091631	Hs.135501	Homo sapiens two pore potassium channel KT3.3	4.7
	434551	BE387162	Hs.280858	ESTs; Highly similar to XPB_HUMAN DNA-REPAIR PRO	4.7
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	4.7
	426300	U15979	Hs.169228	della-like homolog (Drosophila)	4.7
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37kD)	4.7
50	446102	AW168067	Hs.252956	ESTs	4.7
	420547	AF155140	Hs.98738	gonadotropin-regulated testicular RNA helicase	4.7
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	4.7
	429944	R13949	Hs.228440	Homo sapiens clone 24881 mRNA sequence	4.7
	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HEMBA1004610	4.7
55	434988	AJ418055	Hs.161160	ESTs	4.6
	452571	W31518	Hs.34665	ESTs	4.6
	434381	AF129755	Hs.117772	ESTs	4.6
	406400	#(NOCAT)		0	4.6
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	4.6
60	418945	AW290975	Hs.118923	ESTs	4.6
	428301	AW628668	Hs.98440	ESTs	4.6
	430153	AW968128		gb:EST380338 MAGE resequences, MAGJ Homo sapiens c	4.6
	431349	AA503653	Hs.156942	ESTs; Moderately similar to ALU2_HUMAN ALU SUBFA	4.6
	446254	BE179829	Hs.178852	Homo sapiens cDNA FLJ12832 fis, clone NT2RP2003137	4.6
65	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (from clone	4.6
	448027	AJ458437	Hs.177224	ESTs	4.6
	449611	AJ970394	Hs.197075	ESTs	4.6
	459574	AJ741122	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone NT2RP4000035	4.6
	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	4.6
70	409387	AW384900	Hs.123526	ESTs	4.6
	424078	AB006625	Hs.139033	paternally expressed gene 3	4.6
	435244	N77221	Hs.187824	ESTs	4.6
	404996	#(NOCAT)		0	4.6
	407905	AW103655	Hs.252905	ESTs	4.6
75	411560	AW851186		gb:IL3-CT0220-150200-071-H05 CT0220 Homo sapiens c	4.6
	424341	AA385074		gb:EST98673 Thyroid Homo sapiens cDNA 5' end simil	4.6
	441675	AJ914329	Hs.5461	ESTs	4.6
	452172	H00797	Hs.133207	Homo sapiens mRNA for KIAA1230 protein, partial cd	4.6
	420276	AA290938	Hs.190561	ESTs; Highly similar to mosaic protein LR11 [H.sap	4.5
80	402820	#(NOCAT)		0	4.5
	419699	AA248998	Hs.31246	ESTs	4.5
	422529	AW015128	Hs.256703	ESTs	4.5
	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	4.5
	441826	AW503603	Hs.129915	phosphotriesterase related	4.5
	453931	AL121278	Hs.25144	ESTs	4.5

	435538	AB011540	Hs.4930	low density lipoprotein receptor-related protein 4	4.5
	457465	AW301344	Hs.195969	ESTs	4.5
	418848	AI820961	Hs.193465	ESTs	4.5
5	408321	AW405882	Hs.44205	coristatin	4.5
	447499	AW262580	Hs.147674	KIAA1621 protein	4.5
	424513	BE385864	Hs.149894	mitochondrial translational initiation factor 2	4.5
	432731	R31178	Hs.287820	fibronectin 1	4.5
	448275	BE514434	Hs.20830	synaptic Ras GTPase activating protein 1 (homolog	4.5
10	430371	D87466	Hs.240112	KIAA0276 protein	4.5
	448693	AW004854	Hs.228320	Homo sapiens cDNA: FLJ23537 fis, clone LNG07690	4.5
	407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MAMMA100042	4.4
	448141	AI471598	Hs.197531	ESTs	4.4
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HEMBB1001304	4.4
15	417718	T86540	Hs.193981	ESTs	4.4
	436464	AI016176	Hs.269783	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMIL	4.4
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S. cerevisia	4.4
	409092	AI735283	Hs.172608	ESTs	4.4
	416241	N52639	Hs.32683	ESTs	4.4
20	432005	AA524190	Hs.120777	ESTs, Weakly similar to ELL2_HUMAN RNA POLYMER	4.4
	440234	AW117264	Hs.126252	ESTs	4.4
	448743	AB032962	Hs.21896	KIAA1136 protein	4.4
	451389	N73222	Hs.21738	KIAA1008 protein	4.4
	453331	AI240665	Hs.8895	ESTs	4.4
25	454036	AA374756	Hs.93560	ESTs, Weakly similar to unnamed protein product [H	4.4
	448133	AA723157	Hs.73769	folate receptor 1 (adul)	4.4
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain 9 (melt	4.4
	453279	AW893940	Hs.59698	ESTs	4.4
	409459	D86407	Hs.54481	low density lipoprotein receptor-related protein 8	4.4
30	431708	AI698138	Hs.108873	ESTs	4.4
	433906	AI167816	Hs.43355	ESTs	4.4
	437958	BE139550	Hs.121668	ESTs	4.4
	441423	AI793299	Hs.126877	ESTs	4.4
	429876	AB028977	Hs.225974	KIAA1054 protein	4.3
35	446770	AV660309	Hs.154986	ESTs, Weakly similar to AF137386 1 plasminogen [H	4.3
	412078	X89699	Hs.73149	paired box gene 8	4.3
	422093	AF151852	Hs.111449	CGI-94 protein	4.3
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE; Human selenium	4.3
	448390	AL035414	Hs.21068	hypothetical protein	4.3
40	453628	AW243307	Hs.170187	ESTs	4.3
	449722	BE280074	Hs.23960	cyclin B1	4.3
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein product [H	4.3
	431592	R69016	Hs.293871	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMIL	4.3
	432383	AK000144	Hs.274449	Homo sapiens cDNA FLJ20137 fis, clone COL07137	4.3
45	419926	AW900592	Hs.93798	DKFZP586D2223 protein	4.3
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	4.3
	401644	#(NOCAT)		0	4.3
	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leucine heptad	4.3
	413775	AW409934	Hs.75528	nucleolar GTPase	4.3
50	424296	AI631874	Hs.169391	ESTs	4.3
	431118	BE284901	Hs.250502	carbonic anhydrase VIII	4.3
	432201	AI538613	Hs.135657	TMPSR33a mRNA for serine protease (ECHOS1) (TADG-1	4.3
	451073	AI758905	Hs.206063	ESTs	4.3
	451592	AI805416	Hs.213897	ESTs	4.3
55	452453	AI902519		gb:QV-BT009-101198-051 BT009 Homo sapiens cDNA, m	4.3
	441020	W79283	Hs.35962	ESTs	4.2
	439024	R66966	Hs.35598	ESTs	4.2
	453619	H87648	Hs.33922	H.sapiens novel gene from PAC 117P20, chromosome 1	4.2
	453459	BE047032	Hs.257789	ESTs	4.2
60	408427	AW194270	Hs.177236	ESTs	4.2
	419311	AA689591		gb:mv66a12.s1 NCJ_CGAP_GCB1 Homo sapiens cDNA clo	4.2
	426460	D79721	Hs.183702	Homo sapiens cDNA FLJ11752 fis, clone HEMBA1005582	4.2
	444540	AI693927	Hs.265165	ESTs	4.2
	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	4.2
65	453913	AW004683	Hs.233502	ESTs	4.2
	417847	AI521558	Hs.288312	Homo sapiens cDNA: FLJ22316 fis, clone HRC05262	4.2
	428856	AA436735	Hs.183171	Homo sapiens cDNA: FLJ22002 fis, clone HEP06638	4.2
	428679	AA431765		gb:zw80c03.s1 Soares_testis_NHT Homo sapiens cDNA	4.2
	441006	AW605267	Hs.7627	CGI-60 protein	4.2
70	436209	AW850417	Hs.254020	ESTs, Moderately similar to unnamed protein produc	4.2
	446936	H10207	Hs.47314	ESTs	4.2
	406076	AL390179	Hs.137011	Homo sapiens mRNA: cDNA DKFZp547P134 (from clone	4.2
	428819	AL135623	Hs.193914	KIAA0575 gene product	4.2
	406671	AA129547	Hs.285754	mel proto-oncogene (hepatocyte growth factor recep	4.2
75	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedin C)	4.2
	417048	AI088775	Hs.55498	geranylgeranyl diphosphate synthase 1	4.2
	431750	AA514986	Hs.283705	ESTs	4.2
	439314	AA382413	Hs.178144	ESTs	4.2
	448582	AI538880	Hs.94812	ESTs	4.2
80	449554	AA682382	Hs.59982	ESTs	4.2
	455700	BE068115		gb:CM1-BT0368-061299-060-g07 BT0368 Homo sapiens c	4.2
	409073	AA053458		gb:z71a07.s1 Soares_pineal_gland_N3HPG Homo sapie	4.1
	433929	AI375499	Hs.27379	ESTs	4.1
	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMIL	4.1
	444381	BE387335	Hs.283713	ESTs	4.1

5	451024	AA442176		gbzw63b08.r1 Soares_total_fetus_Nb2HF8_9w Homo sa	4.1
	415539	AI733881	Hs.72472	BMPIR-lb; bone morphogenetic protein receptor; typ	4.1
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, long form	4.1
	420736	AI263022	Hs.82204	ESTs	4.1
	453293	AA382267	Hs.10653	ESTs	4.1
	409564	AA045857	Hs.54943	fracture callus 1 (rat) homolog	4.1
	418378	AW962081		gb:EST374154 MAGE resequences, MAGG Homo sapiens	4.1
	428628	H09604	Hs.13268	ESTs	4.1
10	439635	AA477288	Hs.94891	Homo sapiens cDNA: FLJ22729 fis, clone HSI15685	4.1
	440452	AI925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN CALCYPHOSIN	4.1
	443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780 1 retinal short-c	4.1
	448816	AB033052	Hs.22151	KIAA1226 protein	4.1
	452795	AW392555	Hs.18878	hypothetical protein FLJ21620	4.1
15	443171	BE281128	Hs.9030	TONDU	4.1
	425322	U63630	Hs.155637	protein kinase; DNA-activated; catalytic polypeptid	4.1
	442717	R88362	Hs.180591	ESTs, Weakly similar to R06F6.5b [C.elegans]	4.1
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosis)	4.1
	417300	AI765227	Hs.55610	solute carrier family 30 (zinc transporter), membe	4.1
20	417389	BE260964	Hs.82045	Mdkline (neurite growth-promoting factor 2)	4.1
	448105	AW591433	Hs.170675	ESTs, Weakly similar to TMS2_HUMAN TRANSMEMBR	4.1
	419131	AA062933	Hs.301622	ESTs	4.1
	406348	#(NOCAT)		0	4.1
25	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT2RP4000515	4.1
	419790	U79250	Hs.93201	glycerol-3-phosphate dehydrogenase 2 (mitochondria	4.1
	420908	AL049974	Hs.100261	Homo sapiens mRNA; cDNA DKFZp5648222 (from clone	4.1
	421039	NM_003478	Hs.101299	culin 5	4.1
	426890	AA393167	Hs.41294	ESTs	4.1
30	428571	NM_006531	Hs.2291	Probe hTg737 (polycystic kidney disease, autosomal	4.1
	452834	AI536627	Hs.105685	ESTs	4.1
	428771	AB028992	Hs.193143	KIAA1069 protein	4.0
	437849	U78519	Hs.41654	ESTs	4.0
	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT2RP4000448	4.0
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	4.0
35	418375	NM_003081	Hs.84389	synaptosomal-associated protein, 25kD	4.0
	447204	AI366881	Hs.157897	ESTs, Moderately similar to ALUC_HUMAN !!!! ALU CL	4.0
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane protein 3	4.0
	412314	AA825247	Hs.250899	heat shock factor binding protein 1	4.0
	436291	BE558452	Hs.5101	ESTs; Highly similar to protein regulating cytokin	4.0
40	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	4.0
	426991	AJ001536	Hs.285803	Homo sapiens cDNA FLJ12852 fis, clone NT2RP2003445	4.0
	409365	AA702376	Hs.226440	Homo sapiens clone 24881 mRNA sequence	4.0
	410784	AW803201		gb:IL2-UM0077-070500-080-E06 UM0077 Homo sapiens c	4.0
	413374	NM_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	4.0
45	413425	F20956		gb:HSPD05390 HM3 Homo sapiens cDNA clone 032-X4-1	4.0
	417655	AA780791	Hs.14014	ESTs, Weakly similar to KIAA0973 protein [H.sapien	4.0
	424783	AA913909	Hs.153088	TATA box binding protein (TBP)-associated factor,	4.0
	425024	R39235	Hs.12407	ESTs	4.0
	445941	AI267371	Hs.172636	ESTs	4.0
50	448595	AB014544	Hs.21572	KIAA0644 gene product	4.0
	453448	AL036710	Hs.209527	ESTs	4.0
	458944	N93227	Hs.98403	ESTs	4.0
	400284			Estrogen receptor 1	4.0
	441134	W29092	Hs.7678	cellular retinoic acid-binding protein 1	4.0
55	408798	AA688292	Hs.118553	ESTs	4.0
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	4.0
	438913	AI380429	Hs.172445	ESTs	4.0
	402408			0	4.0
	411830	U42349	Hs.71119	Pulative prostate cancer tumor suppressor	4.0
60	450701	H39960	Hs.289467	Homo sapiens cDNA FLJ12280 fis, clone MAMMA100174	4.0
	439780	AL109688		gb:Homo sapiens mRNA full length insert cDNA clone	4.0
	418301	AW976201	Hs.187618	ESTs	4.0
	420077	AW512260	Hs.87767	ESTs	4.0
	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	4.0
65	403721			0	4.0
	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncogene homolo	4.0
	408584	R61377	Hs.12727	hypothetical protein FLJ21610	4.0
	414869	AA157291	Hs.72163	ESTs	4.0
	437980	R50393	Hs.278436	KIAA1474 protein	4.0
70	451050	AW937420	Hs.69662	ESTs	4.0

TABLE 148:

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey	CAT Number	Accession
409073	109851_1	AA063458 AA063018 AJ444822
410784	1221005_1	AW803201 BE079700 BE062940
411560	1249443_1	AW851186 AW996967 BE143456
413425	136885_1	F20956 AA129374 AA133740 AW819878
414315	143512_1	Z24878 AA494098 F13654 AA494040 AA143127
418378	174656_1	AW962081 AA218925 AA354237
418804	179138_1	AA809632 AI917245 AJ701732 AA228406
419311	183793_1	AA689591 AW974261 AA236240 AJ077451 AA631399 AW974262

420637 195241_1 AW976153 AA278945 AA747691
 424341 238294_1 AA385074 AA339054 AA339115 AW956359
 428002 285602_1 AA418703 AA418711 BE071915 BE071920 BE071912
 428679 294049_1 AA431765 AA432015
 429163 300543_1 AA884766 AW974271 AA592975 AA447312
 430153 313709_1 AW968128 AA468102 AA468165
 431229 330060_1 AA496479 T89859 AW020056 AW135251 AJ221100 AA628705 AJ263148 T78074
 431322 331543_1 AW970622 AA503009 AA502998 AA502989 AA502805 T92188
 434415 385931_1 BE177494 AW276909 AA632849
 436812 427323_1 AW298067 AA731645 AA810101 AW194180 AJ690673 AW978773
 437938 44573_2 AJ950087 N70208 R97040 N36809 AJ308119 AW967677 N35320 AJ251473 H59397 AW971573 R97278 W01059 AW967671 AA908598
 AA251875 AJ820501 AJ820532 W87891 T85904 U71458 T82391 BE328571 T75102 R34725 AA884922 BE328517 AJ219788 AA884444 N92578
 F13493 AA927794 AJ560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AJ890387 AJ950344 AJ741346
 AJ689062 AA282915 AW102898 AJ872193 AJ763273 AW173586 AW150329 AJ653832 AJ762688 AA988777 AA488892 AJ356394 AW103813
 AJ539642 AA642789 AA856975 AW505512 AJ961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538
 AA180009 AA337499 AW961101 AA251669 AA251874 AJ819225 AW205862 AJ683338 AJ858509 AW276905 AJ633006 AA972584 AA908741
 AW072629 AW513996 AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 AJ022058 AA780419 AA551005 W80701 AW613456
 AJ373032 AJ564269 F00531 H83488 W37181 W78802 R66055 AJ002839 R87840 AA300207 AW959581 T63226 F04005
 AW979074 AA834841 AA828650
 AA828995 AA834879 AJ926361
 AW979172 AA829595 R96050
 AL109688 R23665 R26578
 AA955998 AJ916584 R61781 T77332 F07756 F08149 F07647
 AJ624049 AW117770 AJ858360
 AA442176 AA259181
 AJ902519 AJ902518 AJ902516
 BE068115 BE068104 BE068102 BE068096 BE068103 BE068154 BE068198
 AJ630223 AJ630470

TABLE 14C:

Key: Unique number corresponding to an Eos probe set

Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495

Strand: Indicates DNA strand from which exons were predicted

Nt_position: Indicates nucleotide positions of predicted exons

Key	Ref	Strand	Nt_position
401844	8576138	Plus	82655-83959
402408	9796239	Minus	110326-110491
402606	9909429	Minus	81747-82094
402820	6456853	Minus	82274-82443
403381	9438267	Minus	26009-26178
403657	8843996	Minus	156223-156370
403721	7528046	Minus	156647-157368
404253	9367202	Minus	55675-56055
404561	9795880	Minus	69039-70100
404939	6862697	Plus	175318-175476
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
405547	1054740	Plus	124361-124520,124914-125050
406348	9255985	Minus	71754-71944
406367	9256126	Minus	58313-58489
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

Table 15A lists about 499 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to be extracellular or cell-surface proteins. These were selected as for Table 14A, except that the ratio was greater than or equal to 3.0, and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g., Ig, fn3, egf, 7tm domains). Predicted protein domains are noted.

TABLE 15A: ABOUT 499 UP-REGULATED GENES ENCODING EXTRACELLULAR/CELL SURFACE PROTEINS, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES

Key: Primekey

UG ID: UniGene ID

Title: UniGene title

Prot. Dom.: Predicted protein structural domains

ratio: ration tumor vs normal tissues

Key	Ex. Accn	UG ID	Title	Prot. Dom.	ratio
415989	AJ267700	Hs.111128	ESTs	TM	42.7
428579	NM_005756	Hs.184942	G protein-coupled receptor 64	TM	30.5
428153	AW513143	Hs.98367	similar to SRY-box containing gene 17	TM	30.1
436982	AB018305	Hs.5378	spondin 1, (I-spondin) extracellular matrix	SS	29.4
427585	D31152	Hs.179729	collagen; type X; alpha 1 (Schmid metaphy	C1q.Collagen	27.0
430591	C14187	Hs.103538	ESTs	TM	26.2
418007	M13509	Hs.83169	Matrix metalloproteinase 1 (interstitial collag	SS,Peptidase_M10	20.6
400292	AA250737	Hs.72472	BMFR-1b; bone morphogenetic protein rec	TM	20.6
424086	AJ351010	Hs.102267	lysyl oxidase	Lysyl oxidase	17.7
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related kin	pkase,kinase	17.4
427356	AW023482	Hs.97849	ESTs	TM	17.4
407638	AJ404672	Hs.288593	EST	TM	17.1
427469	AA403084	Hs.269347	ESTs	TM	17.0
438993	AA828995		Integrin; beta 8	SS,Integrin_B	16.7
421155	H87879	Hs.102267	lysyl oxidase	SS	16.1
431989	AW972870	Hs.291069	ESTs	SS	15.9
428976	AL037824	Hs.194695	ras homolog gene family, member I	ras	15.1
416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, hom	TM	15.0

5	413623	AA825721	Hs.246973	ESTs	TM	14.8
	447350	AJ375572	Hs.172634	ESTs; HER4 (c-erb-B4)	SS,TM,Furin-like,ptkinase	14.2
	428227	AA321849	Hs.2248	INTERFERON-GAMMA INDUCED PRO	IL8	14.1
	452461	N78223	Hs.108106	transcription factor	G9a,PHD	13.7
	451106	BE382701	Hs.25960	N-myc	Myc_N_term	13.6
	416208	AW291168	Hs.41295	ESTs	TM	13.5
	452249	BE394412	Hs.61252	ESTs	homeobox	13.4
	416566	NM_003914	Hs.79378	cyclin A1	cyclin	12.8
10	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	TM	12.6
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	SS,Cys_knot	12.3
	458027	L49054	Hs.85195	ESTs, Highly similar to (3;5)(q25.1;p34) t	TM	12.2
	408460	AA054726	Hs.285574	ESTs	TM	12.2
	415263	AA948033	Hs.130853	ESTs	histone	11.9
15	400298	AA032279	Hs.61635	STEAP1	TM	11.8
	421451	AA291377	Hs.50831	ESTs	TM	11.6
	443715	AJ583187	Hs.9700	cyclin E1	cyclin	11.5
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affinity gl	TM,SDF	11.5
	410102	AW248508	Hs.279727	ESTs	SS	11.4
20	408562	AJ436323	Hs.31141	Homo sapiens mRNA for KIAA1568 prote	TM	11.4
	442353	BE379594	Hs.48136	ESTs	TM	11.3
	427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3	TM,neur_chan	11.2
	453160	AJ263307	Hs.146228	ESTs	histone	11.2
	412723	AA640459	Hs.179912	ESTs	TM	11.1
25	400250			0	Hist_deacetyl+F105	11.1
	438167	R28363	Hs.24286	ESTs	7tm_1	11.1
	434539	AW748078	Hs.214410	ESTs	TM	10.9
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain	TM	10.8
	400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromelysin 2	SS,homopaxin	10.8
30	446142	AJ754693	Hs.145968	ESTs	Cadherin_C_term	10.7
	421285	NM_000102	Hs.1363	cytochrome P450, subfamily XVII (steroid	TM,p450	10.6
	433496	AF064254	Hs.49765	VERY-LONG-CHAIN ACYL-COA SYNT	SS,TM	10.6
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	TM	10.5
	433447	U29195	Hs.3281	neuronal pentraxin II	SS	10.4
35	414245	BE148072	Hs.75850	WAS protein family, member 1	TM	10.3
	426462	U59111	Hs.169993	dermatan sulphate proteoglycan 3	SS,LRRNT	10.3
	418601	AA279490	Hs.86368	calmagin	SS	10.3
	415227	AW821113	Hs.72402	ESTs	TM	10.2
	409269	AA576953	Hs.22972	Homo sapiens cDNA FLJ13352 fis, clone O	TM	10.1
40	426471	M22440	Hs.170009	transforming growth factor, alpha	SS,EGF	9.8
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfotran	SS	9.7
	445537	AJ245671	Hs.12844	EGF-like domain; multiple 6	SS,EGF	9.7
	414972	BE263782	Hs.77695	KIAA0008 gene product	TM	9.4
	435509	AJ458679	Hs.181915	ESTs	TM	9.3
45	445413	AA151342	Hs.12677	CGI-147 protein	UPF0099	9.2
	446999	AA151520	Hs.279525	hypothetical protein PRO2605	TM	9.1
	414569	AF109298	Hs.118258	Prostate cancer associated protein 1	TM	9.1
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	hemopexin	9.0
	408908	BE296227	Hs.48915	serine/threonine kinase 15	pkase, TM	9.0
50	451807	W52654	Hs.27099	DKFZP564J0863 protein	TM	8.8
	420159	AJ572490	Hs.99785	ESTs	TM	8.8
	432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:poly	TM,Ricin_B_lectin	8.7
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfotran	TM	8.7
	438885	AJ886558	Hs.184987	ESTs	TM	8.7
55	447342	AJ199268	Hs.19322	ESTs; Weakly similar to IIII ALU SUBFAM	TM	8.6
	437212	AJ765021	Hs.210775	ESTs	UDPGT	8.5
	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	wnt	8.4
	450505	NM_004572	Hs.25051	plakophilin 2	TM	8.4
	436398	AJ683487	Hs.299112	Homo sapiens cDNA FLJ11441 fis, clone H	wnt	8.3
60	425695	NM_005401	Hs.159238	protein tyrosine phosphatase, non-receptor	Y_phosphatase	8.3
	447268	AJ370413	Hs.36563	Homo sapiens cDNA: FLJ22418 fs, clone	Ribosomal_S8	8.2
	400195			0	TM	8.1
	424906	AJ566086	Hs.153718	Homo sapiens mRNA for Hmob33 protein,	TM	8.1
	438202	AW169287	Hs.22588	ESTs	TM	8.1
65	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	TM	8.0
	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	TM,Fz,Frizzled	8.0
	424001	W67883	Hs.137476	KIAA1051 protein	TM	8.0
	442655	AW027457	Hs.30323	ESTs	TM	7.8
	445657	AW612141	Hs.279575	ESTs	7tm_1	7.8
70	426320	W47595	Hs.169300	transforming growth factor, beta 2	SS,TGF-beta	7.8
	412170	D16532	Hs.73729	very low density lipoprotein receptor	TM,kil_recept_b,EGF	7.6
	436476	AA326108	Hs.53631	ESTs	TM	7.6
	414132	AJ801235	Hs.48480	ESTs	TM	7.6
	437789	AJ581344	Hs.127812	ESTs, Weakly similar to AF141326 1 RNA	TM	7.6
75	450192	AA263143	Hs.24596	RAD51-interacting protein	TM	7.6
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	TM	7.5
	413627	BE182082	Hs.246973	ESTs	TM	7.4
	446293	AJ420213	Hs.149722	ESTs	LM,homeobox	7.4
	409242	AL080170	Hs.51692	DKFZP434C091 protein	TM,7tm_1	7.3
80	450262	AW409872	Hs.271166	ESTs, Moderately similar to ALU7_HUMA	TM	7.3
	451659	BE379761	Hs.14248	ESTs, Weakly similar to ALU8_HUMAN A	TM	7.3
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane g	TM	7.2
	429126	AW172356	Hs.99083	ESTs	7tm_1	7.1
	421464	AA291553	Hs.190086	ESTs	TM	7.0
	420362	U78734	Hs.97206	huntingtin interacting protein 1	TM	7.0

444743	AA045648	Hs.11817	nudix (nucleoside diphosphate linked moiety)	TM	7.0
415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 TFP12	Kunitz_BPTI,G-gamma	6.9
429418	AJ381028	Hs.99283	ESTs	AAA	6.9
409178	BE393948	Hs.50915	kallikrein 5	SS,trypsin	6.9
425905	AB032959	Hs.161700	KIAA1133 protein	TM	6.9
428532	AF157326	Hs.184786	TBP-interacting protein	TM	6.9
433426	H69125	Hs.133525	ESTs	TM	6.9
448674	W31178	Hs.154140	ESTs	TM	6.8
432415	T16971	Hs.289014	ESTs	TM	6.7
418203	X54942	Hs.83758	CDC28 protein kinase 2	TM	6.6
438394	BE379523	Hs.27693	CGI-124 protein	pro_isomerase	6.6
452097	AB002364	Hs.27916	ADAM-TS3 ; a disintegrin-like and metal	Reprolysin	6.6
453745	AA952989	Hs.63908	Homo sapiens HSPC316 mRNA, partial cd	TGFb_propeptide	6.6
423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	filament	6.6
452281	T93500	Hs.28792	ESTs	TGF-beta	6.5
424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic; stratum corneum	SS,trypsin	6.5
452594	AJ076405	Hs.29981	solute carrier family 26 (sulfate transporter)	TM,Sulfate_transp	6.5
434149	Z43829	Hs.19574	ESTs, Weakly similar to katanin p80 subun	pkinase,fn3	6.5
425776	U25128	Hs.159499	parathyroid hormone receptor 2	TM,7tm_2	6.4
409517	X90780	Hs.54668	troponin I, cardiac	Y_phosphatase	6.4
432666	AW204069	Hs.129250	ESTs, Weakly similar to unnamed protein p	TM	6.4
448706	AW291095	Hs.21814	class II cytokine receptor ZCYTOR7	SS	6.4
413582	AW295647	Hs.71331	Homo sapiens cDNA: FLJ21971 fis, clone	TM	6.4
424163	AA451737	Hs.141496	MAGE-like 2	TM	6.4
441081	AJ584019	Hs.169006	ESTs, Moderately similar to plakophilin 2b	PAX	6.4
443539	AJ076182	Hs.134074	ESTs	TM	6.4
418384	AW149266	Hs.25130	ESTs	TM	6.3
425371	D49441	Hs.155981	mesothelin	SS	6.3
449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induced g	SS	6.3
437117	AL049258	Hs.122593	ESTs	TM	6.3
453370	AJ470523	Hs.182356	ESTs, Moderately similar to translation init	ABC_tran	6.3
426514	BE918633	Hs.301122	bone morphogenetic protein 7 (osteogenic p	SS,TGF-beta	6.3
452904	AL157581	Hs.30957	Homo sapiens mRNA; cDNA DKFZp434E	TM	6.2
457030	AJ301740	Hs.173381	dihydropyrimidinase-like 2	TM	6.2
436281	AW411194	Hs.120051	ESTs	TM	6.1
415139	AW975942	Hs.48524	ESTs	TM	6.1
449448	D60730	Hs.57471	ESTs	TM	6.1
457979	AA776655	Hs.270942	ESTs	TM	6.1
422867	L32137	Hs.1584	cartilage oligomeric matrix protein	SS,EGF,isp_3	6.0
421502	AF111856	Hs.105039	solute carrier family 34 (sodium phosphale)	TM	6.0
412733	AA984472	Hs.74554	KIAA0080 protein	C2	6.0
422095	AJ868972	Hs.288966	carboxylasmin (ferroxidase)	SS	6.0
418845	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alp	Chromo_shadow	6.0
410555	U92649	Hs.84311	a disintegrin and metalloproteinase domain	TM,disintegrin,Reprolysin	5.9
437099	N77793	Hs.48659	ESTs, Highly similar to LMA1_HUMAN L	laminin_EGF	5.9
453431	AF094754	Hs.32973	glycine receptor, beta	TM,neur_chan	5.9
417866	AW067903	Hs.82772	*collagen, type XI, alpha 1*	TSPN,Collagen,COLFI	5.9
430291	AV660345	Hs.238126	CGI-49 protein	TM	5.9
405547	#(NOCAT)		0	TM,ABC_membrane	5.9
435793	AB037734	Hs.4993	ESTs	TM	5.8
440138	AB033023	Hs.6982	hypothetical protein FLJ10201	TM	5.8
425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	SS,Collagen,TSPN	5.7
419335	AW950146	Hs.284137	Homo sapiens cDNA FLJ12888 fis, clone N	TM	5.7
452971	AJ873878	Hs.91789	ESTs	TM	5.7
428927	AA441837	Hs.90250	ESTs	TM	5.7
419247	S65791	Hs.89764	fragile X mental retardation 1	TM	5.7
445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 (H.sap	TM	5.7
447078	AW885727	Hs.301570	ESTs	kazal	5.6
421247	BE391727	Hs.102910	general transcription factor IIH, polypeptid	TM	5.6
432030	AJ908400	Hs.143789	ESTs	SS	5.6
443270	NM_004272	Hs.9192	Homer, neuronal immediate early gene, 18	TM	5.6
411096	U80034	Hs.68583	mitochondrial intermediate peptidase	Peptidase_M3	5.5
419558	AW953679	Hs.278394	ESTs	SS	5.5
427386	AW836261	Hs.177486	amyloid beta (A4) precursor protein (protea	TM	5.5
427961	AW293165	Hs.143134	ESTs	TM	5.5
407216	N91773	Hs.102267	lysyl oxidase	TM	5.5
413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	ras,TM	5.5
414315	Z24878		gb:HSB65D052 STRATAGENE Human sk	TM	5.5
441645	AJ222279	Hs.201555	ESTs	SS	5.5
449318	AW236021	Hs.108788	ESTs, Weakly similar to zeste [D.melanoga	TM	5.4
441433	AA933809	Hs.42746	ESTs	TM	5.4
445495	BE622641	Hs.39489	ESTs	I_LWEQ,ENTH	5.4
410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone N	Glycos_transf_2	5.4
442611	BE077155	Hs.177537	ESTs	TM	5.4
452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced protein	Xlink,CUB	5.4
419948	AB041035	Hs.93847	NADPH oxidase 4	TM	5.3
427718	AJ798680	Hs.25933	ESTs	histone	5.3
453867	AJ929383	Hs.108196	HSPC037 protein	TM	5.3
408298	AJ745325	Hs.271923	ESTs, Moderately similar to !!! ALU SUB	Glycos_transf_2,OSPC	5.3
448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P	TM	5.3
433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMA	TM	5.3
449532	W74653	Hs.271593	ESTs	TM	5.3
452822	X85689	Hs.288617	Homo sapiens cDNA: FLJ22621 fis, clone	TM,EGF,fn3	5.3
418379	AA218940	Hs.137516	tdgfin-like 1	AAA	5.2

	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	TM, trypsin	5.2
	413384	NM_000401	Hs.75334	exosomoses (multiple) 2	TM	5.2
	445236	AK001676	Hs.12457	hypothetical protein FLJ10814	TM	5.2
5	406367	#(NOCAT)		0	proteasome, trypsin	5.2
	442500	AJ819068	Hs.209122	ESTs	SS	5.2
	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	TM	5.2
	419140	AJ82647	Hs.215725	ESTs	TM	5.2
	417791	AW955339	Hs.111471	ESTs	Ald_Xen_dh_C	5.1
10	437496	AA452378	Hs.170144	Homo sapiens mRNA; cDNA DKFZp547J1	TSPN, Folate_carrier	5.1
	418849	AW474547	Hs.53565	ESTs, Weakly similar to B0491.1 [C.elegan	TM	5.1
	428093	AW594506	Hs.104830	ESTs	TM	5.1
	408621	AJ970572	Hs.46638	chromosome 11 open reading frame 8; feta	TM	5.1
	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	TM	5.1
	404939			0	TM	5.0
15	447020	T27308	Hs.16986	hypothetical protein FLJ11046	TM	5.0
	410824	AW994813	Hs.33264	ESTs	TM	5.0
	417423	AA197341	Hs.111164	ESTs	TM	5.0
	421477	AJ904743	Hs.104650	hypothetical protein FLJ10292	TM	5.0
	443555	N71710	Hs.21398	ESTs, Moderately similar to GNPI_HUMA	Glucosamine_iso	5.0
20	424539	L02911	Hs.150402	activin A receptor, type I	SS, Activin_recpt, kinase	4.9
	416565	AW000960	Hs.44970	ESTs	TM	4.9
	431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic protein ty	SS	4.9
	408938	AA059013	Hs.22607	ESTs	TM	4.9
25	436754	AJ061288	Hs.133437	ESTs, Moderately similar to gonadotropin I	TM	4.9
	409049	AJ423132	Hs.146343	ESTs	TM	4.9
	458627	AW088642	Hs.97984	ESTs; Weakly similar to WASP-family pro	TM	4.8
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	TM, ABC_membrane	4.8
	422505	AL120862	Hs.124165	ESTs; (HSA)PAP protein (programmed ce	TM	4.8
30	428555	NM_002214	Hs.184908	integrin, beta 8	SS, integrin_B	4.8
	452909	NM_015368	Hs.30985	pannexin 1	TM	4.8
	449535	W15267	Hs.23672	low density lipoprotein receptor-related pro	SS, ldl_recept_a, EGF	4.8
	452232	AW020603	Hs.271698	ESTs	TM	4.8
	423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N	Cadherin_C_term	4.7
35	428405	Y00762	Hs.2266	cholinergic receptor, nicotinic, alpha polype	TM, neur_chan	4.7
	433330	AW207084	Hs.132816	ESTs	TM	4.7
	443933	AJ091631	Hs.135501	Homo sapiens two pore potassium channel	TM	4.7
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	TM	4.7
	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	TM, EGF	4.7
40	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37kD)	AAA, DEAD, helicase_C	4.7
	429944	R13949	Hs.226440	Homo sapiens clone 24881 mRNA sequenc	TM	4.7
	434988	AJ418055	Hs.161160	ESTs	TM	4.6
	406400	#(NOCAT)		0	trypsin, TM	4.6
	428301	AW628666	Hs.98440	ESTs	TM	4.6
45	446254	BE179829	Hs.179852	Homo sapiens cDNA FLJ12832 fis, clone N	TM	4.6
	459574	AJ741122	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone N	TM	4.6
	409928	AL137163	Hs.57549	hypothetical protein dJ47384	TM	4.6
	435244	N77221	Hs.187824	ESTs	TM	4.6
	404966	#(NOCAT)		0	kinase, fn3	4.6
50	407905	AW103655	Hs.252905	ESTs	Peptidase_C1	4.6
	441675	AJ914329	Hs.5461	ESTs	SS, Ephrin	4.6
	420276	AA290938	Hs.190561	ESTs, Highly similar to mosaic protein LR1	TM	4.6
	422529	AW015128	Hs.256703	ESTs	TM, fn3, ldl_recept_a	4.5
	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	TM	4.5
55	457465	AW301344	Hs.195969	ESTs	Phorboltran	4.5
	418848	AJ820961	Hs.193465	ESTs	TM, pkase	4.5
	447499	AW262580	Hs.147674	KIAA1621 protein	TM	4.5
	432731	R31178	Hs.287820	fibronectin 1	SS	4.5
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone H	Nucleoside_tra2	4.4
60	427528	AJ077143	Hs.179565	minichromosome maintenance deficient (S.	TM	4.4
	409092	AJ735283	Hs.172608	ESTs	TM	4.4
	451389	N73222	Hs.21738	KIAA1008 protein	TM	4.4
	453331	AJ240665	Hs.8895	ESTs	TM	4.4
	448133	AA723157	Hs.73769	folate receptor 1 (adult)	TM	4.4
65	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain	TM	4.4
	453279	AW893940	Hs.59698	ESTs	TM	4.4
	409459	D86407	Hs.54481	low density lipoprotein receptor-related pro	TM, EGF, ldl_recept_a	4.4
	431708	AJ698136	Hs.108873	ESTs	TM	4.4
	433506	AJ167816	Hs.43355	ESTs	TM	4.4
70	441423	AJ793299	Hs.126877	ESTs	TM	4.4
	446770	AV660309	Hs.154986	ESTs, Weakly similar to AF137386 1 plasm	TM	4.3
	412078	X69699	Hs.73149	paired box gene 8	TM	4.3
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE; H	AIRS	4.3
	448390	AL035414	Hs.21068	hypothetical protein	TM	4.3
75	453628	AW243307	Hs.170187	ESTs	TM	4.3
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	TM	4.3
	413775	AW409934	Hs.75528	nucleolar GTPase	MMR_HSR1	4.3
	451592	AJ805416	Hs.213897	ESTs	TM	4.3
80	419311	AA689591		gbmv66a12.s1 NCI_CGAP_GCB1 Homo s	TM	4.2
	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	TM	4.2
	428679	AA431765		gbzw80c03.s1 Soares_testis_NHT Homo s	TM	4.2
	436209	AW850417	Hs.254020	ESTs, Moderately similar to unnamed prote	TM	4.2
	405078	AL390179	Hs.137011	Homo sapiens mRNA; cDNA DKFZp547P	TM	4.2
	428819	AL135623	Hs.193914	KIAA0575 gene product	TM	4.2
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fac	F-actin_cap_A	4.2

	431750	AA514986	Hs.283705	ESTs	TM	4.2
	449554	AA682382	Hs.59982	ESTs	TM	4.2
	409073	AA063458		gbz71a07.s1 Soares_pineal_gland_N3HP	SEA	4.1
	433929	AI375499	Hs.27379	ESTs	TM	4.1
5	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN A	TM	4.1
	444381	BE387335	Hs.283713	ESTs	TM	4.1
	415539	AI733881	Hs.72472	BMPR-1b; bone morphogenetic protein rec	TM	4.1
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase 1, long	TM	4.1
10	453293	AA382267	Hs.10653	ESTs	TM	4.1
	409584	AA045857	Hs.54943	fracture callus 1 (rat) homolog	TM	4.1
	429628	H09604	Hs.13268	ESTs	TM	4.1
	440452	AI925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN	TM	4.1
	443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780 1 retina	TM	4.1
15	425322	U63830	Hs.155637	protein kinase; DNA-activated; catalytic po	TM	4.1
	417300	AI765227	Hs.55610	solute carrier family 30 (zinc transporter), m	TM	4.1
	417389	BE260964	Hs.82045	Midkine (neurite growth-promoting factor 2	SS, TM	4.1
	452834	AI638627	Hs.105685	ESTs	kinesin	4.1
	428771	AB028992	Hs.193143	KIAA1069 protein	PI-PLC-X, PI-PLC-Y	4.0
20	412314	AA825247	Hs.250899	heat shock factor binding protein 1	TM	4.0
	436291	BE568452	Hs.5101	ESTs; Highly similar to protein regulating c	TM	4.0
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	KRAB	4.0
	409365	AA702376	Hs.226440	Homo sapiens clone 24881 mRNA sequenc	TM	4.0
	413374	NM_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	ribonuc_red	4.0
25	417655	AA780791	Hs.14014	ESTs, Weakly similar to KIAA0973 protein	TM	4.0
	445941	AI267371	Hs.172636	ESTs	TM, lectin_c	4.0
	441134	W29092	Hs.7678	cellular retinoic acid-binding protein 1	lipocalin	4.0
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppressor	TM	4.0
	418301	AW976201	Hs.187618	ESTs	TM	4.0
30	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncog	TGF-beta, Myc_N_term	4.0
	408684	R61377	Hs.12727	hypothetical protein FLJ21610	TM	4.0
	414869	AA157291	Hs.72163	ESTs	TM	4.0
	420281	AI623693	Hs.191533	ESTs	Cation_efflux	3.9
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural arachnod	EGF, TB	3.9
35	411274	NM_002776	Hs.69423	kallikrein 10	trypsin, TM	3.9
	437222	AL117688	Hs.299963	ESTs	TM	3.9
	431958	X63629	Hs.2877	Cadherin 3, P-cadherin (placental)	TM, cadherin,	3.9
	430634	AI860651	Hs.26685	ESTs	TM	3.9
	415716	N59294	Hs.301141	Homo sapiens cDNA FLJ11689 fis, clone H	NAP_family	3.9
40	420179	N74530	Hs.21168	ESTs	TM	3.8
	451250	AA491275	Hs.236940	Homo sapiens cDNA FLJ12542 fis, clone N	TM	3.8
	429496	AA453800	Hs.192793	ESTs	TM	3.8
	421764	AI681535	Hs.99342	ESTs, Weakly similar to KCC1_HUMAN C	TM	3.8
	447197	R36075		gbz88b01.s1 Soares placenta Nb2HP Hom	TM, SDF	3.8
45	422939	AW394055	Hs.98427	ESTs	TM	3.8
	414737	AI160386	Hs.125087	ESTs	TM	3.8
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	SS, trypsin	3.8
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin 3)	SS, Peptidase_M10	3.7
	424433	H04607	Hs.9218	ESTs	TM	3.7
50	431846	BE019924	Hs.271580	Uroplakin 1B	TM, transmembrane4	3.7
	407792	AI077715	Hs.39384	putative secreted ligand homologous to fxl1	SS	3.7
	417531	NM_003157	Hs.1087	serine/threonine kinase 2	pkase, kinase	3.7
	434836	AA651629	Hs.118088	ESTs	TM	3.7
	439810	AL109710	Hs.85568	EST	TM	3.7
55	418693	AI750878	Hs.87409	thrombospondin 1	SS, EGF, TSPN	3.7
	407884	AF069291	Hs.40539	chromosome 8 open reading frame 1	TM	3.7
	436304	AA339622	Hs.108887	ESTs	TM	3.7
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (transloco	TM	3.7
	453468	W00712	Hs.32990	DKFZP566F084 protein	TM	3.6
60	428943	AW086180	Hs.37636	ESTs, Weakly similar to KIAA1392 protein	TM	3.6
	411402	BE297855	Hs.69855	NRAS-related gene	CSD, ras, CSD	3.6
	425176	AW015644	Hs.301430	ESTs, Moderately similar to TEF1_HUMA	TM	3.6
	400296	AA305627	Hs.139336	ATP-binding cassette; sub-family C (CFTR	ABC_tran	3.6
	407340	AA810168	Hs.232119	ESTs	TM	3.6
	418524	AA300576	Hs.85769	acidic 82 kDa protein mRNA	TM	3.6
65	438279	AA805166	Hs.165165	ESTs, Moderately similar to ALU8_HUMA	TM	3.6
	439453	BE284974	Hs.6566	thyroid hormone receptor interactor 13	AAA, AAA	3.6
	441111	AI806867	Hs.126594	ESTs	TM	3.6
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	TM	3.6
70	409542	AA503020	Hs.36563	ESTs	Ribosomal_S8	3.6
	425441	AA449644	Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone N	Aa_trans	3.6
	428137	AA421792	Hs.170999	ESTs	AAA	3.6
	433692	AI805860	Hs.208675	ESTs, Weakly similar to neuronal thread pr	TM	3.6
	438689	AW129261	Hs.250565	ESTs	TM	3.6
75	443341	AW631480	Hs.8688	ESTs	TM	3.6
	446261	AA313893	Hs.13399	hypothetical protein FLJ12615 similar to m	ATP-sym_D, PH	3.6
	414343	AL036166	Hs.75914	coated vesicle membrane protein	TM	3.5
	414812	X72755	Hs.77367	monokine induced by gamma interferon	SS, IL8	3.5
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-indu	TM	3.5
80	415786	AW419196	Hs.257924	ESTs	TM	3.5
	427177	AB006537	Hs.173880	Interleukin 1 receptor accessory protein	TM, Ig	3.5
	427687	AW003867	Hs.112403	ESTs	TM, 1	3.5
	444619	BE538082	Hs.8172	ESTs	TM	3.5
	447336	AW139383	Hs.245437	ESTs	AhpC-TSA	3.5
	412519	AA196241	Hs.73980	troponin T1, skeletal, slow	TM	3.5

5	418792	AB037805	Hs.88442	KIAA1384 protein	TM	3.5
	408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone N	TM	3.5
	416892	L24498	Hs.80409	growth arrest and DNA-damage-inducible,	TM	3.5
	418793	AW382987	Hs.88474	prostaglandin-endoperoxide synthase 1 (pro	EGF	3.5
	448089	AI467945	Hs.173696	ESTs	SS	3.5
	422278	AF072873	Hs.114218	ESTs	TM,Fz,Fritzzled	3.5
	442133	AW874138	Hs.129017	ESTs	TM	3.5
	410908	AA121686	Hs.10592	ESTs	GTP_EFTU	3.5
10	452198	AI097560	Hs.61210	ESTs	TM	3.5
	408730	AV660717	Hs.47144	DKFZP586N0819 protein	kinase	3.4
	436488	BE520909	Hs.261023	hypothetical protein FLJ20958	TM	3.4
	409745	AA077391		gb:7B14E12 Chromosome 7 Fetal Brain cD	TM	3.4
	445870	AW410053	Hs.13406	synlaxin 18	TM	3.4
15	451743	AW074266	Hs.23071	ESTs	TM	3.4
	407846	AA426202	Hs.40403	Cbip300-interacting transactivator, with G	TM	3.4
	432350	NM_005865	Hs.274407	protease, serine, 16 (thymus)	SS	3.4
	412848	AA121514	Hs.70832	ESTs	TM	3.4
	413625	AW451103	Hs.71371	ESTs	filament	3.4
20	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like repeat d	SS	3.4
	422972	N59319	Hs.145404	ESTs	TM	3.4
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4; MAP kinase	DSPC,Rhodanese	3.4
	450377	AB033091	Hs.24936	ESTs	TM	3.4
	443475	AI066470	Hs.134482	ESTs	TM	3.4
25	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	TM,kinase,lg,SRF-TF	3.4
	409744	AW675258	Hs.56265	Homo sapiens mRNA; cDNA DKFZp586P	TM	3.4
	422789	AK001113	Hs.120842	hypothetical protein FLJ10251	TM	3.4
	404440	#(NOCAT)		0	TM,neur_chan	3.4
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	SS,TIR,lg	3.4
30	411828	AW161449	Hs.72290	wingless-type MMTV integration site fami	wnt	3.4
	417177	NM_004458	Hs.81452	fatty-acid-Coenzyme A ligase, long-chain 4	SS	3.4
	421013	M62397	Hs.1345	mutated in colorectal cancers	TM	3.4
	427072	H38046		gb:yp58c10.1 Soares fetal liver spleen 1NF	Ribosomal_L22a	3.4
	433703	AA210863	Hs.3532	namo-like kinase	kinase	3.4
35	434294	AJ271379	Hs.21175	ESTs	TM	3.4
	444188	AI393165	Hs.19175	ESTs	TM	3.4
	446109	N67953	Hs.145920	ESTs	TM	3.4
	400881			0	Asparaginase_2	3.3
40	450236	AW162998	Hs.24684	KIAA1376 protein	TM	3.3
	418836	AI655499	Hs.161712	ESTs	TM	3.3
	437951	T34530	Hs.4210	Homo sapiens cDNA FLJ13069 fis, clone N	TM	3.3
	446896	T15767	Hs.22452	Homo sapiens cDNA: FLJ21084 fis, clone	TM	3.3
	430687	BE274217	Hs.249247	heterogeneous nuclear protein similar to rat	rm	3.3
	410060	NM_001448	Hs.58367	glypican-4	SS	3.3
45	419546	AA244199		gb:nc06c05.s1 NCL_CGAP_Pr1 Homo sapi	TM	3.3
	429609	AF002246	Hs.210863	cell adhesion molecule with homology to L	TM,fn3,lg	3.3
	413289	AA128061	Hs.114992	ESTs	TM	3.3
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	TM	3.3
	401435	#(NOCAT)		0	TM	3.3
50	420072	AW961196	Hs.207725	ESTs	TM	3.3
	421426	AA291101	Hs.33020	Homo sapiens cDNA FLJ20434 fis, clone K	TM	3.3
	425851	NM_001490	Hs.159642	glucosaminyl (N-acetyl) transferase 1, core	SS	3.3
	443295	AI049783	Hs.241284	ESTs	TM	3.2
	453116	AI276680	Hs.146086	ESTs	Ribosomal_L5_C	3.2
55	456546	AI690321	Hs.203845	ESTs, Weakly similar to TWIK-related acid	TM	3.2
	430016	NM_004736	Hs.227656	xenotropic and polytropic retrovirus recepto	TM	3.2
	418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9,	asp,Glyco_hydro_18	3.2
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated glyco	TM	3.2
	425159	NM_004341	Hs.154858	carbamoyl-phosphate synthetase 2, aspartat	TM	3.2
60	428882	AA436915	Hs.131748	ESTs, Moderately similar to ALU7_HUMA	carb_anhydrase	3.2
	409533	AW969543	Hs.21291	mitogen-activated protein kinase kinase kin	TM	3.2
	411248	AA551538	Hs.69321	KIAA1359 protein	TM	3.2
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cys-	SS,IL6	3.2
	430259	BE550182	Hs.127826	RatGEF-like protein 3, mouse homolog	TM	3.2
65	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	SS	3.2
	444471	AB020684	Hs.11217	KIAA0877 protein	TM	3.2
	421674	T10707	Hs.296355	neuronal PAS domain protein 2	Ribosomal_L31e	3.2
	434163	AW974720	Hs.25206	ESTs	TM	3.2
	421891	NM_014918	Hs.110488	KIAA0990 protein	SS	3.2
70	409589	AW439900	Hs.256914	ESTs	TM	3.2
	414147	BE091634		gb:IL2-BT0731-240400-069-C03 BT0731	TM	3.2
	414661	T97401	Hs.21929	ESTs	TM	3.2
	437537	AA758974	Hs.121417	ESTs, Weakly similar to unnamed protein p	TM	3.2
	439702	AW085525	Hs.134182	ESTs	A2M	3.1
75	420552	AK000492	Hs.98808	hypothetical protein	TM	3.1
	441028	AI333660	Hs.17558	ESTs	ICE_p20,CARD	3.1
	425264	AA353953	Hs.20369	ESTs, Weakly similar to gonadotropin indu	TM	3.1
	422109	S73265	Hs.1473	gastrin-releasing peptide	SS,Bombesin	3.1
	441859	AW194364	Hs.128022	ESTs, Weakly similar to FIG1 MOUSE FIG	TM	3.1
80	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMA	SS,Ephrin	3.1
	447866	AW444754	Hs.211517	ESTs	homeobox	3.1
	419978	NM_001454	Hs.93974	forkhead box J1	Fork_head	3.1
	446219	AI287344	Hs.149827	ESTs	MIP	3.1
	448428	AF282874	Hs.21201	nectin 3; DKFZP56680846 protein	TM,lg	3.1
	407615	AW753085		gb:PM1-CT0247-151299-005-a03 CT0247	TM	3.1

5	410518	AW976443	Hs.285655	ESTs	RasGEF,PH,RhoGEF	3.1
	418396	AJ765805	Hs.26691	ESTs	TM	3.1
	427855	R61253	Hs.98265	ESTs	TM	3.1
	429272	W25140	Hs.110667	ESTs	TM	3.1
	450171	AL133661	Hs.24583	hypothetical protein DKFZp434C0328	TM	3.1
	414774	X02419	Hs.77274	plasminogen activator, urokinase	SS,kringle,trypsin	3.1
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38kD)	TM	3.1
	420062	AW411096	Hs.94785	hypothetical protein LOC57163	TM	3.1
10	428698	AA852773	Hs.297939	ESTs; Weakly similar to neogenin [H.sapi	TM	3.1
	427051	BE178110	Hs.173374	ESTs	TM	3.1
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic diffe	SS	3.1
	452906	BE207039	Hs.75621	serine (or cysteine) proteinase inhibitor, cla	TM	3.1
	429419	AB023226	Hs.202276	KIAA1009 protein	TM	3.1
15	417517	AF001176	Hs.82238	POP4 (processing of precursor, S. cerevisia	TM	3.1
	406137	#(NOCAT)		#	TM	3.1
	424800	AL035588	Hs.153203	MyoD family inhibitor	TM	3.1
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	TM	3.1
	420392	AI242930	Hs.97393	KIAA0328 protein	SS	3.1
20	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone	voltage_CLC,CBS	3.1
	429334	D63078	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone	Glyco_hydro_2	3.1
	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	TM	3.1
	450506	NM_004460	Hs.418	fibroblast activation protein; alpha	SS,Peptidase_S9	3.0
	433849	BE465884	Hs.280728	ESTs	TM	3.0
25	411984	NM_005419	Hs.72988	signal transducer and activator of transcript	SH2,STAT	3.0
	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	TM	3.0
	422128	AW881145		gb:QV0-OT0033-010400-182-e07 OT0033	TM	3.0
	409757	NM_001898	Hs.123114	cystatin SN	SS,cystatin	3.0
	418727	AA227609	Hs.94834	ESTs	TM	3.0
30	422244	Y08890	Hs.113503	karyopherin (importin) beta 3	TM	3.0
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatidat	TM	3.0
	432358	AI093491	Hs.72830	ESTs	SS	3.0
	416896	AI752862	Hs.5638	KIAA1572 protein	BTB	3.0
	447312	AI434345	Hs.36908	activating transcription factor 1	TM	3.0
35	445021	AK002025	Hs.12251	Homo sapiens cDNA FLJ11163 fis, clone P	TM	3.0
	422611	AA158177	Hs.118722	fucosyltransferase 8 (alpha (1,6) fucosyltran	SS	3.0
	453597	BE281130	Hs.33713	myo-inositol 1-phosphate synthase A1	TM	3.0
	401197	#(NOCAT)		0	arf,Ets	3.0
	403000	BE247275	Hs.151787	U5 snRNP-specific protein, 116 kD	TM	3.0
40	410008	AA079552		gb:zm20h12.s1 Stratagene pancreas (93720	TM,FG-GAP	3.0
	413268	AL039079	Hs.75256	regulator of G-protein signalling 1	RGS	3.0
	414080	AA135257	Hs.47783	ESTs, Weakly similar to T12540 hypotheti	TM	3.0
	426882	AA393108	Hs.97365	ESTs	TM	3.0
	427651	AW405731	Hs.18498	Homo sapiens cDNA FLJ12277 fis, clone M	TM	3.0
45	439444	AI277652	Hs.54578	ESTs	TM	3.0
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	TM	3.0
	444895	AI674383	Hs.301192	EST cluster (not in UniGene)	TM,ASC	3.0
	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone	TM	3.0
	414725	AA769791	Hs.120355	Homo sapiens cDNA FLJ13148 fis, clone N	TM,7tm_1	3.0
50	434241	AF118913	Hs.283607	hypothetical protein PRO3077	SS	3.0
	424962	NM_012288	Hs.153954	TRAM-like protein	TM	3.0
	411987	AA375975	Hs.183380	ESTs, Moderately similar to ALU7_HUMA	TM	3.0
	421977	W94197	Hs.110165	ribosomal protein L26 homolog	TM	3.0
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-conju	TM	3.0
55	407872	AB039723	Hs.40735	frizzled (Drosophila) homolog 3	TM,7tm_2,Fz,Frizzled	3.0
	442577	AA292998	Hs.163900	ESTs	TM	3.0
	416120	H46739		gb:yo14h02.s1 Soares adult brain N2b5HB5	TM	3.0
	443775	AF291664	Hs.204732	matrix metalloproteinase 26	TM,Peptidase_M10,7tm_1	3.0
	414664	AA587775	Hs.66295	Homo sapiens HSPC311 mRNA, partial cd	TM	3.0
60	457590	AI612809	Hs.5378	spondin 1, (f-spondin) extracellular matrix	SS	3.0
	418946	AI798841	Hs.132103	ESTs	TM	3.0
	457940	AL360159	Hs.30445	Homo sapiens mRNA full length insert cDN	TM,SPRY,7tm_1	3.0

TABLE 15B:

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

65	Pkey	CAT Number	Accession
	407615	1005404_1	AW753085 AW753082 AW054744 AW753107 AW753087
70	409073	109851_1	AA063458 AA063018 AI444822
	409745	115237_1	AA077391 AI347618 AI361453 AI088754 AW207491 AW960912 AA921874 AA286833 AA150722 BE152353 AW188822 BE152450
	410008	116812_1	AA079552 BE142525 BE142527
	414147	142127_1	BE091634
75	414315	143512_1	Z24878 AA494098 F13654 AA494040 AA143127
	416120	1571266_1	H46739 H51513 H19779
	419311	183793_1	AA689591 AW974261 AA235240 AI077451 AA631399 AW974262
	419546	185766_1	AA244199 AA244272 H57440
	422128	211994_1	AW881145 AA490718 M85637 AA304575 T05067 AA331991
80	427072	274884_1	H38046 W69645 AA397968 H38047
	428679	294049_1	AA431765 AA432015
	438993	457651_1	AA828995 AA834879 AI926361
	447197	711623_1	R36075 AI366546 R36167

TABLE 15C:

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495

Strand: Indicates DNA strand from which exons were predicted

NL_position: Indicates nucleotide positions of predicted exons

Pkey	Ref	Strand	NL_position
400881	2842777	Minus	91446-91603,92123-92265
401197	9719705	Plus	176341-176452
401435	8217934	Minus	54508-55233
404440	7528051	Plus	80430-81581
404939	6862697	Plus	175318-175476
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
405547	1054740	Plus	124361-124520,124914-125050
406137	9166422	Minus	30487-31058
406367	9256126	Minus	58313-58489
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

Table 16A lists about 92 genes up-regulated in mucinous-type ovarian cancer compared to normal adult tissues. These were selected as for Table 14A, except that the "average" ovarian cancer level was set to the 75th percentile amongst various mucinous-type ovarian cancers, and the tumor/normal tissue ratio was greater than or equal to 2.5.

TABLE 16A: ABOUT 92 UP-REGULATED GENES, MUCINOUS OVARIAN CANCER VERSUS NORMAL ADULT TISSUES

Pkey: Primekey

Ex. Accn: Exemplar Accession

UG ID: UniGene ID

Title: UniGene title

Prot. Dom.: Predicted protein domain structure

ratio: ratio tumor vs. normal tissues

Pkey	Ex. Accn	UG ID	Title	Prot. Dom.	ratio
430691	C14187	Hs.103538	ESTs		34.9
432938	T27013	Hs.3132	steroidogenic acute regulatory protein	START	28.0
418007	M13509	Hs.83169	Matrix metalloproteinase 1 (interstitial collag	SS,Peptidase_M10	22.3
451181	AJ796330	Hs.207461	ESTs		10.8
452838	U65011	Hs.30743	Preferentially expressed antigen in melanom		10.0
407638	AJ404672	Hs.288693	EST		9.3
450159	AJ702416	Hs.200771	ESTs, Weakly similar to CAN2_HUMAN		9.2
426890	AA393167	Hs.41294	ESTs		9.1
421155	H87879	Hs.102267	lysyl oxidase	SS,Lysyl_oxidase	8.9
437099	N77793	Hs.48659	ESTs, Highly similar to LMA1_HUMAN L	laminin_EGF	7.6
453866	AW291498	Hs.250557	ESTs		7.6
435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-rel		7.4
418738	AW388633	Hs.6682	solute carrier family 7, member 11		7.2
431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone P	RA	7.0
449579	AW207260	Hs.134014	prostate cancer associated protein 6		6.7
424586	NM_003401	Hs.150930	X-ray repair complementing defective repa		6.7
445891	AW391342	Hs.199460	ESTs		6.2
424717	H03754	Hs.152213	wingless-type MMTV integration site fami	wnt	6.1
452705	H49805	Hs.246005	ESTs		6.1
421285	NM_000102	Hs.1363	cytochrome P450, subfamily XVII (steroid	TM,p450	5.5
408562	AJ436323	Hs.31141	Homo sapiens mRNA for KIAA1568 prote		5.3
420159	AJ572490	Hs.99785	ESTs		5.3
451105	AJ761324	Hs.146343	gbw60b11.x1 NC1_CGAP_Co16 Homo s		5.2
409049	AJ423132	Hs.146343	ESTs		5.0
448674	W31178	Hs.154140	ESTs	TM	5.0
423811	AW295598	Hs.50895	homeo box C4		4.9
427469	AA403084	Hs.269347	ESTs		4.9
447033	AJ357412	Hs.157601	EST - not in UniGene	PH	4.9
424433	H04607	Hs.9218	ESTs		4.9
448811	AJ590371	Hs.174759	ESTs	TM	4.8
444330	AJ597655	Hs.49265	ESTs		4.8
409041	AB033025	Hs.50081	KIAA1199 protein		4.7
418735	N48769	Hs.44609	ESTs		4.5
416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	KH-domain	4.5
430073	U86136	Hs.232070	telomerase-associated protein 1	WD40	4.4
407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfotran	SS	4.4
422260	AA315993	Hs.105484	ESTs; Weakly similar to LITHOSTATHIN		4.4
421110	AJ250717	Hs.1355	cathepsin E	SS,asp	4.3
445676	AJ247763	Hs.16928	ESTs		4.2
430704	AW813091		gb:RC3-ST0186-240400-111-407 ST0186	Epimerase	3.8
414569	AF109298	Hs.118258	Prostate cancer associated protein 1	TM	3.8
438078	AJ016377	Hs.131693	ESTs		3.7
434032	AW009951	Hs.206892	ESTs		3.7
445657	AW612141	Hs.279575	ESTs	7tm_1	3.6
439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN		3.5
455666	BE065813		gb:RC2-BT0318-110100-012-a08 BT0318		3.5
448844	AJ581519	Hs.177164	ESTs		3.5
449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induced g	SS	3.5
438018	AK001160	Hs.5999	hypothetical protein FLJ10298	TM	3.4
458123	AW892676		gb:CM3-NN0004-280300-131-c12 NN0004		3.4
407385	AA610150	Hs.272072	ESTs, Moderately similar to ALU7_HUMA		3.4
424894	H83520	Hs.153678	reproduction 8	SS,UBX	3.3

	424639	AJ917494	Hs.131329	ESTs		3.3
	414083	AL121282	Hs.257786	ESTs		3.2
	426471	M22440	Hs.170009	transforming growth factor, alpha	SS,EGF	3.2
5	428927	AA441837	Hs.90250	ESTs		3.1
	406129	#(NOCAT)		0	TM,cNMP_binding	3.1
	452699	AW295390	Hs.213062	ESTs		3.1
	425842	AI587490	Hs.159623	NK-2 (Drosophila) homolog B	homeobox	3.1
	428976	AL037824	Hs.194695	ras homolog gene family, member I	ras	3.1
10	436396	AI683487	Hs.299112	Homo sapiens cDNA FLJ11441 fis, clone H	wnt	3.0
	454077	AC005952	Hs.37062	insulin-like 3 (Leydig cell)	SS,Insulin,ptkinase	3.0
	404253	#(NOCAT)		0	histone	2.9
	452461	N78223	Hs.108106	transcription factor	G9a,PHD	2.9
	429597	NM_003818	Hs.2442	a disintegrin and metalloproteinase domain	TM	2.9
15	413289	AA128061	Hs.114992	ESTs		2.9
	429703	T93154	Hs.28705	ESTs		2.9
	407829	AA045084	Hs.29725	Homo sapiens cDNA FLJ13197 fis, clone N		2.8
	424786	AW298244	Hs.293507	ESTs		2.8
	424086	AI351010	Hs.102267	lysyl oxidase	Lysyl_oxidase	2.8
20	408427	AW194270	Hs.177236	ESTs		2.7
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain		2.7
	446999	AA151520	Hs.279525	hypothetical protein PRO2605		2.7
	428819	AL135623	Hs.193914	KIAA0575 gene product		2.7
	422956	BE545072	Hs.122579	ESTs		2.7
25	428949	AA442153	Hs.104744	ESTs, Weakly similar to AF208855 1 BM-0		2.7
	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	TM,EGF	2.6
	420380	AA640891	Hs.102408	ESTs		2.6
	428651	AF196478	Hs.188401	annexin A10	TM,annexin	2.6
	417849	AW291587	Hs.82733	Nidogen 2	EGF,ldl_recept_b	2.6
30	453700	AB009426	Hs.560	apolipoprotein B mRNA editing enzyme, ca	TM	2.6
	417975	AA641836	Hs.30085	Homo sapiens cDNA: FLJ23186 fis, clone		2.6
	448756	AI739241	Hs.171480	ESTs		2.6
	425087	R62424	Hs.126059	ESTs		2.5
	444153	AK001610	Hs.10414	hypothetical protein FLJ10748	Kelch	2.5
35	443211	AI128388	Hs.143655	ESTs		2.5
	415263	AA948033	Hs.130853	ESTs	histone	2.5
	432867	AW016936	Hs.233364	ESTs	GSHPx	2.5
	438639	AI278360	Hs.31409	ESTs		2.5
	455386	AW935875		gb:QV3-DT0019-120100-055-d06 DT0019		2.5
40	419092	J05581	Hs.89603	mucin 1, transmembrane	TM,SEA	2.5
	452055	AI377431	Hs.293772	ESTs		2.5

TABLE 16B:

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

45	Pkey	CAT Number	Accession
	430704	322217_1	AW813091 AW206655 AA484440
50	451105	859083_1	AI761324 AW880941 AW880937
	455386	1287756_1	AW935875 BE069116 BE160261
	455666	1349545_1	BE065813 BE065788 BE065889 BE065832
	458123	479942_1	AW892676 AA853877 D44747

TABLE 16C:

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495

Strand: Indicates DNA strand from which exons were predicted

NL_position: Indicates nucleotide positions of predicted exons

60	Pkey	Ref	Strand	NL_position
	404253	9367202	Minus	55675-56055
	406129	9160131	Plus	2567-3056

Table 17A lists about 183 genes up-regulated in endometrioid-type ovarian cancer compared to normal adult tissues. These were selected as for Table 14A, except that the "average" ovarian cancer level was set to the 75th percentile amongst various endometrioid-type ovarian cancers, and the tumor/normal tissue ratio was greater than or equal to 2.5.

TABLE 17A: ABOUT 183 UP-REGULATED GENES, ENDOMETRIOID OVARIAN CANCER VERSUS NORMAL ADULT TISSUES

Pkey: Primekey

Ex. Accn: Exemplar Accession

UG ID: UniGene ID

Title: UniGene title

Prot. Dom.: Predicted protein domains

ratio: ratio tumor vs. normal tissue

80	Pkey	Ex. Accn	UG ID	Title	Prot. Dom.	ratio
	452838	U65011	Hs.30743	Preferentially expressed antigen in melanoma		38.9
	435094	AI560129	Hs.277523	EST		28.8
	428153	AW513143	Hs.98367	hypothetical protein FLJ22252 similar to SR		24.1
	428187	AI687303	Hs.285529	ESTs		23.9
	449034	AI624049		gb:ts41a09.x1 NCI_CGAP_Ut1 Homo sapi		19.9
	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	TM,Fz,Frizzled	15.7

412925	AI089319	Hs.179243	ESTs		15.7
438817	AI023799	Hs.163242	ESTs		13.6
447033	AI357412	Hs.167601	EST - not in UniGene	PH	13.5
433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMA		13.1
422956	BE545072	Hs.122579	ESTs		12.9
450451	AW591528	Hs.202072	ESTs		11.9
453964	AI961486	Hs.12744	ESTs	homeobox	11.5
442438	AA995998		gboss26b03.s1 NCI_CGAP_Kid5 Homo sa		11.4
431989	AW972870	Hs.291069	ESTs	SS	10.3
413623	AA825721	Hs.246973	ESTs		9.7
440901	AA909358	Hs.128612	ESTs		9.6
416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	KH-domain	9.6
421478	AI683243	Hs.97258	ESTs		9.3
448706	AW291095	Hs.21814	class II cytokine receptor ZCYTOR7	SS,Tissue_fac	9.2
410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone P		8.7
438993	AA828995		integrin; beta 8	SS,Integrin_B	8.7
427121	AI272815	Hs.173656	KIAA0941 protein	C2,	8.4
420610	AI683183	Hs.99348	distal-less homeo box 5	homeobox	8.1
427356	AW023462	Hs.97849	ESTs		8.0
446577	AB040933	Hs.15420	KIAA1500 protein		8.0
431118	BE264901	Hs.250502	carbonic anhydrase VIII	carb_anhydrase	7.5
448112	AW245919	Hs.301018	ESTs, Weakly similar to ALUB_HUMAN		6.9
451106	BE382701	Hs.25960	N-myc	HLH,Myc_N_term	6.6
449433	AI672096	Hs.9012	ESTs		6.3
453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1 (y		6.3
434636	AA083764	Hs.241334	ESTs		6.1
453688	AW381270	Hs.194110	Homo sapiens mRNA; cDNA DKFZp434C		5.9
422805	AA436989	Hs.121017	H2A histone family; member A	histone	5.8
400292	AA250737	Hs.72472	BMPR-1b, bone morphogenetic protein rec		5.7
443179	AB28402	Hs.6933	Homo sapiens cDNA FLJ12684 fis, clone N		5.6
418134	AA397769	Hs.86617	ESTs		5.5
452249	BE394412	Hs.61252	ESTs	homeobox	5.5
409269	AA576953	Hs.22972	Homo sapiens cDNA FLJ13352 fis, clone O	TM,UPF0016	5.5
413335	AB13318	Hs.48442	ESTs		5.4
441081	AB584019	Hs.169006	ESTs, Moderately similar to plakophilin 2b	PAX	5.4
428029	AB05840	Hs.293071	ESTs		5.3
419183	AB06669	Hs.89663	cytochrome P450, subfamily XXIV (vitami	p450	5.3
409094	AW337237		gbxw82f01.x1 NCI_CGAP_Pan1 Homo sa		5.2
432938	BT27013	Hs.3132	steroidogenic acute regulatory protein	START	5.1
410102	AW248508	Hs.279727	ESTs	SS	5.1
447835	AW591623	Hs.164129	ESTs		5.1
438202	AW169287	Hs.22588	ESTs		5.0
423992	AW898292	Hs.137206	Homo sapiens mRNA; cDNA DKFZp564H		5.0
425905	AB032959	Hs.161700	KIAA1133 protein	TM	5.0
452461	N78223	Hs.108106	transcription factor	G9a,PHD	4.9
430691	CI4187	Hs.103538	ESTs		4.8
441675	AB14329	Hs.5461	ESTs		4.7
425595	NM_005401	Hs.159238	protein tyrosine phosphatase, non-receptor	Band_41,Y_phosphatase	4.6
440340	AW895503	Hs.125276	ESTs		4.5
428579	NM_005756	Hs.184942	G protein-coupled receptor 64	TM	4.5
444783	AK001468	Hs.62180	ESTs	PH	4.4
451459	AI797515	Hs.270560	ESTs, Moderately similar to ALU7_HUMA		4.4
413395	AI266507	Hs.145689	ESTs		4.3
415263	AA948033	Hs.130853	ESTs	histone	4.2
413988	M81883	Hs.75668	glutamate decarboxylase 1 (brain, 67kD)	pyridoxal_deC	4.2
452030	AL137578	Hs.27607	Homo sapiens mRNA; cDNA DKFZp564N		4.1
418852	BE537037	Hs.273294	hypothetical protein FLJ20069		4.1
446431	R45652	Hs.153486	ESTs		4.1
434891	AA814309	Hs.123583	ESTs		4.0
415139	AW975942	Hs.48524	ESTs	G-patch	4.0
453197	AB16269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN A		4.0
447112	H17800	Hs.7154	ESTs		3.9
420633	NM_014581	Hs.99526	odorant-binding protein 2B	TM,lipocalin	3.9
459574	AT741122	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone N		3.9
415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 TFPI2	Kunitz_BPTI,G-gamma	3.9
414083	AL121282	Hs.257786	ESTs		3.7
442006	AW975183	Hs.292663	ESTs		3.7
409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblastoma	Thymosin	3.7
424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein,		3.7
456662	NM_002448	Hs.1494	msh (Drosophila) homeo box homolog 1 (fo	homeobox	3.7
429125	AA446854	Hs.271004	ESTs		3.6
435538	AB011540	Hs.4930	low density lipoprotein receptor-related pro		3.6
458861	AI630223	Hs.85339	gb:ad06g08.r1 Proliferating Erythroid Cells	PHD	3.5
418508	AA084248	Hs.124027	G protein-coupled receptor 39		3.5
423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE; H	AIRS,AIRS	3.4
437960	AI669586	Hs.222194	ESTs		3.4
400298	AA032279	Hs.61635	STEAP1	TM	3.4
407162	N63855	Hs.142634	zinc finger protein		3.4
408621	AI970672	Hs.46638	chromosome 11 open reading frame 8; beta		3.3
445829	AI452457	Hs.145526	ESTs		3.3
450262	AW409872	Hs.271166	ESTs, Moderately similar to ALU7_HUMA		3.3
457979	AA776555	Hs.270942	ESTs	TM	3.3
402606	#(NOCAT)				3.2
426471	M22440	Hs.170009	transforming growth factor, alpha	SS,EGF	3.2

5	430294	AI538226	Hs.135184	ESTs	polypreryl_synth	3.2
	448027	AI458437	Hs.177224	ESTs		3.2
	432619	AW291722	Hs.278526	related to the N terminus of tre	TBC	3.2
	413627	BE182082	Hs.246973	ESTs		3.2
	441377	BE218239	Hs.202656	ESTs		3.2
10	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone N		3.2
	433527	AW235613	Hs.133020	ESTs		3.2
	450171	AL133661	Hs.24583	hypothetical protein DKFZp434C0328	TM	3.2
	419807	R77402		gb:75f11.s1 Soares placenta Nb2HP Hom		3.1
	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	homeobox	3.1
15	419335	AW960146	Hs.284137	Homo sapiens cDNA FLJ12888 fis, clone N		3.1
	450480	XB2125	Hs.25040	zinc finger protein 239	zf-C2H2	3.1
	420149	AA255920	Hs.88095	ESTs		3.1
	413415	AA828282	Hs.34959	ESTs		3.1
	438966	AW979074		gb:EST391184 MAGE resequences, MAGP		3.1
20	431041	AA490967	Hs.105276	ESTs	Oxysterol_BP	3.1
	415245	N59650	Hs.27252	ESTs		3.0
	412140	AA218591	Hs.73625	RAB6 interacting, kinesin-like (rakinesin6)	kinesin	3.0
	431707	R21326	Hs.267905	hypothetical protein FLJ10422		3.0
	448816	AB033052	Hs.22151	KIAA1226 protein	homeobox	3.0
25	447866	AW444754	Hs.211517	ESTs		3.0
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2		3.0
	406997	U07807	Hs.194762	Human metallothionein IV (MTIV) gene, c		3.0
	433426	H69125	Hs.133525	ESTs	TM	3.0
	420440	NM_002407	Hs.97644	mammaglobin 2	Uteroglobulin	3.0
30	420181	AI380089	Hs.158951	ESTs		3.0
	458627	AW088842	Hs.97984	ESTs; Weakly similar to WASP-family pro		2.9
	452055	AI377431	Hs.293772	ESTs		2.9
	429663	M68874	Hs.211587	Human phosphatidylcholine 2-acylhydrolase	C2,PLA2_B	2.9
	415125	AF061198	Hs.301941	Homo sapiens mRNA for norepinephrine tr	TM,SNF	2.9
35	412708	R26830	Hs.106137	ESTs	TM,7tm_2,Rho_GDI	2.9
	451389	N73222	Hs.21738	KIAA1008 protein		2.9
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	DIX,RGS	2.9
	435185	AA669490	Hs.289109	dimethylarginine dimethylaminohydrolase		2.9
	428054	AI948688	Hs.266619	ESTs		2.9
40	448243	AW369771	Hs.77496	ESTs		2.9
	425723	NM_014420	Hs.159311	diclkopf (Xenopus laevis) homolog 4	SS	2.9
	432415	T16971	Hs.289014	ESTs		2.9
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin)		2.9
	400195			0		2.9
45	449874	AA135688	Hs.10083	ESTs		2.8
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	Hydrolase	2.8
	428093	AW594506	Hs.104830	ESTs		2.8
	409640	U78722	Hs.55481	zinc finger protein 165	TM,zf-C2H2,SCAN	2.8
	424169	AA336399	Hs.153797	ESTs	mlto_carr	2.8
50	409638	AW450420	Hs.21335	ESTs		2.8
	440048	AA897461	Hs.158469	ESTs; Weakly similar to envelope protein [2.8
	426890	AA393167	Hs.41294	ESTs		2.8
	452771	T05477		gb:EST03366 Fetal brain, Stratagene (cat93		2.8
	422505	AL120862	Hs.124165	ESTs; (HSA)PAP protein (programmed ce		2.8
55	416624	H69044		gb:77h05.s1 Soares fetal liver spleen 1NF	zf-C3HC4	2.8
	445870	AW410053	Hs.13406	syntaxin 18	TM	2.7
	441952	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone		2.7
	447342	AI199268	Hs.19322	ESTs; Weakly similar to HSA ALU SUBFAM		2.7
	421247	BE391727	Hs.102910	general transcription factor IIF, polypeptid		2.7
60	419752	AA249573	Hs.152618	ESTs		2.7
	410658	AW105231	Hs.192035	ESTs		2.7
	437698	R61837	Hs.7990	ESTs		2.7
	458027	L49054	Hs.85195	ESTs; Highly similar to t(3;5)(q25.1;p34) t		2.7
	438689	AW129261	Hs.250565	ESTs		2.7
65	439876	AI376278	Hs.100921	ESTs; Weakly similar to ALU7_HUMAN A	SCAN	2.7
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to M	pkinase	2.7
	436406	AW105723	Hs.125346	ESTs		2.7
	437938	AI950087		ESTs; Weakly similar to Gag-Pol polyprote		2.7
	419917	AA320068	Hs.93701	Homo sapiens mRNA; cDNA DKFZp434E		2.7
70	434836	AA651629	Hs.118088	ESTs		2.7
	448404	BE089973		gb:RC6-BT0709-310300-021-G07 BT0709		2.7
	444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-	WD40	2.7
	409757	NM_001898	Hs.123114	cystatin SN	SS,cystatin	2.6
	443775	AF291664	Hs.204732	matrix metalloproteinase 26	TM,Peptidase_M10,7tm_1	2.6
75	427961	AW293165	Hs.143134	ESTs		2.6
	426668	AW136934	Hs.97162	ESTs		2.6
	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	wnt	2.6
	434669	AF151534	Hs.92023	core histone macroH2A2.2	histone_A1pp,DUF27	2.6
	417389	BE260964	Hs.82045	Midkine (neurite growth-promoting factor 2	SS,TM,PTN_MK	2.6
80	451009	AA013140	Hs.115707	ESTs		2.6
	429774	AI522215	Hs.50883	ESTs	pkinase	2.6
	439951	AI347067	Hs.124636	ESTs	TM	2.6
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfera	AIRS,formyl_transf	2.5
	416806	NM_000288	Hs.79993	peroxisomal biogenesis factor 7	WD40	2.5
	420900	AL045633	Hs.44269	ESTs	Ald_Xan_dh_C	2.5
	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	Dihydroorolase	2.5
	459583	AI907673		gb:JL-BT152-080399-004 BT152 Homo sa		2.5
	440870	AI687284	Hs.150539	Homo sapiens cDNA FLJ13793 fis, clone T	PAX	2.5

446693	AW750373	Hs.42315	Homo sapiens cDNA FLJ13036 fis, clone N	TM	2.5
407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone M		2.5
400882			0		2.5
431322	AW970622		gbc:EST382704 MAGE resequences, MAGK		2.5
424081	NM_006413	Hs.139120	ribonuclease P (30kD)		2.5
451996	AW514021	Hs.245510	ESTs		2.5
403381	#(NOCAT)		0		2.5
419488	AA316241	Hs.90691	nucleophosmin/nucleoplasmin 3	SS	2.5
418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	TM,ABC_membrane	2.5

TABLE 17B:

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey	CAT Number	Accession
409094	1099611_1	AW337237 AW861642 AW861655 AW858008 AW857990 AW858007
416624	1604694_1	H69044 T47567 H75691 T50292
419807	188262_1	R77402 AA262462 AA250988 R06794
431322	331543_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188
437938	44573_2	AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875
		AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493
		AA927794 AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488954 AA283144 AI890387 AI950344 AI741346 AI689062
		AA282915 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539642
		AA642789 AA856975 AW505512 AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW855538 AA180009 AA337499
		AW961101 AA251669 AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996
		AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531
		H83488 W37181 W78802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005
438966	467436_1	AW979074 AA834841 AA828650
438993	467651_1	AA828995 AA834878 AI926361
442438	542469_1	AA959998 AI916584 R61781 T77332 F07756 F08149 F07647
448404	761515_1	BE089973 AI498612 AW805032
449034	794817_1	AI624049 AW117770 AI858360
452771	930983_1	T05477 T07855 AI917711
458861	798085_1	AI630223 AI630470

TABLE 17C:

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495

Strand: Indicates DNA strand from which exons were predicted

NL_position: Indicates nucleotide positions of predicted exons

Pkey	Ref	Strand	NL_position
400882	2842777	Minus	110431-110708
402606	9909429	Minus	81747-82094
403381	9438267	Minus	26009-26178

Table 18 lists 178 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode proteins that are secreted into blood, lymph, or other bodily fluids. These genes, and/or their protein products, in combination or alone, are ideal candidates for the early diagnosis of ovarian cancer. These were selected from 59680 probesets on the Affymetrix/Eos HuO3 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 2.4, and that are likely to encode secreted or extracellularly-shed proteins. The "average" ovarian cancer level was set to the 90th percentile amongst various ovarian cancer samples. The "average" normal adult tissue level was set to the 90th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various 149 non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 18: ABOUT 178 UP-REGULATED GENES ENCODING SECRETED PROTEINS, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES

Pkey: Primekey

Ex. Accn: Exemplar Accession

UG ID: UniGene ID

Title: UniGene title

ratio: ratio tumor vs. normal tissues

Pkey	Ex. Accn	UG ID	Title	ratio
428579	NM_005756	Hs.184942	G protein-coupled receptor 64	30.5
436982	AB018305	Hs.5378	spondin 1, (I-spondin) extracellular mat	29.4
427585	D31152	Hs.179729	collagen; type X; alpha 1 (Schmid metaph	27.0
423739	AA398155	Hs.97600	ESTs	22.7
418007	M13509	Hs.83169	Matrix metalloproteinase 1 (interstitial c	20.6
438993	M73780	Hs.52620	Integrin; beta 8	16.7
428664	AK001668	Hs.189095	similar to SALL1 (sal (Drosophila)-like	16.5
439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	16.5
400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin	16.2
421155	H87879	Hs.102267	lysyl oxidase	16.1
431989	AW972870	Hs.291069	ESTs	15.9
426635	BE395109	Hs.129327	ESTs	15.9
424581	M52062	Hs.150917	catenin (cadherin-associated protein), a	15.7
428976	AL037824	Hs.194695	ras homolog gene family, member l	15.1
416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	15.0
439706	AW872527	Hs.59761	ESTs	14.7
452055	AI377431	Hs.293772	ESTs	13.2
410102	AW248508	Hs.279727	ESTs	12.5
428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	12.4

402608	AA434329	Hs.36563	hypothetical protein FLJ22418	11.5
443715	AI583187	Hs.9700	cyclin E1	10.7
433496	AF064254	Hs.49765	VLCS-H1 protein	10.6
418601	AA279490	Hs.86368	calmegin	10.3
409269	AA576953	Hs.22972	Homo sapiens cDNA FLJ13352 fis,	10.1
445537	AJ245671	Hs.12844	EGF-like domain; multiple 6	9.9
427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor	9.7
428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	9.7
429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	9.5
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabidnes	9.4
407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	9.4
435509	AI458679	Hs.181915	ESTs	9.3
408908	BE286227	Hs.48915	serine/threonine kinase 15	9.0
433764	AW763676	Hs.39982	ESTs	9.0
445413	AA151342	Hs.12677	CGI-147 protein	8.7
438078	AI016377	Hs.131693	ESTs	8.6
447342	AI199268	Hs.19322	ESTs; Weakly similar to IIII ALU SUBFA	8.1
415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 TFP12	7.7
418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	7.5
426320	W47595	Hs.169300	transforming growth factor, beta 2	7.5
424001	W67883	Hs.137476	KIAA1051 protein	7.4
458861	NM_007358	Hs.31016	DNA-BINDING PROTEIN M96	7.3
425465	L18964	Hs.1904	protein kinase C, iota	7.2
425776	U25128	Hs.159499	parathyroid hormone receptor 2	7.1
424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic; stratum com	7.0
409178	BE393948	Hs.50915	kallikrein 5	6.8
433159	AB035898	Hs.150587	khesin-like protein 2	6.6
410530	M25809	Hs.64173	ESTs, Highly similar to VAB1	6.5
449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	6.5
422095	AI868872	Hs.288966	ceruloplasmin (ferroxidase)	6.4
425371	D49441	Hs.155981	mesothelin	6.4
448706	AW291095	Hs.21814	class II cytokine receptor ZCYTOR7	6.4
441081	AI584019	Hs.169006	ESTs, Moderately similar to plakophilin	6.4
447207	AA442233	Hs.17731	hypothetical protein FLJ12892	6.3
420440	NM_002407	Hs.97644	mammaglobin 2	6.2
457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	6.2
415139	AW975942	Hs.48524	ESTs	6.1
440870	AI687284	Hs.150539	Homo sapiens cDNA FLJ13793 fis, clone TH	6.0
417866	AW067903	Hs.82772	"collagen, type XI, alpha 1"	6.0
437960	AI669586	Hs.222194	ESTs	6.0
410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	5.9
433447	U29195	Hs.3281	neuronal pentraxin II	5.9
437099	N77793	Hs.48659	ESTs, Highly similar to LMA1	5.9
427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	5.9
422867	L32137	Hs.1584	cartilage oligomeric matrix protein	5.8
444478	W07318	Hs.240	M-phase phosphoprotein 1	5.7
445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 (Hsapi	5.7
453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	5.6
419917	AA320058	Hs.93701	Homo sapiens mRNA; cDNA DKFZp434E232	5.6
424539	L02911	Hs.150402	activin A receptor, type I	5.5
441845	AI222279	Hs.201555	ESTs	5.5
424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT	5.4
426514	BE816633	Hs.301122	bone morphogenetic protein 7 (osteogenic	5.4
425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	5.4
416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	5.3
445236	AK001676	Hs.12457	hypothetical protein FLJ10814	5.2
452930	AW195285	Hs.194097	ESTs	5.2
431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic protein	5.1
411571	AA122393	Hs.70811	hypothetical protein FLJ20516	5.1
432158	W33155	Hs.55548	ESTs, Weakly similar to unknown protein	5.0
447020	T27308	Hs.16988	hypothetical protein FLJ11046	5.0
443268	AI800271	Hs.129445	hypothetical protein FLJ12496	4.9
448133	AA723157	Hs.73769	folate receptor 1 (adult)	4.9
418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	4.8
428555	NM_002214	Hs.184908	Integrin, beta 8	4.8
427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	4.7
406400	AA343629	Hs.104570	kallikrein 8 (neuropilin/ovasin)	4.7
439024	R96696	Hs.35598	ESTs	4.6
426300	U15979	Hs.169228	delta-like homolog (Drosophila)	4.6
448027	AI458437	Hs.177224	ESTs	4.6
404996	NM_001333	Hs.87417	Cathepsin L2	4.6
443933	AI091631	Hs.135501	ESTs	4.5
409459	D86407	Hs.54481	low density lipoprotein receptor-related	4.4
414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosi	4.3
423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE	4.3
448275	BE514434	Hs.20830	synaptic Ras GTPase activating protein 1	4.2
419926	AW900992	Hs.93796	DKFZP586D2223 protein	4.1
420736	AI263022	Hs.82204	ESTs	4.1
419790	U79250	Hs.93201	glycerol-3-phosphate dehydrogenase 2 (mi	4.1
414343	AL036166	Hs.75914	coated vesicle membrane protein	4.0
450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	4.0
445808	AV655234	Hs.298083	ESTs	3.9
417389	BE260964	Hs.82045	Midkine (neurite growth-promoting factor	3.9
425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	3.8

430634	AI860651	Hs.26685	ESTs	3.8
431846	BE019924	Hs.271580	Uroplakin 1B	3.7
416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	3.7
407792	AI077715	Hs.39384	putative secreted ligand homologous to f	3.7
420585	AW505139	Hs.279844	hypothetical protein FLJ10033	3.7
407756	AA116021	Hs.38260	ubiquitin specific protease 18	3.6
411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	3.6
421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	3.5
431958	XG3629	Hs.2877	Cadherin 3, P-cadherin (placental)	3.5
410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	3.5
418793	AW382987	Hs.88474	prostaglandin-endoperoxide synthase 1 (p	3.5
422278	AF072873	Hs.114218	ESTs	3.5
431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	3.4
408730	AV660717	Hs.47144	DKFZP586N0819 protein	3.4
419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	3.3
421841	AA908197	Hs.108850	KIAA0936 protein	3.3
439864	AI720078	Hs.291997	ESTs	3.3
456546	AI690321	Hs.203845	ESTs, Weakly similar to TWIK-related aci	3.2
410687	U24389	Hs.65436	lysyl oxidase-like 1	3.2
414774	X02419	Hs.77274	plasminogen activator, urokinase	3.2
420552	AK000492	Hs.98806	hypothetical protein	3.1
421991	NM_014918	Hs.110488	KIAA0990 protein	3.1
418140	BE613836	Hs.83551	microfibrillar-associated protein 2	3.1
458924	BE242158	Hs.24427	DKFZP566O1646 protein	3.1
411789	AF245505	Hs.72157	Homo sapiens-mRNA; cDNA DKFZp564i19	3.1
434241	AF119913	Hs.283607	hypothetical protein PRO3077	3.1
422611	AA158177	Hs.118722	fucosyltransferase 8 (alpha (1,6) fucosy	3.1
409533	AW969543	Hs.21291	mitogen-activated protein kinase kinase	3.1
416391	AI878927	Hs.79284	mesoderm specific transcript (mouse) hom	3.1
412604	AW978324	Hs.47144	DKFZP586N0819 protein	3.1
425851	NM_001490	Hs.159642	glucosaminyl (N-acetyl) transferase 1, c	3.0
431259	NM_006580	Hs.251391	claudin 16	3.0
418557	BE140602	Hs.246645	ESTs	3.0
428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	3.0
419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	3.0
457590	AI612809	Hs.5378	spondin 1, (I-spondin) extracellular mat	2.9
418741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.9
426330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	2.9
417315	AI080042	Hs.180450	ribosomal protein S24	2.9
438777	AA825487	Hs.142179	ESTs, Weakly similar to ORF2 [M.musculus	2.9
442295	AI827248	Hs.224398	ESTs	2.9
428248	AI126772	Hs.40479	ESTs	2.9
403019	AA834626	Hs.66718	RAD54 (S.cerevisiae)-like	2.8
436252	AI539519	Hs.120969	Homo sapiens cDNA FLJ11562 fis	2.8
419488	AA316241	Hs.90691	nucleophosmin/nucleoplasmin 3	2.8
434288	AW189075	Hs.116265	ESTs	2.7
407872	AB009723	Hs.40735	frizzled (Drosophila) homolog 3	2.7
431611	U58766	Hs.264428	tissue specific transplantation antigen	2.7
443881	R64512	Hs.237146	Homo sapiens cDNA FLJ14234 fis, clone NT	2.7
453779	N35187	Hs.43388	ESTs	2.7
433068	NM_006456	Hs.288215	sialyltransferase	2.7
426841	AI052358	Hs.193726	ESTs	2.7
428778	AK000530	Hs.193326	fibroblast growth factor receptor-like 1	2.7
451346	NM_006338	Hs.26312	glioma amplified on chromosome 1 protein	2.6
443883	AA114212	Hs.9930	serine (or cysteine) proteinase inhibitor	2.6
420162	BE378432	Hs.95577	cyclin-dependent kinase 4	2.6
447149	BE299857	Hs.326	TAR (HIV) RNA-binding protein 2	2.6
433656	AW974941	Hs.282385	ESTs	2.6
408210	N81189	Hs.43104	ESTs	2.6
430651	AA961694	Hs.105187	kinesin protein 9 gene	2.5
422599	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)	2.5
421802	BE261458	Hs.108408	CGI-78 protein	2.5
446211	AI021993	Hs.14331	S100 calcium-binding protein A13	2.5
404029	W72881	Hs.266470	protocadherin beta 2	2.5
453012	T95804	Hs.31334	putative mitochondrial outer membrane pr	2.5
419981	AA897581	Hs.128773	ESTs	2.5
448153	Y10805	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	2.5
419220	AA811938	Hs.291759	ESTs	2.5
432180	Y18418	Hs.272822	RuvB (E coli homolog)-like 1	2.4
406850	AI624300	Hs.172928	collagen, type I, alpha 1	2.4
409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	2.4
421654	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	2.4
409956	AW103364	Hs.727	H.sapiens actin beta-A subunit (exon 2	2.4
407584	W25945	Hs.18745	ESTs	2.4
448796	AA147829	Hs.33193	ESTs, Highly similar to AC007228 3 BC372	2.4

Table 19 lists about 17 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode proteins that are secreted into blood, lymph, or other bodily fluids. These genes, and/or their protein products, in combination or alone, are ideal candidates for the early diagnosis of ovarian cancer. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 2.4, and that are likely to encode secreted or extracellularly-shed proteins. The "average" ovarian cancer level was set to the 90th percentile amongst various ovarian cancer samples. The "average" normal adult tissue level was set to the 90th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 19: ABOUT 17 GENES, AND COMBINATIONS THEREOF, USEFUL FOR DIAGNOSIS OF OVARIAN CANCER

UG ID: UniGene ID

Title: UniGene Title

% tumors: percent of tumors detected expressing gene

Single genes:

UG ID	Title	% tumors
Hs.5378	spondin 1, (I-spondin) extracellular matrix protein	77
Hs.12844	EGF-like-domain 6	86
Hs.151254	kallikrein 7 (chymolytic; stratum corneum)	66
Hs.97644	mammaglobin 2	73
Hs.155981	mesothelin (cytokine)	57
Hs.2258	Matrix Metalloproteinase 10 (Stromelysin 2)	21
Hs.50915	kallikrein 6	27
Hs.301122	bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)	54
Hs.79361	kallikrein 6 (neurosin, zyma)	38
Hs.83169	MMP 1 (interstitial collagenase)	23
Hs.72026	protease, serine, 21 (testisin)	16
Hs.39384	putative secreted ligand homologous to fix1	46
Hs.2719	epididymis-specific; whey-acidic protein type; four-disulfide core	91
Hs.155324	matrix metalloproteinase 11 (stromelysin 3)	11
Hs.1584	cartilage oligomeric matrix protein	25
Hs.169300	TGF beta 2	21
Hs.2250	leukemia inhibitory factor (cholesterol differentiation factor)	23

Exemplary Combinations:

EGF-like-domain 6 + mammaglobin 2	93
kallikrein 7 + mesothelin	71
mammaglobin 2 + bone morphogenetic protein 7	88
EGF-like-domain 6 + bone morphogenetic protein 7	91
kallikrein 7 + bone morphogenetic protein 7 + testisin	75
kallikrein 7 + mammaglobin 2 + mesothelin	84
mammaglobin 2 + bone morphogenetic protein 7 + TGF beta 2	91
EGF-like-domain 6 + bone morphogenetic protein 7 + MMP 1	95

Table 20A lists about 1025 genes up-regulated in ovarian cancer compared to normal adult tissues. Genes associated with ovarian cancer were selected from the 53462 probesets such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 5.0. The "average" ovarian cancer level was set to the 93rd percentile value amongst various ovarian cancer specimens; the "average" normal adult tissue level was set to the 96th percentile value amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Tables 20B-24B list accession numbers for Pkey's lacking UnigenelD's for tables 20A-24A. For each probeset is listed a gene cluster number from which oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Tables 20C-24C list genomic positioning for Pkey's lacking UnigenelD's and accession numbers in tables 20A-24A. For each predicted exon is listed genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

TABLE 20A:

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigenelD: UnigenelD number

UnigenelD Title: UniGene title

Pred. Protein Dom.: Predicted protein domain

R1: Ratio of tumor to normal body tissue

Pkey	ExAccn	UniGene ID	UnigenelD Title	Pred. Protein Dom.	R1
421296	NM_002666	Hs.103253	perlepin	perlepin,SS	32.5
453028	AB006532	Hs.31442	RacQ protein-like 4	DEAD, helicase_C, Fork_head	27.6
422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS	SS, TM, pkinase, fn3, jg	26.5
437897	AA770561	Hs.146170	hypothetical protein FLJ22969	SS, TM, zf-DHHC	26.3
446374	AA329256	Hs.24756	ESTs, Moderately similar to al		22.6
441021	AW578716	Hs.7644	H1 histone family, member 2		22.3
409518	BE384836	Hs.3454	KIAA1821 protein	SS	21.3
413436	AF238083	Hs.68061	sphingosine kinase 1	DAGKc	21.2
424420	BE614743	Hs.146688	prostaglandin E synthase	MAPEG, SS, TM, MAPEG	20.7
422645	L40027	Hs.118890	glycogen synthase kinase 3 alp	pkinaase, SS, Ets	20.7
422098	H03117	Hs.111497	similar to mouse neuronal prot	TM	20.2
429556	AW139399	Hs.98988	ESTs	SS, pkinase, PMP22, Claudin	20.1
436485	X59135	Hs.156110	immunoglobulin kappa constant	SS, jg, SS	19.9
423652	AF052122	Hs.130712	Homo sapiens clone 23929 mRNA	ABC1, SS, PID, PID	19.8
431773	BE409442	Hs.268557	pleckstrin homology-like domain	PH, SS, LIM, Troponin	19.4
422179	AF091619	Hs.112667	dynein, axonemal, intermediate	WD40, SS	19.3
420839	AI792682	Hs.282960	hypothetical protein MGC10870	SS, DS, UPF0139, Glyco_hydro	18.5
441355	BE384361	Hs.182885	ESTs, Weakly similar to JC5024	SS, TM, ank	18.5
424659	AW891298	Hs.331601	Homo sapiens, Similar to cyste	SS, Fork_head	18.4
439924	AI985897	Hs.125293	ESTs	SS	18.1
458814	AI498957	Hs.170861	ESTs, Weakly similar to Z195_H	SS, TM, jdl_recept, a_kdl_re	17.5
451643	M64437	Hs.234799	breakpoint cluster region	RhoGEF, RhoGAP, PH, C2	17.2
439108	AW163034	Hs.6467	synaptogyrin 3	Synaptogyrin, SS, TM, PDZ, WD	16.9
432945	AL043683		hypothetical protein FLJ10803	SS	16.8

5	410418	D31382	Hs.63325	transmembrane protease, serine	SS,TM,Idl_recept_a,trypsl	16.8
	438424	AJ912498	Hs.25895	hypothetical protein FLJ14996	SS,TM	16.7
	409435	AJ810721	Hs.95424	ESTs	SS	16.4
	418969	W33191	Hs.28907	hypothetical protein FLJ20258	SH3,SH3	16.2
	421612	AF161254	Hs.106196	8D6, antigen	Idl_recept_a,SS,TM	16.0
	456177	NM_012391	Hs.79414	prostate epithelium-specific E	Ets,SAM_PNT	15.7
	414837	U24266	Hs.77448	aldehyde dehydrogenase 4 fam1	aldadh	15.6
	432631	H08379	Hs.165563	hypothetical protein DKFZp434N	TM,DnaJ,UBA,ArlGap,homeob	15.5
10	454017	AW023617	Hs.347130	hypothetical protein FLJ22709	SS,TM,myosin_head,RA,DAG_	15.5
	401278			Target Exon	Band_41	15.4
	444804	AJ084452	Hs.22156	hypothetical protein FLJ21988	SS	15.4
	410259	AK000337	Hs.61485	hypothetical protein	GFO_IDH_MocA,GFO_IDH_MocA	15.4
	406620	M81105	Hs.146550	myosin, heavy polypeptide 9, n	myosin_head,Myosin_tail,	15.1
15	423081	AF262992	Hs.123169	sperm associated antigen 4	TM	14.9
	421495	AJ583067	Hs.149152	ESTs, Weakly similar to RHOP M		14.7
	416893	AA455588	Hs.62406	hypothetical protein FLJ22573	SS,rm,SS	14.7
	413244	AW955951	Hs.159265	kruppel-related zinc finger pr	SS,TM,BTB,Pep_M12B_propep	14.6
	406901	M14624		gb:Human 4-beta-galactosyltran		14.6
20	416006	AA324251	Hs.78950	branched chain keto acid dehyd	E1_dehydrog	14.6
	436186	BE390717	Hs.5074	similar to S. pombe dim1	DIM1,SS	14.5
	455557	AW995839		gb:CV4-BN0044-110200-108-h07 B	Metallophos	14.4
	434518	H56995	Hs.37372	Homo sapiens DNA binding pept	SS	14.2
	421489	AJ922821	Hs.32433	ESTs	SS,PI-PLC-X,PI-PLC-Y,C2	14.1
25	444441	AW613841	Hs.301394	hypothetical protein MGC3101		14.0
	435017	AA336522	Hs.12854	angiotensin II, type I recepto		14.0
	446572	AV659151	Hs.282961	ESTs		13.9
	434058	AA977935	Hs.127274	ESTs	SS	13.7
30	432481	AW451645	Hs.151504	Homo sapiens cDNA FLJ11973 fis	SS,Collagen,COLFI,TSPN	13.7
	447304	Z98883	Hs.18079	phosphatidylinositol glycan, c	SS,Peptidase_C2	13.6
	421182	AA284855	Hs.104480	ESTs	SS,Topoisomerase_I,Topois	13.3
	407767	W15398	Hs.38628	hypothetical protein	SS,zf-CCCH	13.3
	456642	AW451623	Hs.109752	putative c-Myc-responsive		13.3
	437457	AA757900	Hs.270823	ESTs, Weakly similar to S65657	SQS_PSY	13.2
35	430178	AW449612	Hs.152475	ESTs	SS	13.1
	430399	AJ916284	Hs.199671	ESTs	Sec7,PH	12.9
	436725	BE045223	Hs.136912	hypothetical protein MGC10796		12.9
	410219	T98226	Hs.171952	occludin	SS,TM,Occludin,BIR	12.7
40	442620	C00138	Hs.8535	Homo sapiens mRNA for KIAA1668	SS,RNA_pol_K	12.7
	439233	AA831893	Hs.292767	hypothetical protein FLJ23109	zf-C3HC4,TM,Sulfate_trans	12.7
	425018	BE245277	Hs.154196	E4F transcription factor 1	zf-C2H2,LIM,SS,Exo_endo_p	12.6
	423801	NM_015071	Hs.132942	GTPase regulator associated wi	RhoGAP,SH3,PH	12.6
	417826	T85105	Hs.15471	ESTs	SS,cadherin,Cadherin_C_te	12.6
45	409261	BE315042	Hs.19210	hypothetical protein MGC11308		12.6
	420568	F09247	Hs.247735	protocadherin alpha 10	cadherin,SS,TM,cadherin	12.6
	411570	BE144584	Hs.314341	ESTs		12.5
	430397	AJ924533	Hs.105607	bicarbonate transporter relate	HCO3_cotransp,SS,TM	12.5
	423767	H18283	Hs.132753	F-box only protein 2	F-box,SS,F-box,HORMA	12.4
50	441805	AA285136	Hs.301914	neuronal specific transcriptio	LIM,SS,LIM	12.3
	402365			Target Exon	SS,SS,TM,lg	12.2
	414371	AJ905865		thymosin, beta 4, X chromosome	Thymosin	12.2
	446780	R31107		gb:yb61g01.s1 Soares placenta		12.1
	428782	X12830	Hs.193400	interleukin 6 receptor	SS,TM,fn3,lg,SS,TM	12.1
	427695	R88483	Hs.172862	intron of Bicucal D homolog 1		12.1
55	400460			C11002253*gl 129091 sp P23267	SS,TM,SCAN,zf-C2H2,KRAB	12.0
	407341	AA918886	Hs.204918	ESTs, Weakly similar to ALU8_H	SS,TM	12.0
	424049	AB014524	Hs.138380	KIAA0624 protein	SS	11.9
	422872	BE326786	Hs.187646	ESTs	TM	11.9
	450800	BE395161	Hs.1390	proteasome (prosome, macropain	SS	11.8
60	428648	AF052728	Hs.188021	potassium voltage-gated channe	cNMP_binding	11.7
	432329	NM_002962	Hs.2960	S100 calcium-binding protein A	S_100,efhand,SS,efhand,S_	11.7
	417051	AJ675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis	CTF_NFI	11.6
	451195	U10492	Hs.438	mesenchyme homeo box 1	homeobox,SS	11.5
	417595	AA424317	Hs.6259	KIAA1698 protein	SS,TM,Glyco_hydro_31,Glyc	11.5
65	426500	NM_014638	Hs.170156	KIAA0450 gene product	SS	11.4
	433124	U51712	Hs.13775	hypothetical protein SMAP31		11.4
	444001	AJ095087	Hs.152299	ESTs, Moderately similar to S6		11.4
	419298	AA053479	Hs.89890	pyruvate carboxylase	CPSase_L_chain,PYC_OADA,H	11.4
	428593	AW207440	Hs.185973	degenerative spermatocyte (hom	SS	11.3
70	411408	U76666	Hs.69949	calcium channel, voltage-depen	Ion_trans,SS,TM	11.2
	404438			Target Exon		11.2
	427448	BE246449	Hs.2157	Wiskott-Aldrich syndrome (ecze	WH1,PBD,WH2,SS	11.2
	406230			Target Exon		11.2
	432125	AW972667	Hs.183006	Homo sapiens cDNA FLJ12300 fis	Band_41,ERM	11.2
75	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_H		11.1
	400206			Eos Control	SS,SS,Glyco_transf_43,COLF	11.1
	450503	R35917	Hs.301338	hypothetical protein FLJ12587	SS	11.0
	407605	W03512	Hs.6479	hypothetical protein MGC13272	SS,Sema,ptkinase,TIG,PSI,e	11.0
	432143	AL040183	Hs.123484	Homo sapiens, clone IMAGE-4178	SS,TM,cys_rich_FGFR	10.9
80	446839	BE091926	Hs.16244	mitotic spindle coiled-coil re	Troponin,SS,glycolytic_en	10.8
	443559	AJ076765	Hs.269899	ESTs, Moderately similar to AL	SS,TM,BIR,UQ_con	10.8
	411298	AW835858		gb:PM0-LT0017-031299-001-h07 L		10.8
	409557	BE182896	Hs.211193	ESTs		10.8
	435158	AW663317	Hs.65588	DAZ associated protein 1	rm,SS,rm	10.8
	444410	BE387360	Hs.33719	ESTs, Moderately similar to S6	SS	10.6

5	428948	BE514362		FK506-binding protein 3 (25kD)	FKBP,PIPSK	10.6
	424707	BE061914	Hs.10844	Homo sapiens cDNA FLJ14476 fis	SS,SS,TM,Sema	10.6
	416819	U77735	Hs.80205	p1m-2 oncogene	pklnase,SS,TM,OTU,K_tetra	10.5
	419341	N71463	Hs.118888	ESTs, Weakly similar to ALU1_H	SS,TM,UPF0016	10.5
	444359	AJ697160	Hs.143594	ESTs, Weakly similar to HS4L_H		10.5
	404333			C7001735-gi 7768636 dbj BAA85	vwd	10.5
	401210			C12000519-gi 7710046 ref NP_05		10.5
	457941	AJ004525	Hs.14587	ESTs, Weakly similar to AF1518	SS,TM,SS,TM	10.4
10	401594			NM_024817:Homo sapiens hypothe		10.3
	441790	AW294909	Hs.132208	ESTs		10.3
	444008	BE544855	Hs.236572	ESTs, Weakly similar to SFR4_H	SS,SS,SAC3_GANP	10.3
	438185	Y19188	Hs.320461	ESTs	SS	10.2
	432031	AF039196	Hs.272367	hairless protein (putative sin	jmiC	10.2
15	410471	T88872		gb:yd31a12s1 Soares fetal liv		10.1
	433573	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G	SS,TM,7tm_2,EGF,cdherin,	10.1
	417371	N74613	Hs.269149	ESTs		10.0
	428167	AA770021	Hs.16332	ESTs	SS,Jg,fn3	10.0
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis		10.0
20	412674	X04106	Hs.74451	catpalm 4, small subunit (30K)	efhand,SS,CAP_GLY	10.0
	425863	U43604	Hs.159901	Human unidentified mRNA, parti		9.9
	427239	NM_007274	Hs.8679	cytosolic acyl coenzyme A thio	Acyl-CoA_hydro,SS,TM	9.9
	429469	M64590	Hs.27	glycine dehydrogenase (decarbo	GDC-P,GDC-P	9.9
	420029	BE258876	Hs.94446	polyamine-modulated factor 1	aldo_ket_red,SS,TM,gla	9.8
25	445625	BE246743		hypothetical protein FLJ22635	SS,TM	9.8
	435339	AJ358300		ESTs	SS,ras	9.8
	407235	D20569	Hs.169407	SAC2 (suppressor of acin muta	SS,TM,Ribosomal_S13,Galac	9.8
	428758	AA433988	Hs.98502	CA125 antigen, muck 16	SS	9.8
	401349			inositol polyphosphate-1-phosp		9.7
30	437915	AJ637993	Hs.202312	Homo sapiens clone N11 Ntera2D		9.7
	424511	BE300512	Hs.193557	ESTs, Moderately similar to AL		9.7
	423366	Z80345	Hs.127610	acyl-Coenzyme A dehydrogenase,	Acyl-CoA_dh,Acyl-CoA_dh_M	9.7
	405143			NM_013432:Homo sapiens nuclea	ank,SS,TM,CPSF_A	9.6
	427497	AW139476	Hs.31240	ESTs		9.6
35	420423	AA827718	Hs.88218	ESTs	SS	9.6
	431512	BE270734	Hs.2795	lactate dehydrogenase A	ldh,ldh_C,SS,ldh	9.6
	450052	AJ681298	Hs.236524	ESTs	zf-C3HC4,zf-B_box	9.5
	412738	N34731	Hs.74562	slah binding protein 1; FBP in	homeobox	9.5
	444202	AL031685	Hs.12785	KJAA0939 protein	SS,TM,Na_H_Exchange,ABC2	9.5
40	451165	AJ340575	Hs.286084	MRIP-1 protein		9.5
	411450	H49619	Hs.127301	ESTs	SS,pkinase	9.5
	405371			NM_005569:Homo sapiens LIM do	kinase,LIM,PDZ	9.5
	435782	N49433	Hs.285737	Homo sapiens cDNA: FLJ20895 fi	SS,G6PD,Glucosamine_iso,G	9.5
	416866	AA297356	Hs.80324	serine/threonine protein phosph	Metallophos,Metallophos	9.4
45	405474			NM_001093:Homo sapiens acetyl	CPSase_L_chain,biotin_jip	9.4
	412837	AJ922293	Hs.58389	hypothetical protein MGC4090		9.3
	448133	AA723157	Hs.73769	folate receptor 1 (adult)	Folate_rec,SS	9.3
	431081	AA491594	Hs.75813	polycystic kidney disease 1 (a	SS,TM	9.3
	427640	AF058293	Hs.180015	D-dopachrome tautomerase	MIF,late_protein_L2,SS,GS	9.2
50	427435	AW938739	Hs.115412	hypothetical protein FLJ13881	SS	9.2
	407688	W25317	Hs.37616	Human D9 splice variant B mRNA		9.2
	407507	U73799		gb:Human dynactin mRNA, parti	SS,TM,HCO3_cotransp,CAP_G	9.2
	400833			C11000890-gi 3746443 gb AAC639	SS,TM,7tm_1	9.2
	422064	AW452589	Hs.335742	ESTs	TM	9.2
55	452434	D30934	Hs.29549	C-type lectin-like receptor-1	lectin_C,SS,TM	9.2
	451752	AB032997		KJAA1171 protein	TBC,SS,TM,pkinase,laminin	9.2
	432931	AF174487	Hs.293753	Bcl-2-related ovarian killer p		9.1
	407893	BE408359	Hs.43621	Homo sapiens, Similar to hypot	SS,SS,arf,ras,fn3,ras	9.1
	427397	AJ929685	Hs.177656	calmodulin 1 (phosphorylase ki	efhand,RmaAD,SS,efhand	9.1
60	405159			ENSP00000243337:CDNA FLJ13984		9.1
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45,	CDC45	9.1
	407058	X94563		gb:H.sapiens dbi/acbp gene exo	SS	9.0
	448045	AJ297436	Hs.20166	prostate stem cell antigen	SS,TM,UPAR_LY6,toxin,SS,T	9.0
	400772			NM_003105:Homo sapiens sortil	ldl_recept_a,ln3,ldl_rece	9.0
65	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp5	spectrin,SH3,PH,CH	9.0
	414391	BE409872		gb:601299655F1 NIH_MGC_21 Homo		9.0
	447867	AJ525268	Hs.164303	ESTs	TM	9.0
	422639	AJ929377	Hs.173724	creatine kinase, brain	ATP_gua_Ptrans,ATP_gua_Pt	9.0
70	454319	AW247736	Hs.101617	ESTs, Weakly similar to T32527	SS	8.9
	428781	AF164799	Hs.193384	putative 28 kDa protein		8.9
	408645	AW245738	Hs.109274	hypothetical protein MGC4365	SS,TM	8.9
	428527	AA454184	Hs.289014	ESTs		8.9
	406551	AJ559224		gb:ta32c02.x1 NCI_CGAP_U11 Hom		8.9
	430893	BE502068	Hs.282087	ESTs		8.8
75	414413	BE294877		gb:601174162F1 NIH_MGC_17 Homo	SS	8.8
	413726	AJ278465	Hs.75510	annexin A11	annexin,SS,annexin	8.8
	432211	BE274530	Hs.273333	hypothetical protein FLJ10986		8.8
	421694	BE387430	Hs.106880	bystin-like		8.8
	453683	AL079854	Hs.118598	Homo sapiens mRNA for KJAA1878	SS	8.8
80	456741	W37608	Hs.184492	ESTs	SS,pkinase	8.7
	442995	AA532511	Hs.288455	Homo sapiens cDNA: FLJ23270 fi		8.7
	415898	Z43379	Hs.177193	gb:HSC1AE111 normalized infant		8.7
	456977	AK000252	Hs.169758	hypothetical protein FLJ20245		8.7
	439532	AW410714	Hs.334437	hypothetical protein MGC4248	SS,TM,transmembrane4	8.7
	431462	AW583672	Hs.256311	granin-like neuroendocrine pep	SS	8.7

400128			Eos Control	TM,E1-E2_ATPase,HMA,Hydro	8.7
438582	AJ521310	Hs.283365	ESTs, Weakly similar to ALU5_H	SS	8.7
450958	AL137669	Hs.348012	Homo sapiens mRNA; cDNA DKFZp4		8.7
410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	SNF2_N,helicase_C,SS	8.7
415126	D60945		gb:HUM141D048 Clontech human f	SS,TM	8.7
418736	T18979	Hs.87908	Snf2-related CBP activator pro	SS,helicase_C,AT_hook,SS,	8.6
431157	AI823969	Hs.132678	ESTs	SS,MAPEG,SS,MAPEG	8.6
418843	AJ251016	Hs.89230	potassium intermediate/small c	TM,CaMBD,SK_channel,TM	8.6
419167	AI589535	Hs.94875	ESTs, Weakly similar to A35363	SS	8.6
432343	NM_002960	Hs.2961	S100 calcium-binding protein A	S_100,SS,efhand,S_100,eth	8.6
458440	AI095468	Hs.135254	Homo sapiens clone 1 thrombosp		8.6
407065	Y10141		gb:H.sapiens DAT1 gene, partia	SNF,SS,TM	8.6
452851	AW173191	Hs.213117	ESTs	SS,Sema	8.6
422418	AK001383	Hs.116385	hypothetical protein FLJ10521	RhoGEF	8.6
420836	AW958453	Hs.204959	hypothetical protein FLJ14886	SS,ras	8.6
455588	AJ129903	Hs.74669	vesicle-associated membrane pr	synaplobrevin,SS,TM	8.5
431974	AW972689	Hs.200934	ESTs	bZIP	8.5
410720	AF035154	Hs.65756	regulator of G-protein signal	RGS,G-gamma,DEP,SS,RGS,M	8.5
449751	AW207115	Hs.25555	ESTs		8.5
434030	AW162336	Hs.3709	low molecular mass ubiquinone-	SS	8.5
405557			Target Exon	Ets,SAM_PNT	8.5
443780	NM_012068	Hs.9754	activating transcription facto	bZIP,NTP_transf_2,SS,TBC	8.5
428860	U38291	Hs.194301	microtubule-associated protein	M	8.5
421901	AB014554	Hs.109299	protein tyrosine phosphatase,	SAM,SS,TM,mm,PDZ	8.4
401885			Target Exon	kinesin,SS,TM	8.4
449382	AI650407	Hs.197875	ESTs	SS,mm,zf-RanBP	8.4
432862	AW004958	Hs.236720	amionless protein	SS,MATH,zf-TRAF,zf-C3HC4	8.4
441363	AW450211	Hs.126825	ESTs, Weakly similar to A46302	SS,TM,HSP20,7tm_1	8.4
407363	AF035032	Hs.181125	gb:Homo sapiens clone MCA1L my	SS,Jg,SS,G_glu_transsept	8.4
425380	AA358389	Hs.32148	AD-015 protein	SS,TMLRR,P,Peptidase_S8	8.4
424893	AW295112	Hs.153648	Homo sapiens cDNA FLJ13303 fis	SS,SAM,SS,TM,7tm_1	8.4
424080	AW185983	Hs.139119	Homo sapiens cDNA FLJ10967 fis		8.3
439772	AL365406	Hs.10268	Homo sapiens mRNA full length		8.3
431765	AF124249	Hs.268541	novel SH2-containing protein 1	SH2,SS,TM	8.3
404365			Target Exon	SS	8.3
424310	AA338648	Hs.50334	testes development-related NYD	SS,TM	8.3
401935			Target Exon	PH	8.3
434796	AA812046		ESTs	SS,myb_DNA-binding,myb_DN	8.3
423098	AA321980	Hs.204682	ESTs		8.3
434552	AA639618	Hs.325116	Homo sapiens, clone MGC:2962,	SS	8.2
457082	AA470687	Hs.104772	ESTs	SS	8.2
432603	AA554920	Hs.105794	UDP-glucose:glycoprotein gluco	SS,TM	8.2
402445			Target Exon	tn3,SS,TM,BNR	8.2
422078	AW872378	Hs.120170	hypothetical protein FLJ21415	SS	8.2
418361	AW505368	Hs.12460	gb:U1-HF-BNO-alu-4-03-0-ULr1		8.2
431354	BE046956	Hs.251673	DNA (cytosine-5-)-methyltransf	SS,PWWP,PHD	8.2
403885			Target Exon	TM,Sulfate_transp,STAS,HM	8.2
450029	AW073380	Hs.287963	hypothetical protein FLJ10535	SS,Pyridox_oxidase,zf-C2H	8.2
452512	AW363486	Hs.337635	ESTs	SS	8.2
420138	BE268854	Hs.177729	ESTs	SS	8.2
439788	N71241	Hs.119275	ESTs	UQ_con	8.2
423662	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc	SS	8.2
449656	AA002008	Hs.188633	ESTs	PIPSK	8.1
452295	BE379936	Hs.28866	programmed cell death 10	SS,serpin	8.1
448650	AW769385	Hs.204891	ESTs	SS,IL8	8.1
446035	NM_006558	Hs.13565	Sam68-like phosphotyrosine pro	KH-domain	8.1
444406	AJ147237		Immunoglobulin heavy constant	SS	8.1
437215	AL117488		Human clone Z3564 mRNA sequenc	SS	8.1
408891	NM_005577	Hs.284284	ESTs, Highly similar to beta-1	SS,TM,DIX,PDZ,DEP,Disheve	8.1
400409	AF153341		Homo sapiens winged helixfork	SS	8.0
443801	AW206942	Hs.253594	intron of: trichorhinophalang	GATA	8.0
425281	AA444390	Hs.155482	hydroxyacyl glutathione hydrol	lactamase_B,SS	8.0
458216	AW024282	Hs.104938	hypothetical protein MGC15906		8.0
401507			C15000810":g j11131272 sp P793		8.0
401180			eukaryotic translation elongat	SS,TM,Ion_trans,IQ	8.0
454291	AW384847	Hs.213534	ESTs, Weakly similar to MUC2_H	SS,XRCC1_N,BRCT,lactamase	8.0
444014	AI095718	Hs.135015	ESTs		8.0
412128	AW894709		gb:CM1-NN0032-020500-212-d05 N	SCAN,zf-C2H2,KRAB	7.9
408363	NM_003389	Hs.44396	coronin, actin-binding protein	WD40	7.9
425694	U51333	Hs.159237	hexokinase 3 (white cell)	hexokinase,hexokinase2,he	7.9
425263	NM_001197	Hs.155419	BCL2-interacting killer (apopt	SS,TM,TspO_MBR	7.9
447045	AW392394		sorting nexin 17	SS,JF-2B,PP2C	7.9
457613	AA598869	Hs.173770	ESTs		7.9
410338	W03445	Hs.38205	gb:za05g11.1.r1 Soares melanocyt	pk kinase	7.9
402545			Target Exon		7.9
454246	AW245185	Hs.6996	ESTs		7.9
410079	U94362	Hs.58589	glycogenin 2	Glyco_transf_8	7.9
443678	AW009605	Hs.231923	ESTs	SS	7.9
404676			Target Exon		7.9
406649	AI569392		gb:tn86a02.x1 NCL CGAP_U02 Hom	Fork_head,SS,Fork_head	7.9
420230	AL034344	Hs.284186	forkhead box C1	SS,TM	7.8
413534	BE146961		gb:QV4-HT0222-011199-019-b12 H	PAP2,SS,TM	7.8
444628	U01120	Hs.242	glucose-6-phosphatase, catalyt	thioredo,Rho_GDI,gntR,SS,T	7.8
410839	NM_006849	Hs.66581	protein disulfide isomerase		7.8

444046	AJ360834	Hs.135094	ESTs	SS,GTP_EFTU,EFG_C,GTP_EFT	7.8
439501	AF086321	Hs.287452	Homo sapiens cDNA FLJ11760 fis	TM	7.8
415441	R13977	Hs.9634	ESTs		7.8
450461	BE408081	Hs.46736	hypothetical protein FLJ23476	SS	7.8
448993	AI471630		KIAA0144 gene product		7.8
400923			Target Exon	SS,TM,DUF289	7.8
440546	AI491994		gb:to07g09.x1 NCI_CGAP_UI2 Hom	SS,HATPase_c	7.8
419757	AA773820	Hs.63970	ESTs	SS,TM	7.8
451721	NM_006946	Hs.26915	spectrin, beta, non-erythrocyt	spectrin,PH,CH,SS,Peptida	7.8
458834	AI566883	Hs.196446	ESTs		7.8
422633	X56832	Hs.118804	enolase 3, (beta, muscle)	enolase,SS,TM,kinesin,FHA	7.7
438452	AI220911	Hs.288959	hypothetical protein FLJ20920	SS	7.7
421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054	asp,SS,TM,ion_trans,K_tet	7.7
434743	AI363410		ribosomal protein S18	SS,TM	7.7
450635	AW403954	Hs.25237	mesenchymal stem cell protein	4HBT	7.7
442394	R62926	Hs.285193	ESTs		7.7
434333	AA186733	Hs.292154	stromal cell protein		7.7
427221	L15409	Hs.174007	von Hippel-Lindau syndrome	VHL,TM	7.7
429099	BE439952	Hs.196177	phosphorylase kinase, gamma 2	pkinase,SS,SNF2_N,helicas	7.7
444670	H58373	Hs.332938	hypothetical protein MGC5370	SS,zf-RanBP,MDM2	7.7
449495	AI652833		gb:wb22c11.x1 NCI_CGAP_GC6 Hom	SS	7.7
444607	AW405635	Hs.293687	ESTs	SS,PI-PLC-X,PH,PI-PLC-Y,C	7.7
449125	AI671439	Hs.196029	Homo sapiens mRNA for KIAA1657	TIMP	7.7
447151	AI022813	Hs.92679	Homo sapiens clone CDABP0014 m	SS,TM,LRR,aminotran_1_2	7.6
446626	WZ7670	Hs.55613	hypothetical protein FLJ22531		7.6
430432	AB037758	Hs.241419	KIAA1337 protein	TM,Patched,TM	7.6
401822			C17001422:gil2695866[emb]CAA75		7.6
428909	AI190714	Hs.98945	ESTs		7.6
414534	BE257293	Hs.76366	BCL2-antagonist of cell death	SS,hormone_rec,zf-C4	7.6
421620	AA446183	Hs.91885	ESTs, Weakly similar to I55214		7.6
441650	AI261960	Hs.132545	ESTs	SS,TM,KOW	7.6
442232	AI357813	Hs.337460	ESTs, Weakly similar to A47582	SS,TM,TGFb_propeptide,TGF	7.6
439539	BE348395	Hs.121589	ESTs	SS,Fork_head	7.5
400286			C16000922:gil7499103[pir]T209	TM,ABC_tran,ABC_membrane	7.5
452833	BE559681	Hs.30736	KIAA0124 protein	WD40	7.5
417390	AA196552	Hs.85852	hypothetical protein MGC3169		7.5
427721	AI582843	Hs.180455	RAD23 (S. cerevisiae) homolog	ubiquitin,UBA,integrin_B,	7.5
450716	T57758	Hs.10255	ESTs		7.5
407435	AF211976		gb:Homo sapiens LENG9 mRNA, pa		7.5
413956	AI821351	Hs.193133	ESTs, Weakly similar to ALU7_H		7.5
427899	AA829286	Hs.332053	serum amyloid A1	SS,SAA_proteins,SS,SAA_pr	7.5
406495			Target Exon	SRCR,TM,Acetyltransf	7.5
430387	AW372884	Hs.240770	nuclear cap binding protein su	rm,SS,TM,rm	7.5
408601	U47928	Hs.86122	protein A	SS,7tm_1,SS,Ig,WD40,zf-UB	7.5
424364	AW383226	Hs.163834	ESTs, Weakly similar to G01763	SS,ras	7.4
409832	AW963293		gb:EST375366 MAGE resequences,	SS	7.4
448043	AI458653	Hs.201881	ESTs	PHD	7.4
421148	AF008936	Hs.102178	synixin 16	Syntaxin,SS,Peptidase_M17	7.4
420970	AA305079	Hs.1342	cytochrome c oxidase subunit V	COX5B	7.4
419295	BE397712	Hs.144027	ESTs	myb_DNA-binding,myb_DNA-b	7.4
448330	AL036449		ESTs		7.4
419639	AK001502	Hs.91753	hypothetical protein		7.4
431488	AB037785	Hs.257594	KIAA1364 protein	SS,CH,LIM,SS	7.4
456467	AF064804		suppressor of Ty (S.cerevisiae)		7.4
448615	AI910868	Hs.212957	ESTs	SS	7.4
427433	D82070	Hs.177972	chromosome 4 open reading fram	SS,pkinase	7.4
441076	N49809	Hs.11187	Homo sapiens, clone IMAGE:3343		7.4
452554	AW452434	Hs.58006	ESTs, Weakly similar to ALU5_H	SS,PAS,HLH	7.4
411448	AA178955	Hs.271439	ESTs, Weakly similar to I38022	rm,POZ	7.4
442318	AI792199		ESTs	SS,zf-C2H2	7.4
426055	AW961959	Hs.96940	ESTs		7.4
412935	BE267045	Hs.75064	tubulin-specific chaperone c	SS,TM,transmembrane4	7.4
403748			Target Exon	TM	7.4
447282	AI989963	Hs.197505	ESTs	TM	7.3
422305	AI928242	Hs.293438	ESTs, Highly similar to AF1984	SS	7.3
416472	AA180756	Hs.340316	ESTs, Moderately similar to AL	zf-C2H2	7.3
427273	AW139032	Hs.107376	hypothetical protein DKFZp434N	SS,SS,TM	7.3
412265	AA101325	Hs.86154	hypothetical protein FLJ12457	UPP_synthetase,HMG14_17	7.3
447859	AK002194	Hs.19851	peroxisomal biogenesis factor		7.3
432747	NM_014404	Hs.278907	calcium channel, voltage-depen	PMP22_Claudin,SS,TM,PMP22	7.3
405727	AI219282	Hs.2186	eukaryotic translation elongat	SS,G-gamma	7.3
404199			ENSP00000211797*Helicase SKI2	SS,RasGAP,PH,SS,PHD	7.3
445434	BE391690	Hs.9265	hypothetical protein FLJ20917	SS,PWWP,Exonuclease,tipoc	7.2
428550	AW297880	Hs.98661	ESTs	SS,homobox,homobox	7.2
454718	AW815144		gb:QV4-ST0212-120100-075-d10 S	SS,ATP-synt_ab,ATP-synt_La	7.2
407686	AW901268	Hs.126043	chromosome 21 open reading fra	SS,TM,ISK_Channel	7.2
418304	AA215702		gb:zr97g10.x1 NCI_CGAP_GCB1 Ho	serpin	7.2
424263	M77640	Hs.1757	L1 cell adhesion molecule (hyd	fn3,Ig,IRK,SS,TM,fn3,Ig,R	7.2
407581	R48402	Hs.173508	P3ECSL	SS,TM,7tm_1	7.2
430746	AW977370	Hs.222012	ESTs	SS	7.2
402651			NM_000721*Homo sapiens catciu	ion_trans	7.2
407323	AA181183	Hs.143504	gb:zps7c02.s1 Stratagene endot	SS,Ribosomal_S4e,ubiquiti	7.2
407619	AL050341	Hs.37165	collagen, type IX, alpha 2	SS,Collagen,SS,Collagen	7.2
434035	AI762074	Hs.204769	ESTs, Weakly similar to T28770	SS,TM	7.2

	400419	AF084545		Target	EGF,lg,lectin_c,sushi,XII	7.2
	424241	AW955948	Hs.182339	Homo sapiens pyruvate dehydrog	SAM_PNT	7.2
	445837	AI261700		ESTs		7.2
5	427725	U66839	Hs.180533	mitogen-activated protein kina	pkinae	7.1
	421879	AW955907		gb:EST371677 MAGE resequences,		7.1
	418285	H68616	Hs.293756	ESTs	SS,EMP24_GP25L	7.1
	442893	H78133		gb:yu86c11.s1 Soares fetal liv		7.1
	437829	AI358522	Hs.103834	ESTs		7.1
10	450873	BE464016	Hs.238956	ESTs	SS,zf-C2H2,rm	7.1
	433396	AJ742071	Hs.133205	ESTs	SS,TM	7.1
	415595	R54144	Hs.278707	chromosome 21 open reading fra	SS	7.1
	436629	AA861011	Hs.249795	ESTs	TM	7.1
	414593	BE386764		gb:601273249F1 NIH_MGC_20 Homo		7.1
	422765	AW409701	Hs.1578	baculoviral IAP repeat-contain	BIR,TK,SS,TM	7.1
15	419823	AW271708	Hs.118918	ESTs, Weakly similar to M2OM_H	SS,TM	7.1
	405247			Target Exon	SS	7.1
	455778	BE088746		gb:CM2-BTD693-210300-123-409 B		7.1
	431005	AA490544	Hs.127269	ESTs, Weakly similar to T02345	WD40	7.1
20	435717	AF227905	Hs.105794	UDP-glucose:glycoprotein gluco	Glyco_transf_8	7.1
	405113			Target Exon	SS	7.1
	428070	T63918	Hs.182313	retinol-binding protein 2, cel	lipocalin, lipocalin, WD40	7.1
	429029	AA443443	Hs.85524	for muscle specific ring finger	SS	7.1
	430354	AA954810	Hs.239784	human homolog of Drosophila Sc	SS,TM,Ig	7.0
25	412970	AB026438	Hs.177534	dual specificity phosphatase 1	Rhodanese,DSPc,SS,DSPc	7.0
	438701	AA937112	Hs.207788	ESTs	TM,sushi	7.0
	454756	AW619273		gb:CM2-ST0284-061299-046-a12 S		7.0
	401264			C180000907:glj6678656[ref]NP_0	SS,laminin_Nterm,laminin_	7.0
	408080	AW149754	Hs.248652	ESTs, Weakly similar to T00273	SS	7.0
30	418641	BE243136	Hs.86947	a disintegrin and metalloprote	disintegrin, Reprolysin,Pe	7.0
	413402	AA743534	Hs.250861	ESTs		7.0
	423790	BE152393		gb:CM2-HT0323-171189-033-a08 H	SS	7.0
	450688	AW272352	Hs.60450	ESTs	TM	7.0
	405928			Target Exon	SS,cystatin,Coprogen_oxid	7.0
35	454438	AA224053		cell division cycle 27	SS,TM,SPRY,7tm_3,ANF_rece	7.0
	407281	AJ307226	Hs.164421	ESTs	SS	6.9
	423386	AW136098	Hs.314081	ESTs	SS,WD40,EPO_TPO	6.9
	459360	BE384526	Hs.25734	gb:601277913F1 NIH_MGC_20 Homo		6.9
	420187	AK001714	Hs.95744	hypothetical protein similar t	ank,TM	6.9
40	431549	AA507036	Hs.170673	ESTs		6.9
	423384	AL133632	Hs.127808	Homo sapiens mRNA; cDNA DKFZp4		6.9
	454577	AW809272		gb:MR4-ST0118-040100-034-c08_1		6.9
	438118	AW753311		ESTs	SS,lipocalin	6.9
	416233	AA176633		gb:zfp13g01.s1 Stralagene fetal		6.9
45	417012	N38970	Hs.194214	ESTs		6.9
	452399	BE513301	Hs.29344	hypothetical protein, clone 24	SS,perilipin	6.9
	439963	AW247529	Hs.6793	platelet-activating factor ace	PAF-AH_Ib,Lipase_GDSL,SS,	6.9
	418416	U11700	Hs.84999	ATPase, Cu transporting, beta	E1-E2_ATPase,HMA,Hydrolas	6.9
	404956			C10032107:glj6912582[ref]NP_03	PI3_P14_kinase,PI3K_C2,PI	6.9
50	451606	AA018791	Hs.7945	AIE-75 binding protein protein	SS	6.9
	438525	AW368528	Hs.100855	ESTs	SS	6.9
	400908			C18000324:glj12229928[sp]Q9PTW		6.9
	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA13	SS	6.8
	406834	AJ318680		gb:ta49g09.x1 NC1_CGAP_Lu25 Ho		6.8
55	414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/m	SS,COesterase,SS,COestera	6.8
	424198	AB029010	Hs.143026	KIAA1087 protein	SS,TM,Na_Ca_Ex_Cab-beta,	6.8
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytop	SS,PABP,rm,kinase,14-3-	6.8
	439605	AF086431	Hs.22380	ESTs	SS,TM	6.8
	432284	AA532807	Hs.105822	ESTs	SS,TM,kinase	6.8
60	421904	BE143533	Hs.109309	hypothetical protein FLJ20035		6.8
	443136	NM_001440	Hs.9018	exostoses (multiple)-like 3	Exostosis,SS,TM	6.8
	421758	BE397336	Hs.1422	Gardner-Rasheed feline sarcoma	SH2,SH3,kinase	6.8
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	PHD,Virus_HS,SS,IChn_chan	6.8
	400205			NM_006265:Homo sapiens RAD21	SS	6.8
65	434315	AW196608		ESTs		6.8
	418184	AA367375		Homo sapiens cDNA FLJ14015 fis		6.8
	431898	AK000020	Hs.272018	hypothetical protein FLJ20013		6.7
	438627	AJ087335	Hs.123473	ESTs	TM,Reticulon	6.7
	409649	AA159216	Hs.55505	hypothetical protein FLJ20442	Y_phosphatase,DSPc,TM	6.7
70	429712	AW245825	Hs.211914	ENSP00000233627:NADH-ubiquino	oxidored_q6,SS,TM,rm	6.7
	456886	AW089093	Hs.144996	ESTs, Weakly similar to I38022		6.7
	427461	AA531527	Hs.332040	hypothetical protein MGC13010	SS,TM,ACAT,LRR	6.7
	434000	BE002846	Hs.112984	ESTs		6.7
	432530	AF131786	Hs.278303	Homo sapiens clone 25220 mRNA	SS,proteasome	6.7
75	436141	AA970001	Hs.150319	Homo sapiens, clone IMAGE:3610	SS,TM	6.7
	441794	AW197794		ESTs		6.7
	450287	AW291483	Hs.255909	ESTs		6.7
	441523	AW514263		ESTs, Weakly similar to ALUF_H	SS	6.7
	452798	AJ918771	Hs.257170	ESTs	SS,TM,TNFR_c6	6.7
80	451937	AF119664	Hs.27299	transcriptional regulator prot	SS,Integrin_B,fn3,Cabx-be	6.7
	421417	AA291004	Hs.326088	ESTs		6.7
	440317	BE561888		gb:601346093F1 NIH_MGC_8 Homo		6.7
	421321	NM_005309	Hs.103502	glutamic-pyruvate transaminase	aminotran_1_2,SS,TM,LRR	6.7
	444904	AW452054	Hs.161139	ESTs		6.7
	449730	R72290	Hs.117557	ESTs, Weakly similar to I38022	RasGAP,thyroglobulin_1,RJ	6.7

5	450622	AJ560285	Hs.58210	ESTs, Highly similar to ITIH4_H	SS,TM,vwa	6.7
	425424	NM_004954	Hs.157199	ELKL motif kinase	pk kinase,KA1,UBA,SS	6.7
	435864	AL036499	Hs.188491	ESTs		6.7
	410397	AF217517	Hs.63042	DKFZp564J157 protein	SS,homeobox,UPF0160,DUF23	6.7
	454262	AW612232	Hs.254835	ESTs	SS,TM,voltage_CLC,C8S	6.7
	453023	AW028733	Hs.31439	serine protease inhibitor, Kun	Kunitz_BPTI,SS,TM,ion_tra	6.6
	419157	AA234540	Hs.23871	ESTs	pk kinase	6.6
	412464	T78141	Hs.22826	ESTs, Weakly similar to I55214	SS,cadherin,crystal	6.6
10	407332	AI801565	Hs.200113	Homo sapiens cDNA FLJ11379 fls	SS,adh_short,Transglutami	6.6
	456643	AW751497	Hs.98370	cytochrome P450, subfamily IIS		6.6
	411490	R39474		gb:YH55b09.1 Soares placenta	SS	6.6
	455885	BE153524		gb:PM0-HTD339-241199-002-C03 H	SS,PK kinase	6.6
	438857	AI627912	Hs.130783	Forssman synthetase	SS,RA,RasGEF,RasGEFN	6.6
15	420307	AW502869	Hs.66219	ESTs	SS,TM	6.6
	453496	AA442103	Hs.33084	solute carrier family 2 (faci)	sugar_tr,SS,TM	6.6
	419182	AA234822	Hs.66147	ESTs	SS,TM,ion_trans,ion_trans	6.6
	406301			Target Exon	TM	6.6
	433938	AF161538	Hs.284292	ubiquitin-cytochrome c reducta	TM	6.6
20	448980	AL137527	Hs.269038	hypothetical protein MGC4126		6.6
	454095	AW178110	Hs.191705	gb:IL3-HT0061-010999-013-H04 H	SS,TM,homeobox,trypsin,PD	6.6
	459702	AI204995		gb:an03c03.x1 Stratagene schiz		6.6
	422201	NM_001505	Hs.113207	G protein-coupled receptor 30	7tm_1,SS,TM	6.6
	406779	AA412048	Hs.279574	CGI-39 protein; cell death-reg	SS,SS	6.6
25	404149			C602509*gi5031885[ref]NP_00	SS,TM,kringle	6.6
	418576	AW968159	Hs.302740	Epithelial calcium channel 2,	SS,TM	6.6
	421363	NM_001381	Hs.103854	docking protein 1, 62kD (downs	PH,IRS,TM,PH,IRS,trypsin,	6.6
	458919	AI681567	Hs.13349	KIAA0756 protein	TM	6.6
	427502	AI811865	Hs.7133	Homo sapiens, clone IMAGE:3161	SS,TM,ABC_tran,Glyco_tran	6.5
30	412289	AW935967	Hs.170162	KIAA1357 protein	SS	6.5
	447105	AW377610	Hs.11123	DKFZP564G092 protein	SS,TM	6.5
	444672	Z95636	Hs.11669	laminin, alpha 5	laminin_EGF,laminin_G,EGF	6.5
	429299	AI620463	Hs.347408	hypothetical protein MGC13102	SS,TM,gla	6.5
	420003	AA256906	Hs.111364	ESTs, Weakly similar to ubiqui	SS,TM	6.5
35	431849	AI670823	Hs.85573	hypothetical protein MGC10911	SS,TM	6.5
	430396	D49742	Hs.241363	hyaluronan-binding protein 2	trypsin,kringle,EGF,SS	6.5
	437662	AA765387		ESTs	WD40,RCC1,SPRY	6.5
	436543	NM_002212	Hs.5215	integrin beta 4 binding protai	elf8	6.5
40	405375			CX000741*gi4885461[ref]NP_00	SS,TM	6.5
	430116	AA465350	Hs.119400	ESTs	SS,TM,adh_short	6.5
	406109			Target Exon		6.5
	414871	BE549179	Hs.29008	gb:601078714F1 NIH_MGC_12 Homo		6.5
	440656	AI979248	Hs.148221	ESTs		6.5
	438951	U51336	Hs.6453	inositol 1,3,4-triphosphate 5/	SS,oxidored_nitro,SS	6.5
45	405376			Target Exon	SS,TM	6.5
	426925	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fl	SS	6.5
	400500			Target Exon		6.5
	408294	BE141732		gb:QV0-HT0101-061099-032-e07 H	Ammonium_transp	6.4
	447904	AW206303		ESTs		6.4
50	439211	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fl	SS	6.4
	426828	NM_000020	Hs.172670	activin A receptor type II-like	pk kinase,Activin_rec,SS,T	6.4
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.	SS,TM	6.4
	442146	R52599		gb:yg81g01.r1 Soares infant br	TM	6.4
	425041	AI377150	Hs.150914	ESTs	SS	6.4
55	457584	AA147979	Hs.285005	mitochondrial import receptor	Josephin	6.4
	435449	AA682379	Hs.303460	EST		6.4
	406284			Homo sapiens mRNA full length		6.4
	425944	AK000864	Hs.164256	hypothetical protein FLJ20657		6.4
	453367	AW732847	Hs.70573	PKC-1-related HIT protein	SS,TM	6.4
60	419725	U66048	Hs.92683	Homo sapiens clone 161455 brea		6.4
	412452	AA215731		suppression of tumorigenicity	SS	6.4
	421273	AJ245416	Hs.103106	U6 snRNA-associated Sm-like pr	Sm,SS,IRNA-syn1,GST_C,G	6.4
	432746	AA564512	Hs.24301	polymerase (RNA) II (DNA direc	SS,TM,EF1B0	6.4
	429398	AA452239		KIAA0970 protein		6.4
65	404430			C8000066*gi10432395[emb]CAC1	SS	6.4
	427339	AI734109	Hs.97984	SRY (sex determining region Y)		6.4
	436389	AI811706		CHMP1.5 protein		6.4
	428890	AA525228	Hs.303293	ESTs, Moderately similar to I5		6.4
	445333	BE537641	Hs.44278	hypothetical protein FLJ12538	SS	6.4
70	414756	AW451101	Hs.159489	ESTs, Moderately similar to JC	hexokinase2,hexokinase	6.4
	423847	U16997	Hs.133314	RAR-related orphan receptor C	hormone_rec,zf-C4,SS,TM,h	6.4
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (mus	PGAM,BRCT,RNA_pol_L	6.4
	439569	AW602168	Hs.222399	CEGP1 protein	CUB,EGF,SS	6.4
	457274	AW674193	Hs.227152	mannan-binding lectin serine p	SS,TM,SS,TM,Claudin_Ig_c	6.4
75	444550	BE250716	Hs.87614	ESTs	SS	6.4
	407198	H91679		gb:yy04a07.s1 Soares fetal liv	BIR	6.4
	423228	AL137491	Hs.125511	Homo sapiens mRNA; cDNA DKFZp4	SS,TM,sushi	6.4
	422682	W05238	Hs.94316	ESTs, Weakly similar to T31613	SS,TM,DEAD,helicase_C,Lam	6.3
	447887	AA114050	Hs.19949	caspase 8, apoptosis-related c	ICE_p20,DED,ICE_p10	6.3
80	400137			Eos Control		6.3
	408784	AW971350	Hs.63386	ESTs	SS	6.3
	435028	AW193035	Hs.187370	ESTs		6.3
	438113	AI467908	Hs.8882	ESTs	SS,TM,7tm_1	6.3
	417810	D28419	Hs.82609	hydroxymethylbilane synthase	Porphobil_deam	6.3
	436050	AI057205	Hs.14584	ESTs		6.3

5	403672			C4001244:g 539933 pir A61275	tubulin,TM	6.3
	448269	BE622358	Hs.61260	hypothetical protein FLJ13164		6.3
	430217	N47863	Hs.180450	ribosomal protein S24	Ribosomal_S24e	6.3
	426675	AW084791	Hs.133122	hypothetical protein FLJ14524	SS,TM,aminotran_1_2	6.3
	423510	AB000824	Hs.129712	trehalase (brush-border membra	Trehalase	6.3
	428573	AA430651	Hs.209249	ESTs		6.3
	457052	BE167242	Hs.47099	hypothetical protein FLJ21212	SS	6.3
	445099	BE163341		gb:QV3-HT0458-230200-099-b01 H		6.3
10	450334	AF035959	Hs.24879	phosphatidic acid phosphatase	PAP2,SS	6.3
	416000	R82342	Hs.79856	ESTs, Weakly similar to S65657	SS,TM,sugar_tr	6.3
	427880	AA436011	Hs.98187	ESTs		6.3
	426722	U53823	Hs.171952	occludin	Occludin,SS,TM,BIR	6.3
	452072	BE258857	Hs.27744	RAB3A, member RAS oncogene fam	ras,arf,SS,PDEase	6.2
15	431161	AA493591		gb:nh01a12s1 NCI_CGAP_Thy1 Ho	SS	6.2
	413055	AV655701	Hs.75183	cytochrome P450, subfamily IIE	p450	6.2
	431250	BE264649	Hs.251377	taxol resistance associated ge		6.2
	406373			Target Exon	SS,TM,vwa,FG-GAP,Integrin	6.2
	403003			NM_024944*:Homo sapiens hypoth	TM	6.2
20	437834	AA769294		gb:nz36p03.s1 NCI_CGAP_GCB1 Ho	SS	6.2
	406299			Target Exon		6.2
	439327	AF086141	Hs.50760	ESTs, Highly similar to BimL [SS	6.2
	414246	BE391090	Hs.280278	EST		6.2
	427812	AA770424	Hs.98162	ESTs	SS	6.2
	420926	AA830402	Hs.221216	ESTs	UQ_con	6.2
25	443766	N91071	Hs.109650	ESTs		6.2
	431082	AA491600		gb:ne80a11.s1 NCI_CGAP_Ew1 Hom		6.2
	420530	A1218431		coagulation factor VIII-associ		6.2
	407360	X13075		gb:Human 2a12 mRNA for kappa-I		6.2
30	449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)		6.2
	409946	AW162263	Hs.312468	ESTs, Weakly similar to ALUC_H	RasGAP,C2,PH,BTK	6.2
	413272	AA127923		ESTs	SS	6.2
	445050	AW205483	Hs.147260	ESTs	SS,trypsin,kingle,m2,EG	6.2
	458130	AA115811	Hs.6838	ras homolog gene family, membe	ras,arf	6.2
35	449940	AW291126	Hs.187520	Homo sapiens, clone IMAGE:3834	SS,zf-C2H2	6.2
	440390	AW207385	Hs.36475	KIAA0493 protein		6.2
	423108	NS2572	Hs.13702	ESTs, Moderately similar to AL		6.2
	402501			sperm specific antigen 2	ig,MHC_I,SS	6.1
	431470	AA832417	Hs.139650	ESTs	SS,ig,kinase,LRR,LRRCT	6.1
40	416597	H66891		gb:yr71c03.r1 Soares fetal liv		6.1
	412122	AW852707		G-rich RNA sequence binding fa	SS,WD40	6.1
	415056	AB004662	Hs.77867	adenosine A1 receptor	7tm_1,SS,TM	6.1
	400358	AF181286		Homo sapiens mutant dystrophin		6.1
	405473			NM_001093*:Homo sapiens acetyl	CPase_L_chain,biotin_lip	6.1
45	422625	AW504698	Hs.155976	cullin 4B	SS,SS,Cullin,Cullin	6.1
	422262	AL022315	Hs.113987	lectin, galactoside-binding, s	Gal-bind_lectin	6.1
	401121			C12001638*:g 7291960 gb AA47		6.1
	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	TM	6.1
	457216	AA452554	Hs.283697	ESTs, Weakly similar to AA4796	bZIP_Maf,SS,P5CR,EF1BD	6.1
50	456021	BE246628	Hs.250726	gb:TCBAP1D5030 Pediatric pre-B	SS,TM,SS	6.1
	420319	AW406289	Hs.96593	hypothetical protein	ras,arf	6.1
	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	SS,HECT,phoslip	6.1
	450593	AF129085	Hs.25197	STIP1 homology and U-Box conta	TPR,SS,TM,Rhomboid,lactam	6.1
	437050	AA766420		ESTs	SS	6.1
55	458835	AI868753	Hs.76372	ESTs	SS	6.1
	412777	AI335773		ESTs		6.1
	454364	BE263928	Hs.323806	gb:601191272F1 NIH_MGC_7 Homo	SS,TM	6.1
	448877	AI583696	Hs.253313	ESTs		6.1
	413045	X92121	Hs.75180	protein phosphatase 5, catalyt	Metallophos,TPR	6.1
60	408054	AW816490	Hs.8102	ESTs		6.1
	417852	AJ250562	Hs.82749	transmembrane 4 superfamily me	transmembrane4,SS,TM	6.1
	410445	AA199830		gb:zq75h01.r1 Stratagene hNT n		6.1
	415870	H15578	Hs.21017	ESTs		6.1
	438723	M34429		gb:Human PVT-IGLC fusion prote		6.1
65	441307	AW071696	Hs.209065	hypothetical protein FLJ14225	SS,TM	6.0
	406575			Target Exon	SS,pkinase,pkinase_C,RFK_	6.0
	401488			Target Exon	Glyco_hydro_1	6.0
	437650	AA814338	Hs.292297	ESTs		6.0
	439827	AA846538	Hs.187389	ESTs	pkinase,DAG_PE-bind,PH	6.0
70	456373	BE247706	Hs.89751	membrane-spanning 4-domains, s	SS,TM	6.0
	454513	BE159271	Hs.109731	gb:MR0-HT0407-180100-004-h05 H		6.0
	414944	C15044		gb:C15044 Clontech human aorta	SS,TM	6.0
	451277	AK001123	Hs.26176	hypothetical protein FLJ10261	TM,SS,TM,death,DED	6.0
	421190	U95031	Hs.102482	mucin 5, subtype B, tracheobro	Cys_knot,wvc	6.0
75	401215			C12000457*:g 7512178 pir T30	trypsin,SS,TM	6.0
	408117	AL138255		ESTs, Weakly similar to I38022	SS,zf-C3HC4,BIR	6.0
	426357	AW753757	Hs.12396	gb:RC3-CT0283-271099-021-a08 C		6.0
	418630	AI351311	Hs.251946	poly(A)-binding protein, cytop	SS,pkinase	6.0
	400389	AL135841		olfactory receptor, family 2,	7tm_1,SS,TM,CSD	6.0
	447128	AJ271898		cyclin K		6.0
80	431297	AA651771	Hs.3076	ESTs		6.0
	431857	W19144	Hs.271742	ADP-ribosyltransferase (NAD; p	PARP,PARP_reg,SS,TM,Pepti	6.0
	430023	AA158243	Hs.227729	FK506-binding protein 2 (13kD)	SS,FKBP,SS,PDGF,C2,PI-PLC	6.0
	453101	AW952776	Hs.94943	ESTs	TM	6.0
	407383	AA532576		ESTs, Moderately similar to AL	SS,Patatin,ank	6.0

430132	AA204686	Hs.234149	hypothetical protein FLJ20647	SS,SS,TM,Ig	6.0
459111	AU077013	Hs.28757	transmembrane 9 superfamily me	EMP70	6.0
405770			NM_002362:Homo sapiens melanom	MAGE	6.0
415811	T26376		gb:AB123C11R Infant brain, LLN	SS,TM,rm,sushi	6.0
453413	AJ003294		gb:AJ003294 Selected chromosom	SS,Folate_carrier	6.0
424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	enolase,SS,Atrophin-1,Atr	5.9
426048	AJ768653	Hs.134478	ESTs	TM	5.9
435750	AB029012	Hs.4990	KIAA1089 protein	SS,TM	5.9
439469	W69836		gb:zd48a02r1 Soares fetal_hes	SS,kinase,C2,kinase_C,D	5.9
445664	AW968638	Hs.237691	ESTs, Weakly similar to KIAA06		5.9
418830	BE513731	Hs.88959	hypothetical protein MGC4816	TM,COP-OH_P_transf	5.9
452113	AJ859393		gb:wm11a02.x1 NCI_CGAP_U14 Hom	actin	5.9
449101	AA205847	Hs.23016	G protein-coupled receptor	7tm_1,SS,TM	5.9
437640	AA764893	Hs.272155	ESTs, Weakly similar to I38022		5.9
400748			NM_022122:Homo sapiens matrix	SS,Peptidase_M10,hemopexi	5.9
442370	AJ143593	Hs.129419	ESTs		5.9
442419	AJ749693	Hs.270532	ESTs, Weakly similar to I38022	Adaptin_N,Alpha_adaptinC2	5.9
439986	AW750272	Hs.128608	ESTs	SS,TM,JSK_Channel	5.9
407553	Z11168		gb:H.sapiens 5HT1A receptor re	SS,TM	5.9
431424	AJ228699		ESTs	SS	5.9
442297	NM_006202	Hs.89901	phosphodiesterase 4A, cAMP-spe	PDEase	5.9
457845	H93040	Hs.297729	ESTs	SS,TM,WD40	5.9
446912	AJ347650	Hs.128521	ESTs, Moderately similar to AL	SS	5.9
451381	BE241831	Hs.172330	hypothetical protein MGC2705	SS,Ribosomal_L28a	5.9
416024	AW886484	Hs.343522	ATPase, Ca transporting, plasm	E1-E2_ATPase,Hydrolase,Ca	5.9
446329	NM_013272	Hs.14805	solute carrier family 21 (orga	kazal,OATP_N,OATP_C	5.9
431321	AW136372	Hs.1852	acid phosphatase, prostate	SS,TM,acid_phosphat	5.9
420039	NM_004605	Hs.94581	sulfotransferase family, cytos	Sulfotransfer,SS,DAGKc	5.9
428223	AA424313	Hs.98402	ESTs	HECT	5.9
433333	AJ016521	Hs.71816	v-akt murine thymoma viral onc	homeobox,kinase,PH,pkina	5.9
450251	BE080483		gb:QV1-BT0630-280200-086-a05 B	SS	5.9
408511	AW206404	Hs.27268	ESTs		5.9
414348	AF041430	Hs.75922	brain protein I3	SS,SH3	5.9
456950	AF111170	Hs.306165	Homo sapiens 14q32 Jagged2 gen	SS,TM,DSL	5.9
412173	T71071		gb:yc50b05.r1 Stratagene liver	CPSase_L_chain	5.8
404001			Target Exon		5.8
445263	H57646	Hs.42586	KIAA1560 protein	SS	5.8
441583	AJ791499	Hs.205742	ESTs, Weakly similar to ALUA_H		5.8
430168	AW968343		DKFZP434I1735 protein	SS,TM,efhand,efhand	5.8
454682	AW816029		gb:MR3-ST0220-151299-027-b10 S	filament	5.8
453829	AL138200		gb:DKFZp547N052_r1 547 (synony	SS,TM,ATP-synt_L,C,Galactos	5.8
437372	AA323968	Hs.283631	hypothetical protein DKFZp547G	SS	5.8
421726	AK001237	Hs.319088	hypothetical protein FLJ10375	TM	5.8
451045	AA215672		gb:zr96a09.s1 NCI_CGAP_GCB1 Ho	SS,Peptidase_C1,zl-C2H2	5.8
439616	BE018635	Hs.58582	Homo sapiens cDNA FLJ12789 fis	SS,TM	5.8
455679	BE066529		gb:RC3-BT0333-300300-017-a12 B	UBX	5.8
457125	AW444451	Hs.134812	ESTs	SS	5.8
430600	AW950967	Hs.274348	HLA-B associated transcript-3	ubiquitin,SS,TM,G-patch,a	5.8
421707	NM_014921	Hs.107054	lectomedin-2	Latrophilin,OLF,7tm_2,Gal	5.8
436127	W94824	Hs.11565	RIKEN cDNA 2010100012 gene	Corona_7,SS,TM	5.8
414347	BE275835		gb:601121639F1 NIH_MGC_20 Homo	SS	5.8
439910	H66765	Hs.339397	ESTs	SS	5.8
410382	AW664971	Hs.259546	ESTs	LM	5.8
426391	AW161050	Hs.169611	second mitochondria-derived ac	SS	5.8
423358	AJ815474	Hs.343866	gb:au47f110.y1 Schneider fetal	SS	5.8
440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fi	SS	5.8
402189			ENSP00000247423*-D-siglec prec	Peptidase_M1	5.8
439949	AW979197	Hs.292073	ESTs, Weakly similar to ALU7_H		5.8
457978	AA776638		gb:ae78g04.s1 Stratagene schiz	SS,PH,IQ,RasGEF,RasGEFN,R	5.8
436685	W28661	Hs.5288	Homo sapiens mRNA; cDNA DKFZp4	SS,TM,kinase,Activin_rec	5.8
411602	L01406	Hs.767	growth hormone releasing hormo	7tm_2,HRM	5.8
433357	T05639		gb:EST03528 Fetal brain, Strat	SS	5.8
404311			Target Exon	TM	5.8
428092	AW879141		ESTs	SS,TM	5.8
452620	AA436504	Hs.119286	ESTs	SS	5.8
401938			Target Exon	SS,PHD,proteasome	5.7
407202	N58172	Hs.109370	ESTs	SS,F5_F8_type_C,kinase,E	5.7
458882	R34993	Hs.226666	ESTs, Moderately similar to I5	SS,CRAL_TRIO,PKI	5.7
452357	AJ638176	Hs.283865	ESTs	SS,TM,SS,TM	5.7
452625	AA724771	Hs.61425	ESTs		5.7
430281	AJ878842	Hs.237924	CGI-69 protein	mito_carr,SS,TM	5.7
430490	AW902951	Hs.301723	Homo sapiens cDNA FLJ12974 fis	TM	5.7
450122	BE313765	Hs.343443	ESTs, Weakly similar to I38022	SS,TM,Y_phosphatase,LONA	5.7
450801	AJ739013	Hs.203348	ESTs	SS,TM,HinLH_signal	5.7
413413	D82520	Hs.132390	zinc finger protein 36 (KOX 18	SS,rm,DUF185	5.7
445631	AK001822		Homo sapiens cDNA FLJ10960 fis		5.7
419390	AJ701162	Hs.90207	hypothetical protein MGC11138	SS,TM,PMP22_Claudin,PMP22	5.7
423139	AW402725	Hs.288560	hypothetical protein FLJ21106		5.7
426221	AB007881		KIAA0421 protein	PI3_P14_kinase,FATC,SS,TM	5.7
443785	AW449952	Hs.190125	basic-helix-loop-helix-PAS pro		5.7
417900	BE250127	Hs.82906	CDC20 (cell division cycle 20,	WD40,SS,TM,fn3,EGF,fn3,Ig	5.7
446596	AW204515	Hs.156113	ESTs, Weakly similar to G01025		5.7
432353	NM_016558	Hs.274411	SCAN domain-containing 1	SCAN	5.7
427625	AF008216	Hs.285013	putative human HLA class II as		5.7

5	421543	AK000519	Hs.105606	hypothetical protein FLJ20512	TM	5.7
	418087	AA961613	Hs.127838	ESTs		5.7
	432751	AF152099	Hs.278911	interleukin 17C	SS	5.7
	433943	AA992805	Hs.44865	lymphoid enhancer-binding fact		5.7
	414274	AW300961	Hs.334684	Homo sapiens, clone IMAGE:4127	SS,Vps26,Acyl-CoA_dh	5.7
	431328	AA502999	Hs.291591	ESTs		5.7
	451481	AA300228	Hs.295866	hypothetical protein DKFZp434N		5.7
10	430344	AA476827	Hs.171012	hypothetical protein FLJ22349	HLH	5.6
	419516	H82550		ATP-binding cassette, sub-famil	SS,TM,ABC_tran,ABC_membra	5.6
	413564	BE260120		gb:601146990F1 NIH_MGC_19 Homo		5.6
	415958	H10942		gb:ym05c11.1 Soares Infant br	SS,TM	5.6
	401402			Target Exon		5.6
	456145	BE299427	Hs.21446	KIAA1716 protein	SS,DIX,PDZ,DEP,Dshvella	5.6
15	431536	AL133066	Hs.341906	ESTs	TM,SAM_decarbox,SS,ptinas	5.6
	456266	L29073	Hs.198726	cold shock domain protein A	CSD,homoeobox,SS,TM,7tm_2,	5.6
	435800	AI248285	Hs.118348	ESTs	TM,ECH,chromo	5.6
	449285	AI912702	Hs.139135	ESTs		5.6
	418256	AW845318	Hs.12271	f-box and leucine-rich repeat	SS,SS,TM,HSF_DNA-bind	5.6
20	417442	AA199940	Hs.124039	ESTs		5.6
	405931			Target Exon		5.6
	455286	BE144384		gb:MR0-HT0166-191199-004-c11 H	SS	5.6
	446931	AI348856	Hs.21627	gb:tb05a05.x2 NCL_CGAP_Lu26 Ho		5.6
	446548	AJ769392	Hs.200215	ESTs	SS,TM,Ribosomal_S25,sugar	5.6
25	401984			C17000146:gij2143629[pir]A57	pktnase,SS,TM,PZX_recepto	5.6
	404066			Target Exon	SS,IRNA-synt_2b,HGTP_ant	5.6
	418363	AA218628	Hs.202977	ESTs		5.6
	458198	AI286100		ESTs		5.6
30	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	SS,TM,GNS1_SUR4,SS,TM,Rho	5.6
	432328	AI572739	Hs.195471	6-phosphofructo-2-kinasefruct	PGAM,6PF2K	5.6
	421871	AK001416	Hs.306122	glycoprotein, synaptic 2	TM,Steroid_dh,SS	5.6
	415514	F11301	Hs.138329	ESTs	SS,TM	5.6
	426208	AI370379	Hs.132216	ESTs	SS,TM	5.6
	429367	AB007867	Hs.278311	plexin B1	Sema,PSI,TIG,SS,TM,TIG,Se	5.6
35	405939			Target Exon		5.6
	457331	AV647405	Hs.18443	aldehyde dehydrogenase 8 famil	GTP_EFTU	5.6
	438705	AI049524	Hs.283390	ESTs, Weakly similar to 210926	SS,E2F_TDP,E2F_TDP	5.6
	428624	AI125222	Hs.98712	hypothetical protein DKFZp434H	SS,TM,ras,MSP_domain	5.6
	419389	AI074951	Hs.319095	ESTs	SS,DPPIV_N_term	5.6
40	447595	AW379130	Hs.18953	phosphodiesterase 9A	PDEase	5.6
	408015	AW136771	Hs.244349	epidermal differentiation comp		5.6
	413041	BE061580	Hs.61622	gb:MR0-BT0249-091299-201-c07 B	SS	5.5
	452849	AF044924	Hs.30792	hook2 protein	bZIP,SS,AhpC-TSA	5.5
	434357	AW732284	Hs.3828	mevalonate (diphospho) decarbo	GHMP_kinases,SS,TM	5.5
45	455274	BE151622		gb:PM0-HT0302-271099-001-a08 H	SS,TM,RNA_pol_L	5.5
	453904	AW003821		ESTs		5.5
	424624	AB032947	Hs.151301	Ca2-dependent activator protel	Fork_head	5.5
	426576	AA381720		gb:EST94853 Activated T-cells	vwa,Integrin_A,FG-GAP	5.5
	440682	AW362152	Hs.27181	nuclear receptor binding facto		5.5
50	419125	AA642452	Hs.130881	B-cell CLL/lymphoma 11A (zinc	SS	5.5
	450207	T87615	Hs.14716	ESTs		5.5
	405211			C7000900:gij4508027[re]NP_003	SS	5.5
	413937	H65775	Hs.207915	ESTs		5.5
	426793	X89887	Hs.172350	HIR (histone cell cycle regula	WD40,Claithrin,Claithrin_pr	5.5
55	412091	R06185		gb:ye94d03.r1 Soares fetal liv	SS,TM,IBR,IBR	5.5
	446536	W74413	Hs.15251	hypothetical protein	SS	5.5
	451117	AA015752	Hs.205173	ESTs		5.5
	409547	AW409885	Hs.335877	Homo sapiens, clone MGC:4558,	TM	5.5
	412673	AL042957	Hs.31845	ESTs		5.5
60	426440	BE382756	Hs.169902	solute carrier family 2 (faci	sugar_tr,SS,TM,sugar_tr	5.5
	449225	R39108	Hs.6777	ESTs	SS,TM,Na_sulph_symp	5.5
	403938			Target Exon	Ephrin	5.5
	441197	BE244638	Hs.166	sterol regulatory element bind	HLH	5.5
	455604	BE011183		gb:PM3-BN0218-100500-003-d09 B		5.5
65	457468	AW971345	Hs.292715	ESTs		5.5
	447677	AI419235	Hs.344456	gb:t21d02.x1 NCL_CGAP_Bm23 H	SS,zf-C2H2,SCAN,SCAN,zf-C	5.5
	415473	R39986	Hs.12778	ESTs	TM,Ion_trans	5.5
	408422	AW977031	Hs.143554	ESTs, Highly similar to B45036		5.5
	442780	AI017521		ESTs	SS,TM,7tm_1	5.5
70	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-famil	ABC_tran,SRP54,SS,TM,ECH	5.5
	439422	AW452791	Hs.249625	ESTs	SS,TM	5.5
	423479	NM_014326	Hs.129208	death-associated protein kinas	pktnase	5.5
	459558	AI539821	Hs.298799	ESTs, Weakly similar to 210926	SS	5.5
	441187	AW195237	Hs.7734	hypothetical protein FLJ22174	SS,TM,tubulin	5.5
75	420894	AA744597	Hs.88854	ESTs	SS,ank	5.5
	404710			C9001584:gij7499208[pir]T2099		5.5
	447827	U73727	Hs.19718	protein tyrosine phosphatase,	Y_phosphatase,fn3,ig,MAM,	5.5
	448387	AI874402	Hs.292590	ESTs		5.5
	419541	AW749617	Hs.280776	lankyrase, TRF1-interacting an		5.5
80	449686	AW072813	Hs.270868	ESTs, Moderately similar to AL		5.5
	426315	AA854219	Hs.348137	Homo sapiens, clone IMAGE:3542	SS,crystal	5.5
	451312	AJ769831	Hs.337054	ESTs	SS	5.5
	432538	BE258332	Hs.278362	male-enhanced antigen	SS,TM,AAA,Ribosomal_L2	5.5
	446790	AW452105		ESTs	SS,zf-C2H2	5.5
	448682	T09471	Hs.250820	hypothetical protein FLJ14827		5.5

5	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022	SS	5.5
	411219	AW832917		gb:QV2-TT0003-161199-013-h06 T		5.5
	439742	A1827721	Hs.284298	Homo sapiens mRNA full length	SS	5.5
	432004	BE018302	Hs.2894	placental growth factor, vascu	PDGF,SS	5.5
	402916			ENSP00000202587: Bicarbonate t	HCO3_cotransp,SS	5.5
	405346			Rag C protein	RCC1	5.5
	415976	R43144	Hs.21919	ESTs	TM	5.4
	435064	T70740	Hs.31433	ESTs	SS,MDM2	5.4
10	440024	AA969333	Hs.160098	ESTs		5.4
	431525	AA506656	Hs.6185	KIAA1557 protein		5.4
	458644	AW270149		ESTs, Moderately similar to GG		5.4
	410895	AW809679		gb:MR4-ST0124-261099-015-f05 S		5.4
	441350	AB020690	Hs.7782	paraneoplastic antigen MA2		5.4
15	413034	BE392896	Hs.129126	Homo sapiens, clone MGC:10992,	SS	5.4
	444664	N26362	Hs.11615	map kinase phosphatase-like pr	DSPc,Rhodanese,SS,TM	5.4
	443887	NM_004729	Hs.9933	Ac-like transposable element	zf-BED	5.4
	445871	A1702901	Hs.145582	ESTs, Weakly similar to FORA M	SS,TM,efhand,efhand	5.4
	411992	AW816214	Hs.143055	ESTs	SS,TM	5.4
20	458341	AW373583	Hs.221994	gb:QV4-BT0534-281299-053-e08 B		5.4
	451677	AA059222	Hs.33538	ESTs, Weakly similar to oxygen		5.4
	432656	NM_000246	Hs.3076	MHC class II transactivator	LRR	5.4
	417739	Z43995		gb:HSC1QB121 normalized infant	SS,ArfGap,vwa,TSPN,fn3,Co	5.4
	424618	L29472	Hs.1802	major histocompatibility compl	TM,Ig,MHC_II_beta,SS,TM,A	5.4
25	446847	T51454	Hs.82845	Homo sapiens cDNA: FLJ21930.6	SS,TM,BNR,fn3,Idl_recept	5.4
	436094	A1798701		ESTs		5.4
	433168	A1085436		gb:ow84g06.s1 Soares_fetal_jiv	SS,TM,PID	5.4
	417359	T99264	Hs.191117	ESTs		5.4
	436014	AF281134	Hs.283741	exosome component Rrp46	RNase_PH,RNase_PH_C,SS,TG	5.4
30	435154	AA688764	Hs.301637	ESTs	SS,TM	5.4
	431630	NM_002204	Hs.265829	Integrin, alpha 3 (antigen CD4	Integrin_A,FG-GAP,Rhbd_g	5.4
	444064	W85970	Hs.16292	ESTs	SS,TM,Dihydroorotase	5.4
	415970	H23333	Hs.29002	KIAA1706 protein		5.4
	445303	AW362198	Hs.12503	Interleukin 15 receptor, alpha	SS,sushi,SS	5.4
35	421542	AA411607	Hs.118964	ESTs, Weakly similar to KIAA11	SS,SS	5.4
	459704	AA719572	Hs.274441	Homo sapiens mRNA; cDNA DKFZp4		5.4
	402285			sclerostin	SS,TM	5.4
	431543	AW969619	Hs.259768	adenylate cyclase 1 (brain)	TM	5.4
40	431534	AL137531	Hs.258890	Homo sapiens mRNA; cDNA DKFZp4	SS,TM,ras	5.4
	417516	AA203473	Hs.81529	ESTs	TM	5.4
	423233	BE048021	Hs.11067	ESTs, Highly similar to T46395		5.4
	420733	AW291446	Hs.88651	ESTs	SS	5.4
	404807			Target Exon	UPF0027	5.4
	436483	AJ272063	Hs.283010	vanilloid receptor subtype 1	SS,TM,ank,ion_trans,SS,TM	5.4
45	425316	AA354977	Hs.99010	ESTs, Moderately similar to T1	SS,pkinase,Ig	5.4
	425565	AA359485	Hs.173084	gb:EST68511 Fetal lung II Homo		5.4
	413341	H78472	Hs.191325	ESTs, Weakly similar to T18967		5.4
	401203			Target Exon	filament	5.4
	422452	AL110255	Hs.116808	Homo sapiens mRNA; cDNA DKFZp5	SS,asp,PGAM	5.4
50	436718	AW015227	Hs.289053	hypothetical protein FLJ14733	SS,TM	5.4
	428501	AL041162	Hs.98587	ESTs	TM	5.4
	439695	W28548	Hs.285050	ESTs	TM,ion_trans,K_tetra,Kv2c	5.3
	417514	AA203445	Hs.325819	ESTs		5.3
	441358	AW173212		ESTs		5.3
55	401722			Target Exon	TM,PLAT,SS	5.3
	408905	AV655783	Hs.661	Target CAT		5.3
	454453	AW752781		hypothetical protein FLJ12614		5.3
	410312	AW850953	Hs.75350	gb:IL3-CT0220-150200-068-A11 C	Vinculin	5.3
	437926	BE383605	Hs.300816	small GTP-binding protein	SS,TM,TPR	5.3
60	458682	AV659151	Hs.282961	ESTs		5.3
	411605	AW006831		ESTs	TM,synaptobrevin	5.3
	409164	AA706639		gb:ag90e09.r1 Stralagena hNT n	SS,TM,Hnt,HH_signal,tubu	5.3
	438868	AW246243	Hs.334800	hypothetical protein FLJ20974		5.3
	439034	AF075083		gb:Homo sapiens full length in	filament,filament	5.3
65	411426	BE141714		gb:QV0-HT0101-061099-032-c04 H	SS	5.3
	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A,	Glyco_hydro_38,SS,TM,Pept	5.3
	438470	AW936329	Hs.227823	pM5 protein	SS,TM	5.3
	427789	AA412428	Hs.48642	hypothetical protein FLJ23093		5.3
	430220	BE257724	Hs.236361	seb4D	rm,SS,2-Hacid_DH,WD40	5.3
70	434314	BE392921	Hs.3797	RAB26, member RAS oncogene fam	ras,arf,SS	5.3
	428539	AW410063	Hs.184877	solute carrier family 25 (mito	mito_carr,SS,TM,profilin,	5.3
	414927	T83587	Hs.186476	ESTs	SS,Sulfatase	5.3
	404596			Target Exon	SS	5.3
	454151	AA047169	Hs.154088	hypothetical protein FLJ22756	SS,TM,Glycos_transf_4	5.3
75	431627	AW609720		HSPC042 protein		5.3
	422379	AA932860	Hs.133864	ESTs		5.3
	426765	AA743803	Hs.172108	nucleoporin 88kD	MAM33	5.3
	433325	AW206986	Hs.143905	ESTs	SS	5.3
80	403128			KIAA1033 protein	SS,TM,tubulin,EGF,F5_F8_1	5.3
	447730	A1421251	Hs.114085	Homo sapiens mRNA for KIAA1755	SS,Transglutamin_C,Transg	5.3
	405085			Target Exon	SS,SS,SNF2_N,helicase_C	5.3
	438080	AA777381	Hs.291530	ESTs, Weakly similar to ALUC_H		5.3
	439091	AA830144	Hs.135613	ESTs, Moderately similar to I3	KH-domain	5.3
	427326	A1287878		gb:qv23f06.x1 NCI_CGAP_Lym6 Ho	SS,TM,7m_1,SS,TM	5.3
	427859	AA416856	Hs.98170	ESTs	SS,TM,DUF60,trypsin,CUB,u	5.3

421779	AI879159	Hs.108219	wingless-type MMTV integration	SS,wnt,SS	5.3
408270	AW177805		gb:IL3-HT0059-180899-007-B06 H		5.3
418437	AA771738	Hs.348000	ESTs, Moderately similar to AL		5.3
409879	BE063422	Hs.56851	hypothetical protein MGC2668	SS,TM	5.3
428304	AF743177		ESTs	SS,TM	5.3
418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-	SS,TM,zf-C2H2	5.3
436540	BE397032	Hs.14468	hypothetical protein MGC14226	SS,TM	5.2
437161	AA054477	Hs.25391	ESTs	SS,TM	5.2
400171			ENSP00000211797:Helicase SKI2W	SS,proteasome	5.2
431461	BE299671	Hs.256310	likely ortholog of mouse ZFP28		5.2
402197			Target Exon	SS,TM,ATP1G1_PLM_MAT8,lg,	5.2
449514	AW970440	Hs.23642	protein predicted by clone 236	SS,PX,arf,lipocalin,PHD,z	5.2
442472	AW806859		gb:MR0-ST0020-081199-004-c03 S	SS,TM,Inos-1-P_synth,Ocd	5.2
409679	BE250521		ras homolog gene family, membe	SS,homeobox,CUT	5.2
439150	AF086008		gb:Homo sapiens full length in	SS	5.2
412934	BE011437		gb:CM4-BN0220-080500-170-403 B		5.2
435186	AL119470		ESTs	SS	5.2
400668			Target Exon	CARD,ICE_p20,SS,ICE_p20,I	5.2
409125	R17268	Hs.343567	axonal transport of synaptic v	SS,kinesin,PH,FHA,kinesin	5.2
445904	AW449920	Hs.248855	ESTs	SS,homeobox	5.2
414567	BE281057	Hs.184519	hypothetical protein FLJ12949	SS,TM,ank,Adap_comp_sub	5.2
414551	AI815639	Hs.76394	enoyl Coenzyme A hydratase, sh	ECH,Peptidase_U7,SS,TM	5.2
432872	AI908984	Hs.279623	selenoprotein X, 1	DUF25,SS,Ribosomal_L3,PDZ	5.2
419492	AA243547	Hs.19447	PDZ-LIM protein mystique	LIM,SS,SH3,Sorb,Metalloph	5.2
407478	L77559		gb:homo sapiens DGS-B partial		5.2
457892	AA744389		gb:ny51e10.s1 NCL_CGAP_Pr18 Ho		5.2
457228	U15177	Hs.206984	Human cosmid CRI-JC2015 at D10	6PF2K,PGAM	5.2
437536	X91221	Hs.144465	ESTs	SS,TM,Na_Ca_Ex	5.2
420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN		5.2
431275	T56571	Hs.10041	ESTs	SS,HLH	5.2
428021	AI022287	Hs.111991	ESTs, Weakly similar to T33900	SS	5.2
422400	AA974434	Hs.128353	ESTs		5.2
446442	BE221533	Hs.257858	ESTs		5.2
415585	R59946	Hs.184852	KIAA1553 protein	SS	5.2
438429	D16918	Hs.12547	Homo sapiens cDNA: FLJ23388 f	TM	5.2
401677			BAI1-associated protein 3	SS,TM,zf-C2H2,kinesin,Vau	5.2
405637			Target Exon		5.2
450437	X13956	Hs.24998	hypothetical protein MGC10471	SS	5.2
408215	BE614290		syntactin 10	SS,SS,TM,HLH,TRM,zf-CCHC	5.2
452666	AW194601	Hs.13219	ESTs	PI-PLC-X,PI-PLC-Y,C2,PH	5.2
401553			Target Exon		5.2
447541	AK000288	Hs.18800	hypothetical protein FLJ20281	zf-CCHC	5.2
453434	AJ271378	Hs.333243	ESTs		5.2
450351	BE547267	Hs.59791	hypothetical protein MGC13183	SS,TM	5.2
411456	AW847588		gb:IL3-CT0213-161299-038-G09 C	SS,TM	5.2
445634	AI624849	Hs.344612	ESTs, Weakly similar to NEL1_H	vwd	5.2
453740	AL120295	Hs.311809	ESTs, Moderately similar to PC		5.2
426318	AA375125	Hs.147112	Homo sapiens cDNA: FLJ22322 f	SS,TM,EPH_1bd,pkinase,fn3	5.1
416470	N90464	Hs.303023	beta tubulin 1, class VI	SS,tubulin,SS	5.1
432022	AL162042	Hs.272348	Homo sapiens mRNA; cDNA DKFZp7		5.1
457579	AB030816	Hs.36761	HRAS-like suppressor	TM	5.1
438484	AW021671	Hs.293330	ESTs, Weakly similar to p40 [H		5.1
422802	NM_004278	Hs.27008	phosphatidylinositol glycan, c	DUF158,ank	5.1
401724			C16001374:gil755086[ref]NP_03	TM,PLAT,SS	5.1
438670	AI275803	Hs.123428	ESTs		5.1
414757	U46922	Hs.77252	fragile histidine triad gene	HIT	5.1
425098	AW295349	Hs.8038	ESTs	SS,TM	5.1
431898	AW297844	Hs.101428	ESTs	SS	5.1
416732	H81066	Hs.285017	hypothetical protein FLJ21799	SS	5.1
404571			NM_015902*:Homo sapiens prog	HECT,zf-UBR1,PABP	5.1
433675	AW977653	Hs.75319	ribonucleotide reductase M2 po	SS	5.1
426358	AA376438		gb:EST88856 HSC172 cells II Ho	TM	5.1
456767	AI086412	Hs.129064	Homo sapiens chromosome 19, co	SS,TM,trypsin,kringle,UPA	5.1
412915	AW087727	Hs.74823	NM_004541:Homo sapiens NADH de		5.1
443553	AL040535	Hs.9573	ATP-binding cassette, sub-fami	ABC_tran,SS	5.1
415888	Z42737		gb:HSC05E081 normalized infant	SS	5.1
401674			C16001417:gil7500345[pir]T21	FAD-oxidase_C,FAD_binding	5.1
424266	AA337810	Hs.149152	ESTs, Weakly similar to RHOP M		5.1
455035	AW851734		gb:MR2-CT0222-011199-007-e10 C		5.1
408567	S72921		ciliary neurotrophic factor	CNTF	5.1
436616	AW799109	Hs.226755	ESTs	14-3-3	5.1
409078	AW327515		ESTs		5.1
447976	AW972653	Hs.293691	ESTs, Highly similar to CR2_HU		5.1
457720	AA992835	Hs.186776	ESTs		5.1
400528			NM_020975*:Homo sapiens ret pr	cadherin,pkinase,SS	5.1
407757	BE048414	Hs.165215	hypothetical protein MGC5395	SS,EF1G_domain,GST_C,GST_	5.1
452446	AA086123	Hs.297856	ESTs	nm,NTF2	5.1
450807	AJ739262		gb:aw17b08.x1 NCL_CGAP_Co16 Ho		5.1
432540	AI821517	Hs.105868	ESTs	SS,TM	5.1
449324	AI638706		ESTs, Weakly similar to A47582		5.1
426434	M17755	Hs.2041	thyroid peroxidase	EGF,sushi,An_peroxidase,p	5.1
407652	W27953	Hs.292911	ESTs, Highly similar to S60712	Troponin	5.1
443952	AI149106		ESTs	SS,pkinase	5.1
448869	AI792798	Hs.12496	ESTs, Weakly similar to ALU4_H	SS,TM	5.1

5	422837	U25441	Hs.121478	dopamine receptor D3	7tm_1,SS,TM,7tm_1	5.1
	407143	C14076	Hs.332329	EST	SS,TM	5.1
	442298	NM_007275	Hs.8186	lung cancer candidate	SS,TM,Glyco_hydro_56,Glyc	5.1
	407722	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin	pkB,SS	5.1
	427336	NM_005658	Hs.2134	TNF receptor-associated factor	MATH,SS,MATH,A2M_N,A2M,NT	5.1
	447960	AW954377	Hs.26412	ring finger protein 26	SS,TM,Cbl_N,Cbl_N2,Cbl_N3	5.1
	400863			C11002296.gij11692557[gblAAG39	SS,TM	5.1
	409034	A1684149	Hs.172035	hypothetical protein similar t	SS	5.1
10	421696	AF035306	Hs.106890	Homo sapiens clone 23771 mRNA		5.1
	427587	BE348244	Hs.284239	ESTs, Weakly similar to I78885	SS,UDPGT	5.1
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_H	SS,histone,histone	5.1
	454219	X75042	Hs.44313	v-rel avian reticuloendothelio	RHD,TIG	5.1
	430513	AA012008	Hs.241588	G6C protein	SS,TM,GST_C,abhydrolase	5.1
15	435902	AA701867	Hs.297726	ESTs		5.1
	442743	A1801351	Hs.302110	ESTs, Weakly similar to MUC2_H	SS,fibrinogen_C,Rhodanese	5.1
	454923	AW697236		gb:CM0-NN0057-150400-335-c06 N	SS,Catdesmon	5.1
	440518	AA888046	Hs.233235	ESTs	SS,TM	5.1
	448237	A1471790	Hs.309386	ESTs	TM,Ribosomal_S7	5.1
20	428924	A1016405	Hs.98959	ESTs, Weakly similar to JC5314	SS,TM,lectin_c	5.1
	412081	Z24895	Hs.293818	gb:HSB67F122 STRATAGENE Human	SS,TM,SQS_PSY,GATA	5.1
	437141	BE304917	Hs.31097	hypothetical protein FLJ21478	SS,TM,Glycos_transf_4	5.1
	421658	X84048	Hs.301760	frequenin (Drosophila) homolog		5.1
	423467	AK000214	Hs.129014	hypothetical protein FLJ20207	SS,TM,GDPD,SS,TM,SH3,PDZ,	5.0
25	417151	AA194055	Hs.293858	ESTs	PH	5.0
	408307	A1761786	Hs.204674	ESTs	Armadoilo_seg	5.0
	404752			NM_024778:Homo sapiens hypot		5.0
	453126	AA032155	Hs.61622	ESTs		5.0
	413983	BE348384	Hs.279194	ESTs		5.0
30	405366			NM_003371:Homo sapiens vav 2	SS	5.0
	412425	AW949156		gb:QV4-FT0005-110500-205-b06 F		5.0
	437036	A1571514	Hs.133022	ESTs	SS,TM,Glycos_transf_2	5.0
	448455	A1252625	Hs.269860	ESTs, Moderately similar to S6	SS,TM	5.0
	411413	BE379438	Hs.211573	heparan sulfate proteoglycan 2	lg,laminin_B,laminin_EGF,	5.0
35	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis	CARD,SS,HSF_DNA-bind,E2F_	5.0
	424874	AA347951		Homo sapiens cDNA FLJ20812 fis	SS	5.0
	408023	BE018269	Hs.279688	ESTs		5.0
	411758	AW860667		gb:QV0-CT0383-210400-204-d03 C	homeobox,homeobox	5.0
	410660	A1061118	Hs.65328	Fanconi anemia, complementatio		5.0
40	427411	AA402242		ESTs		5.0
	437018	AA889078		ESTs	SS,TM,ERG4_ERG24	5.0
	427029	AA379596		ESTs	SS,ras	5.0
	452047	N35953	Hs.43510	ESTs, Weakly similar to BOX B	SS	5.0
45	432093	H28383		gb:y152c03.r1 Soares breast 3N	Band_41,ERM	5.0
	453099	H62087	Hs.31659	thyroid hormone receptor-assoc	SS	5.0
	441456	A1458911	Hs.127765	ESTs		5.0
	414356	AW505085	Hs.335147	gb:UH-HF-BN0-als-a-10-0-ULr1	SS,TM	5.0
	434067	H18913	Hs.124023	Homo sapiens cDNA FLJ14218 fis		5.0
	436393	AW022213		ESTs	Galactosyl_T_2	5.0
50	409227	AA806165	Hs.130323	Homo sapiens, clone IMAGE:3960		5.0
	448680	AW245890	Hs.21753	JM5 protein	WD40,SS,TM,KOW,HLH	5.0
	439343	AF086161	Hs.114611	hypothetical protein FLJ11808		5.0
	428079	AA421020	Hs.208919	ESTs	SS,TM,trypsin	5.0
	421951	BE327432	Hs.109804	H1 histone family, member X		5.0
55	427204	AA405404	Hs.215725	ESTs	SS,SS	5.0
	409690	W45393	Hs.55888	activating transcription facto		5.0
	436574	AW293527	Hs.126465	ESTs		5.0
	457761	AW401809	Hs.4779	KIAA1150 protein	SS,IJM,SS	5.0
	435294	T84084	Hs.196008	Homo sapiens cDNA FLJ11723 fis	HMG_box	5.0
60	445372	N36417	Hs.144928	ESTs	SS,PID,PDZ	5.0
	440511	AF132959	Hs.7236	eNOS interacting protein	SS,TM,MAGE_Ribosomal_S17,	5.0
	424437	BE244700	Hs.147049	cut (Drosophila)-like 1 (CCAAT	CUT,homeobox,beta-lactama	5.0
	401539			NM_002675:Homo sapiens promyel	zf-B_box,zf-C3HC4,SS	5.0
	417903	NM_002342	Hs.1116	lymphotoxin beta receptor (TNF	TNFR_c6,SS	5.0
65	442451	AA98080	Hs.129616	ESTs	SS	5.0
	450538	A1699529		gb:tt17a02.x1 NCL_CGAP_GC6 Hom	SS,G-alpha,arf	5.0
	425169	AW292500	Hs.128514	ESTs	SS	5.0
	435262	AA677088		ESTs		5.0
	444855	BE409261	Hs.12084	Tu translation elongation fact	GTP_EFTU,GTP_EFTU_D3,GTP_	5.0
70	433507	A1817336	Hs.191791	ESTs	pkinase	5.0
	432396	AW295956	Hs.11900	hypothetical protein FLJ14972	SS	5.0
	438395	AA017514	Hs.6211	methyl-CpG binding domain prot	MBD,zf-CXXC,SS,zf-CXXC	5.0
	446603	NM_014835	Hs.15519	oxysterol-binding protein-rela	Oxysterol_BP,SS	5.0
	400762			Target Exon		5.0
75	440133	A1056255	Hs.133349	ESTs		5.0
	445903	A1347487	Hs.132781	class I cytokine receptor	SS,TM,EF1B0	5.0
	412940	BE295701	Hs.819	homeo box B7	homeobox,SS,homeobox,home	5.0
	419269	AA235838		gb:z41b04.s1 Soares_NhHMPu_S1	TM	5.0

TABLE 208:

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey	CAT Number	Accession
408117	104000_1	AL138255 BE380045 AA047314 D82381 T18585 H64978 T10798
408215	10478_1	BE614290 AA307674 N35629 AA338538 AI193603 AA781096 AI680061 AI613258 AW276647 BE221263 AI348910 AI985031 AI090078 AI359617 AA665391 AI160210 AI446461 AI355345 AI343638 AI343640 AI275091 M78746 AW262795 AW250002 AA503756 AI934519 AW272086 N26520 AA626639
5	408270	1049980_1 AW177805 AW177895 AW177816 AW177901 BE141597 BE141584 AW177822 AW177818 AW177899
	408294	1050553_1 BE141732 U75823 BE141331 AW178416 AW178430 BE141343 BE141298 BE141702 BE141285
	408567	10563_1 S72921 NM_000614 X55889 X60542 X60477
10	409078	1098756_1 AW327515 AW327774 AW327571
	409164	110421_1 AA706639 AA064707 AL036920 AI651598
	409679	114787_1 BE250521 AA076837 BE249870 AA984291 AW502442 AW501551 AI221491 AA194239 D63046 AA193426 AA773243 AA193293
	409832	115564_1 AW963293 AI866310 AA077791 AA362540
	410445	120374_2 AA199830 AI143895 AW961629 AA322482
15	410471	1204721_1 T88872 AW749857
	410895	1226051_1 AW809679 AW809678 AW810113 AW810182 AW809900 AW809851 AW810110 AW810228 AW810342 AW810181 AW809632 AW809745 AW810372 AW809681 AW809792 AW809806 AW810452 AW809575 AW809964 AW810033 AW810111 AW809846 AW809847 AW809717 AW832917 AW832913 AW832906 AW832788 AW832915 AW832776
	411219	1236055_1 AW835858 AW835836 AW835823 AW835834 AW835831 AW835832 AW835843 AW835816 AW835833 AW835815 AW835849 AW835835
	411298	1237955_1 AW835848 AW835851 AW835852 AW835862 AW835855 AW835825 AW835847 AW835838 BE141714 AW845993 AW845989
20	411426	1245515_1 AW847588 AW847716 AW847664 AW847592
	411458	1246708_1 R39474 AW848420 R76943
	411490	1247428_1 AW006831 AA678298 R12579 W86152 AI123683 AA699780 AI672156 BE092587 AA094230 AI633815 AA526153 W86151
	411605	125123_2 AW006831 AA678298 R12579 W86152 AI123683 AA699780 AI672156 BE092587 AA094230 AI633815 AA526153 W86151
25	411758	1256751_1 AW860667 AW860665
	412091	1276584_1 R06185 AW891805 AW901892 AW901895
	412122	127838_2 AW852707 N57282 AA725075 AI703492 AW612137 AI696372 AI879394 AI653605 W26914
	412128	1278728_1 AW894709 N78140
	412173	1280870_1 T71071 AW902279 AW897608
30	412425	1293726_1 AW949156 AW949003 AW949008
	412452	1297707_1 AA215731 N48523 AA307559 AA130794 BE296746 BE378396 AA190411 AI904194 AA311805 AI356291 AA446714 AI818924 AI609152 AW771476 BE298184 AA295023 AA130708 AI078381 AA114156 AI198283 AA215665 AI201085 AI694848 AI077572 AA102778 AW016425 AI923123 AA577072 AI671
	412777	132672_1 AI35773 AI288496 AA120880
35	412934	1337389_1 BE011437 BE011402 BE011395 BE011428 BE011407 BE011421 BE011406
	413272	135718_1 AA127923 AA127846 AA534131 N53566 AA533669 AW511251 AI174441 AA127875 AI685293 AA127913 N72525 AW770386 N69010 AW070312 H80275 H80289 AA972923
	413534	1375357_1 BE146961 BE146780 BE146788 BE146967 BE146774 BE146963 BE146907
	413564	1376722_1 BE260120 BE148538
40	414347	1437406_1 BE275835 BE390063 BE388764 BE409101
	414371	14388_8 AI905865 BE294801 BE562308 BE297857 AW157051 AI815883 AW162529 BE439610 AW157225 AW157210 AW162675 AW161998 AI816168 AW162599 AI816004 AI815820 AW162158 AW162339 M17733 AW157639 AI879416 BE258811 AW157436 AW162433 AW161633 AW162155 AW157410 AW157269 AW162
	414391	1441921_1 BE409872 BE281460
45	414413	1443696_1 BE294877 BE294759
	414593	1464909_1 BE386764 BE387560
	414944	1509480_1 C15044 D80943 C15696
	415126	1523506_1 D60945 D61346 D81568 D80539
	415611	1540555_1 T26376 F12852 T75058
	415888	1560411_1 Z42737 T08986 H07956
50	415958	1563222_1 H10942 Z42911 R60453
	416233	158010_1 AA176633 AW961842 AA309418
	416597	1603081_1 H66891 R98149 H68467
	417739	1696198_1 Z43995 R12357 R34740
55	418184	172744_1 AA367375 AA486701 BE152479 BE152800 AW816961 AA214097
	418304	173658_2 AA215702 AA368006 AA215703 BE066555 BE006876
	419269	183444_1 AA235838 BE180775
	419516	185533_1 H82550 N43802 AA243820 AL040762 N24315 U66692
	420530	19446_1 AI218431 AA432232 AW183040 X86012 AA668831 AI191788 AA912999 AI204297 AI205744 AI218259 AA428596 AA993742 AA703660 AI018669 AA879431
60	421879	208649_1 AW959607 AA299654 AA579966
	423790	232031_1 BE152393 AA330984 BE073904
	424874	244523_1 AA347851 AI688463 AA883123
	426221	26281_1 AB007881 U32581 AW131202 AW995994 W31964 N24261 AI033045 H98694 AW364848 AI222031 AA907216 AI215730 AA776981 AW473826 W31373
65	426358	265504_1 AA376438 AA376324 AW963848 AW834782
	426576	269378_1 AA381720 AA382040 AW963564
	427029	274544_1 AA397596 AI198827 AA435832
	427326	277229_1 AI287878 AI804160 AA400787
70	427411	278474_1 AA402242 AA813659 AI150316 AA412054
	428092	286920_1 AW879141 AA421182 AI734104 AI733923 AA430600
	428304	289603_1 AI743177 AA425743 AI804283 AI743189
	428948	29737_1 BE514362 AI879343 BE272870 BE616390 AW163444 AW161588 AW378754 AW238803 BE267205 BE047746 BE207213 BE312782 BE266301 BE266413 BE278348 BE280885 BE278833 BE281417 BE407786 BE378176 BE392818 AW377597 BE395951 BE393978 AW327483 BE394175 BE385795 BE275663 BE3
75	428398	303954_1 AA452239 AI262173 AI925886 AI469041 H96628 AI768463 AI671422 AI915624 AA766891 AA521087 AA814103 AW993151 AW005927
	430168	313927_1 AW986343 AA468507 AI478223 AW513008 AI762122 AI554512 AA862642 AA468976
	431082	327710_1 AA491600 AA491645 AI920986
	431161	328713_1 AA493591 AA829120 AA533792
80	431424	333110_1 AI222969 AA806560 AA504839 AA805261
	431627	33581_1 AW609720 AW609735 AA082767 N88831 R23418 N55837 BE549484 AW816584 AW816947 AW816897
	432093	341283_1 H28383 AW972670 H28359 AA525808
	432945	356589_1 AL043683 AA570698 AA907496 AL043682 AW362288
	433168	360235_1 AI085436 AA579438 AA579002
	433357	36402_1 T05639 AF024702

	434315	383402_1	AW196608 AA884617 AA758108 AI126321 AA629291 AW196549 AI208031
	434743	3925_1	AI363410 AI356019 H00141 T78748 ALD49365 AL079911 AI750972 Z42602 AW452523 AI223826 AA215407 AI633829 AA292122 N42783
			AW505595 AF080995 N90340 N63271 AA131836 AW607273 AA527132 T32315 AA421961 T34951 AW966080 M78807 N31947 AA521151
5	434796	393400_1	AA278866 AA044784 AA700
	435186	402143_1	AA812046 AW574514 AA764999 AA649302
	435262	403605_1	AL119470 AA669492 AI628351 AI263835 AL119498
	435339	404485_1	AA677088 AI022246 AA677107
	436094	414444_1	AI358300 AI762981 AA678073 AA988621
10	436389	41894_1	AI798701 AW008826 AA704731
			AI811706 AW297940 AJ227887 AA875850 AA228803 AI610234 AI921618 AI768606 N37039 AA081104 BE172693 D56503 Z28585 T95651
			AA292389 AA293502 N28751
	436393	41903_1	AW022213 AI274032 AJ227898 AI160412 AI084451
	437018	431333_1	AA889078 AA907263 AA742199
	437050	432210_1	AA766420 AA743319 AW976442
15	437215	43473_1	AL117488 ALD44479
	437662	440374_1	AA765387 AA832241 AI222134 AI216405 AI685043
	437834	443674_1	AA769294 AW749299 AW749302 AW749295 AW749304 AW749293 AW749298 AW749299 AW749297 AW749292
			AW749296 AW749289 AW749287 BE535498
20	438118	450293_1	AW753311 AW663081 AA778411
	438723	46392_1	M34429 M34431 M34432 M25802 AW938720
	439034	46802_1	AF075083 H52291 H52528
	439150	46919_1	AF086006 H64722 H65212 H66282
	439469	47274_1	W69836 AF086287 W69557
25	440317	49187_1	BE561888 BE560815 BE562102
	440546	496976_2	AI491994 AW139809 AA889258 AI700895
	441358	515468_1	AW173212 AA983948 AI080705 AA931334
	441523	519049_1	AW514263 AI567908 AI299828 AI299043 N51706 AA936483
	441784	526289_1	AW197794 AW195867 AW197787 AA968466
30	442146	533972_1	R52599 T65201 F11984 F13186 AA977679 T77028 H12167
	442318	538584_1	AI792199 AI733491 AA991378
	442472	543371_1	AW806859 AW806852 AF049582
	442780	551405_1	AI017521 AI017613 AW511133
	442893	553987_1	H78133 H90849 AI023482
35	443952	586524_1	AI149106 AI500318 AI334156 AI093029 AI765679 AI769652 AI167308 AI128885
	444406	605004_1	AI147237 AI800517
	445099	629785_1	BE163341 AI207756 BE171477
	445625	64558_1	BE246743 AA436942 AW024744 AW242177 AA975476 AW385185 R07536 R73462 AV654529 T57442 AI399986 R50073 R48743 AI769689
			AI833005 AA317805 AI678000 AW189963 AI965207 AW471273 R73463 AI335104 AI590161 AI469257 AI954604 H21954 T25141 AA856793
40	445631	6457_1	R50074 AI708253 AI2
			AK001822 AW860325 AA335296 AW965531 AW130957 AW193951 AI347975 AW081323 AW662527 AI343924 AI380749 AA938153 T66966
			AI655000 AW418837 AI380485 AA410698 AI520726 BE501355 AI637925 AW779200 AI524755 AW593995 AI336927 AI336928 AI357036 R60592
			H19058 R11124 T1
	445837	652068_1	AI261700 AI793196 AI469160 AI793007
45	446780	692897_1	R31107 AI341136 AI653198 HD4953
	446790	693032_1	AW452105 AI341280 AI917445
	447045	70510_1	AW392394 AW579531 AW382131 AA010316 BE146145 AW579562 AW579577 BE146152 BE146040 BE145972 BE146099 AW003280 AA868470
			BE146306 T85009 AI087294 BE146299 BE146319 BE146307 W44912 AI703134 AW026017 BE382873 AA903733 AI655933 BE551223 AA847664
			AW173582 AW57240
50	447128	70934_1	AI271898 BE048502 AI452509 AI244810 X84721 AI858001 AI553937 AA149853 H00719 AI765259 AW973696 F25787 F35749 AI568815
	447904	741913_1	AW015380 AA554539 C00201 AA961610 AW059537 R77127
	448330	758690_1	AW206303 AW207644 AI765705
	448993	79225_1	AL036449 AW016705 AI492482
			AI471630 BE540637 BE265481 AW407710 BE513882 BE546739 AA053597 BE140503 BE218514 AW956702 AI656234 AI636283 AI567265
55	449324	804806_1	AW340858 BE207794 AA053085 R69173 AA292343 AA454908 AA293504 AI659741 AI927478 AA399460 AI760441 AA346416 BE047245
	449495	808345_1	AA730380 AA394063 AA454
	450251	829987_1	AI638706 BE550292 R11026
	450536	837848_1	AI652833 AI695904 AW888916
60	450807	847591_1	BE080483 BE080416 AI689298
	451045	85673_1	AI699529 BE161564 BE077251
	451752	8835_1	AI739262 R28418
			AA215672 AI696628 AA013335 H86334 AA017006
			AB032997 N74056 BE467119 AW237035 AI141678 AA934774 AW978722 AI761408 H09497 AI934521 AA716567 H62600 AI479668 Z40632
65	452113	899664_1	AA832081 Z44858 H09496 BE395335 AW295901 BE465977 AI621269 BE465983 M79058 H62533 AA325444
	453413	966269_1	AI859393 BE177742
	453829	982731_1	AJ003294 AJ003315 AJ003293
	453904	986581_1	AL138200 T71830 T71828
	454438	120132_1	AW003821 AW027475 AW025661
			AA224053 AA114150 AA214275 AA224027 T58431 AA211908 AA689657 AA199744 AA630511 AA164864 T58463 AA214394 AA161378
70	454453	1206827_1	AA161386 AA205211 AA167824 AA084940 AA223625 AA191190 AA309486 AW961804
	454577	1225673_1	AW752781 BE143749 AW752727 AW752559 AW752578 AW752584 R45742
			AW809272 AW809169 AW809179 AW809192 AW809166 AW809172 AW809191 AW809165 AW809197 AW809181 AW809237 AW809226
			AW809250 AW809199 AW809259 AW809239 AW809273 AW809270 AW809147 AW809188 AW809245
	454682	1228976_1	AW816029 AW813292 AW816156 AW813333 AW816159 AW813302 AW813344 AW813172
75	454718	1230532_1	AW815144 AW815150 AW810007
	454756	1233646_1	AW819273 AW819283 AW819287 AW819281 AW819274 AW819282 AW819277 AW819286
	454923	1245024_1	AW897236 AW845406
	455035	1249762_1	AW851734 AW851676 AW851693 AW851713 AW851722 AW851616 AW851731 AW851618 AW851648 AW852215
	455274	1272212_1	BE161622 BE151636 AW885648
	455286	1273576_1	BE144384 AW887474 AW887403 BE144386
80	455557	1325974_1	AW995839 AW995907
	455604	1337197_1	BE011183 BE011170 BE011333 BE011188 BE011181 BE011324 BE011161 BE011169
	455679	1349914_1	BE066629 BE066274 BE066390 BE066356 BE066419 BE066345 BE066298 BE066292 BE066359
	455778	1364506_1	BE088746 BE088802 BE088755 BE088876 BE088947 BE088881 BE088952
	455885	1380385_1	BE153524 BE153576 BE153583

456487 19270_1 AF064804 AA320309 N89343 AA564588 AF069734 AA349248 AW964366 T98541 AW511100 T98542 AW070452 AA013172 A1767005 T32140
 W05727 T30969 T30970 N74883 AA903211 A1392796 A1434622 AA829283
 457892 432926_1 AA744389 AA744270 AA744284 AA744299 AA745380 AA744337 AA846905 AA847698
 457978 448900_1 AA776638 BE439540
 458188 504834_1 A1288100 AA952934 AA918305
 458644 670856_1 AW270149 AW664628 A1285912

TABLE 20C:

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495

Strand: Indicates DNA strand from which exons were predicted

Nt_position: Indicates nucleotide positions of predicted exons

	Pkey	Ref	Strand	Nt_position
15	400460	8389428	Plus	35559-36295
	400500	9796136	Minus	120238-120495
	400528	6981824	Plus	472381-472528,474170-474277,475328-475542,475878-476000
20	400668	8118719	Plus	121756-122043
	400748	8119063	Plus	84237-84398
	400762	8131616	Plus	7235-7605
	400772	8131629	Minus	34896-35021,41078-41197
	400833	8705148	Minus	187599-188138
	400863	9798616	Plus	21575-22330
25	400906	9966290	Plus	112863-112989,120162-120266
	400923	7637836	Minus	94518-94659
	401121	8570296	Plus	57211-57525
	401180	9438648	Minus	150981-152128
	401203	9743387	Minus	172961-173056,173868-173928
30	401210	7712287	Plus	166969-167133,169760-169877,171563-171733
	401215	9858408	Plus	103739-103919
	401264	9797154	Plus	130810-130927,133367-133504
	401278	9799936	Plus	98428-98573
	401349	9930791	Plus	72440-73030
35	401402	7710964	Plus	75730-76077
	401488	7341775	Plus	54523-54686,55364-55451,55737-55846,58047-58175,58261-58356
	401507	7534110	Plus	71055-71259
	401539	8072433	Minus	62028-62608
40	401553	8099284	Minus	83990-84161
	401594	7230963	Plus	7997-8170
	401674	7689903	Plus	138786-138927,139157-139298,139440-139599,139960-140159
	401677	9965537	Minus	62856-63086,63603-63884
	401722	7656694	Plus	143861-144054
	401724	7656694	Plus	150063-150241
45	401822	6730824	Plus	88400-89959
	401885	8140731	Plus	148234-148321,150365-150559
	401935	3808091	Plus	46329-46473
	401938	6102666	Plus	151891-152032
50	401984	4454511	Plus	103825-104024
	402189	8576043	Minus	128318-129601
	402197	8576113	Plus	199466-199585
	402285	2689079	Minus	92386-92634
	402365	9454515	Minus	70928-71185
55	402445	9796614	Plus	90925-91064,91172-91331
	402501	9797862	Plus	8601-8876
	402545	9838114	Minus	48547-48678,50604-50737,51384-51467
	402651	7960391	Plus	174215-174380
	402916	7406502	Minus	361-474,541-687
60	403003	5441423	Minus	79403-79560,79712-80021
	403128	7331426	Plus	122884-123018,123134-123283,123372-123695,123779-123940,124059-124256
	403672	7283286	Minus	96600-96681,96951-97280,97393-97594
	403748	7658423	Minus	129503-130344
	403885	7710403	Minus	53259-53524
65	403938	7711795	Plus	48636-48822
	404001	8555948	Minus	137995-138317
	404066	3367505	Minus	71040-71288
	404149	7534008	Plus	121831-121951,124044-124150
	404199	6010176	Minus	1669-2740
70	404311	8570412	Minus	149189-149303
	404333	9802821	Minus	137948-138024,138111-138300
	404365	9964977	Plus	50151-50319,50859-51098
	404430	7407979	Plus	42921-43109
	404438	6984205	Plus	63413-63553
75	404571	7249169	Minus	112450-112648
	404598	9958262	Minus	104807-105043
	404676	9797204	Minus	56167-56342,58066-58189,58891-59048,60452-60628
	404710	9801097	Minus	45190-45339,47509-47622,48137-48264,48805-48946,50073-50345,51467-51588
	404752	7109522	Minus	120168-120326
80	404807	4165210	Minus	124246-124422
	404956	7387343	Plus	55883-56203
	405085	8072509	Minus	44045-44230
	405113	8096927	Plus	170073-170894
	405143	9438278	Plus	5894-5983,7355-7427
	405159	9966252	Plus	79659-79804

5	419167	AI589535	Hs.94875	ESTs, Weakly similar to A35363	SS	18.6
	406663	U24683		immunoglobulin heavy constant	SS	18.5
	429712	AW245825	Hs.211914	ENSP00000233627-NADH-ubiquinol	oxidored_g6,SS,TM,rm	18.5
	425848	BE242709	Hs.159637	valyl-HRNA synthetase 2	GST_C,GST_N,Tropomyosin,S	18.4
	447151	AI022813	Hs.92679	Homo sapiens clone CDABP0014 m	SS,TMLRR,aminotran_1_2	18.4
	413343	BE392026	Hs.334346	hypothetical protein MGC13045	SS,DnaJ	18.2
	450029	AW073380	Hs.267963	hypothetical protein FLJ10535	SS,Pyridox_oxidase,zf-C2H	17.7
	427721	AI582843	Hs.180455	RAD23 (S. cerevisiae) homolog	ubiquitin,UBA,integrin_B,	17.6
10	443780	NM_012068	Hs.9754	activating transcription facto	bZIP,NTP_transf_2,SS,TBC	17.2
	421812	AF161254	Hs.106198	BD6 antigen	ldl_recept_a,SS,TM	17.1
	444607	AW405635	Hs.293687	ESTs	SS,PI-PLC-X,PH,PI-PLC-Y,C	16.7
	406621	X57809	Hs.181125	immunoglobulin lambda locus	SS	16.6
	443496	AJ006973	Hs.9482	target of myb1 (chicken) homol	VHS,GAT,TM,Heme_oxygenase	16.6
15	440104	AA132838	Hs.239894	hypothetical protein MGC2803	SS,DS	16.3
	427640	AF058293	Hs.180015	D-dopachrome tautomerase	MIF,late_protein_L2,SS,GS	16.2
	445625	BE246743		hypothetical protein FLJ22635	SS,TM	16.1
	427461	AA531527	Hs.332040	hypothetical protein MGC13010	SS,TM,ACAT,LRR	15.9
	423366	Z80345	Hs.127610	acyl-Coenzyme A dehydrogenase,	Acyl-CoA_dh,Acyl-CoA_dh_M	15.7
20	409017	T86957	Hs.272299	hypothetical protein RP4-622L5	SS,TM	15.6
	428167	AA770021	Hs.16332	ESTs	SS,Ig,In3	15.5
	420029	BE258876	Hs.94446	polyamine-modulated factor 1	aldo_ket_red,SS,TM,glu	15.5
	400460			C11002253-gil129091[sp]P23267	SS,TM,SCAN,zf-C2H2,KRAB	15.4
	407767	W15398	Hs.38628	hypothetical protein	SS,zf-CCCH	15.4
25	406918	M88357		gbr:Homo sapiens DNA-binding pr	zf-C2H2,SS	15.4
	435158	AW663317	Hs.65588	DAZ associated protein 1	rm,ss,rm	15.3
	407619	AL050341	Hs.37165	collagen, type IX, alpha 2	SS,Collagen,SS,Collagen	15.3
	421273	AJ245416	Hs.103108	U6 snRNA-associated Sm-like pr	Sm,SS,IRNA-sym_L1,GST_C,G	15.1
	402365			Target Exon	SS,SS,TM,Ig	14.9
30	450503	R35917	Hs.301338	hypothetical protein FLJ12587	SS	14.8
	427502	AI811865	Hs.7133	Homo sapiens, clone IMAGE:3161	SS,TM,ABC_tran,Glyco_tran	14.6
	432872	AJ908984	Hs.279623	selenoprotein X, 1	DUF25,SS,Ribosomal_L3,PDZ	14.5
	439233	AA831893	Hs.292767	hypothetical protein FLJ23109	zf-C3HC4,TM,Sulfate_trans	14.5
	416897	M78146	Hs.324700	hypothetical protein MGC2663	SS	14.3
35	447304	Z98883	Hs.18079	phosphatidylinositol glycan, c	SS,Peptidase_C2	14.2
	431543	AW69619	Hs.259768	adenylate cyclase 1 (brain)	TM	14.0
	447544	AA401573	Hs.288284	hypothetical protein FLJ22378	SS,TM	14.0
	417595	AA424317	Hs.6259	KAA1698 protein	SS,TM,Glyco_hydro_31,Glyc	13.8
	436127	W94824	Hs.11565	RIKEN cDNA 2010100012 gene	Corona_7,SS,TM	13.8
40	412623	R28898	Hs.74170	metallothionein 1E (functional	SS,TM,metallothio,DEAD,meta	13.7
	448133	AA723157	Hs.73769	folate receptor 1 (adult)	Folate_rec,SS	13.5
	453367	AW732847	Hs.70573	PKC1-related HIT protein	SS,TM	13.5
	431462	AW583672	Hs.256311	granin-like neuroendocrine pep	SS	13.2
	408724	AI658842	Hs.294143	ESTs, Weakly similar to T22914	SS,pkinase,tubulin	13.2
45	423464	NM_016240	Hs.128856	CSR1 protein	Collagen,SS	13.1
	428539	AW410063	Hs.184877	solute carrier family 25 (mito	mito_car,SS,TM,profilin,	13.0
	436014	AF281134	Hs.283741	exosome component Rrp46	RNase_PH,RNase_PH_C,SS,TG	12.9
	438857	AI627912	Hs.130783	Forsman synthetase	SS,RA,RasGEF,RasGEFN	12.8
	444410	BE387360	Hs.33719	ESTs, Moderately similar to S6	SS	12.8
50	427527	AI809057	Hs.153261	immunoglobulin heavy constant	SS,TM,Ig	12.6
	430168	AW968343		DKFZP434H1735 protein	SS,TM,efhand,efhand	12.5
	437543	H16443	Hs.7117	glutamate receptor, ionotropic	SS,TM,Ig_chan,ANF_recept	12.4
	413711	AW291765	Hs.75486	heat shock transcription facto	NA,SS,E2F_TDP	12.3
	422825	AW504698	Hs.155976	cullin 4B	SS,SS,Cullin,Cullin	12.2
55	443136	NM_001440	Hs.9018	exostoses (multiple)-like 3	Exostosis,SS,TM	12.1
	407143	C14076	Hs.332329	EST	SS,TM	12.1
	424707	BE081914	Hs.10844	Homo sapiens cDNA FLJ14476 fs	SS,SS,TM,Sema	12.1
	426251	Z22521	Hs.155342	protein kinase C, delta	pkinase,DAG_PE-bind,pkina	12.0
	427336	NM_005658	Hs.2134	TNF receptor-associated factor	MATH,SS,MATH,A2M_N,A2M,NT	12.0
60	421572	AA531607		hypothetical protein FLJ22678	SS,TM,TGF-beta,ASC	12.0
	447946	AI566164	Hs.165827	ESTs	SS,PTN_MK,7tm_1,DAGKc,DAG	11.9
	425954	AK000633	Hs.164476	hypothetical protein FLJ20626	SCAN,zf-C2H2,KRAB,SS,KRAB	11.7
	427273	AW139032	Hs.107376	hypothetical protein DKFZp434N	SS,SS,TM	11.7
	427397	AI929685	Hs.177656	calmodulin 1 (phosphorylase ki	efhand,RnaAD,SS,efhand	11.7
65	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	enolase,SS,Atrophin-1,Atr	11.7
	417852	AJ250562	Hs.82749	transmembrane 4 superfamily me	transmembrane4,SS,TM	11.6
	447451	AJ379925	Hs.207525	ESTs	SS,pkinase,PH,pkinase_C	11.5
	410397	AF217517	Hs.63042	DKFZp564J157 protein	SS,homeobox,UFP0160,DUF23	11.4
	430354	AA954810	Hs.239784	human homolog of Drosophila Sc	SS,TM,Ig	11.3
70	419390	AI701162	Hs.90207	hypothetical protein MGC11138	SS,TM,PMP22_Claudin,PMP22	11.3
	422682	W05238	Hs.94316	ESTs, Weakly similar to T31613	SS,TM,DEAD,helicase_C,Lam	11.3
	422178	AL122063	Hs.112645	Homo sapiens mRNA; cDNA DKFZp4	SS,TM	11.2
	450122	BE313765	Hs.343443	ESTs, Weakly similar to I38022	SS,TM,Y_phosphatase,LON,A	11.1
	453968	AA847843	Hs.62711	High mobility group (nonhiston	SS,HMG_box	11.1
75	444744	BE394732	Hs.147562	ESTs	SS	10.9
	423220	BE394920	Hs.125262	aladin	WD40,TM,Activin_rec,pkin	10.9
	417116	Z43916	Hs.7634	hypothetical protein FLJ12287	SS,TM,filament,IF_tail	10.9
	406779	AA412048	Hs.279574	CGI-39 protein; cell death-reg	SS,SS	10.8
	450593	AF129085	Hs.25197	STIP1 homology and U-Box conta	TPR,SS,TM,Rhomboid,Jaclam	10.7
80	406837	R70292	Hs.156110	immunoglobulin kappa constant	SS	10.7
	452434	D30934	Hs.29549	C-type lectin-like receptor-1	lectin_c,SS,TM	10.7
	440150	AW975738	Hs.7001	Homo sapiens, clone IMAGE:3940	SS,TM,SS,TM,Peptidase_M22	10.6
	418641	BE243136	Hs.86947	a disintegrin and metalloprote	disintegrin,Repolyisin,Pe	10.6
	414313	NM_004371	Hs.75887	coatomer protein complex, subu	WD40,SS,WD40,Ribosomal_S2	10.6
	420307	AW502869	Hs.66219	ESTs	SS,TM	10.6

5	414918	AI219207	Hs.72222	hypothetical protein FLJ13459	SS,TM,efhand	10.6
	446562	BE272686	Hs.15356	hypothetical protein FLJ20254	hormone,SS,ptkB	10.5
	419846	NM_015977	Hs.285681	Williams-Beuren syndrome chrom	SS,HLH,SS,TM,WD40	10.4
	453023	AW028733	Hs.31439	serine protease inhibitor, Kun	Kunitz_BPT1,SS,TM,ion_tra	10.4
	438800	AB037108	Hs.6418	seven transmembrane domain orp	SS,TM	10.3
	431275	T56571	Hs.10041	ESTs	SS,HLH	10.3
	407241	M34516		gb:Human omega light chain pro	SS,ig,PH,ig,PH	10.3
	441238	AJ372555	Hs.322456	hypothetical protein DKFZp761D	homeobox,SS,TM,Rho_GDI,th	10.3
10	436325	AL390088	Hs.7393	hypothetical protein from EURO	SS,Synapsin_C,SS	10.3
	435605	AF151815	Hs.4973	hypothetical protein	SS,TM,SS,TM,ABC_tran,ABC	10.3
	444202	AL031685	Hs.12785	KIAA0939 protein	SS,TM,Na_H_Exchange,ABC2	10.3
	425597	U28694	Hs.158324	chemokine (C-C motif) receptor	7tm_1	10.3
	415200	AL040328	Hs.78202	SWI/SNF related, matrix associ	SNF2_N,helicase_C,bromodo	10.2
15	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	NoH1_Nop2_Sun,SS,SNF2_N,h	10.2
	414874	D26351	Hs.77515	inositol 1,4,5-trisphosphate re	TM,RYDR,TTPR,ion_trans,Mi	10.2
	423524	AF055989	Hs.129738	potassium voltage-gated channe	ion_trans,K_tetra,thumal	10.2
	434552	AA639618	Hs.325116	Homo sapiens, clone MGC-2962,	SS	10.2
	406836	AW514501	Hs.156110	immunoglobulin kappa constant	SS	10.1
20	420233	AA256714	Hs.194864	hypothetical protein FLJ22578	SS	10.1
	427458	BE208364	Hs.29283	ESTs, Weakly similar to LKHU p	SS,F5_F8_type_C,EGF,TGT	10.1
	427672	AA356615	Hs.336916	death-associated protein 6	SS,BTB,abhydrolase_2,RasG	10.0
	423218	NM_015896	Hs.167380	BLu protein	zf-MYND,SS,TM,Glyco_hydro	10.0
	403028			Target Exon	SS,tretol	10.0
25	412780	NM_014767	Hs.74583	KIAA0275 gene product	kazal,thyroglobulin_1,zf	10.0
	419823	AW271708	Hs.118918	ESTs, Weakly similar to M2OM_H	SS,TM	10.0
	433886	AA613596	Hs.28412	ESTs	SS	9.9
	428092	AW879141		ESTs	SS,TM	9.8
	450493	M93718	Hs.166373	nitric oxide synthase 3 (endot	flavodoxin,FAD_binding,NO	9.7
30	420423	AA827718	Hs.88218	ESTs	SS	9.7
	452302	AF173867	Hs.28906	glucocorticoid modulatory elem	SAND,SS	9.7
	444681	AJ243937	Hs.288316	chromosome 6 open reading fram	notch,EGF,ank,GoLoco,SS,T	9.7
	414249	AJ797994	Hs.279929	gp25L2 protein	SS,TM,EMP24_GP25L,SS,TM,G	9.6
	424263	M77640	Hs.1757	L1 cell adhesion molecule (hyd	fn3,ig,IRK,SS,TM,fn3,ig,R	9.6
35	438627	AJ087335	Hs.123473	ESTs	TM,Rebculon	9.6
	407065	Y10141		gb:H.sapiens DAT1 gene, partia	SNF,SS,TM	9.6
	441307	AW071696	Hs.209065	hypothetical protein FLJ14225	SS,TM	9.6
	409649	AA159216	Hs.55505	hypothetical protein FLJ20442	Y_phosphatase,DSPc,TM	9.6
	424487	T08754	Hs.6259	KIAA1698 protein	SS,SS,TM,Glyco_hydro_31,G	9.5
40	444633	AF111713	Hs.286218	junctional adhesion molecule 1	ig,SS,TM,HLH	9.4
	427747	AW411425	Hs.180655	serine/threonine kinase 12	pkinaase,SS,TM,synaptobrev	9.4
	450437	X13956	Hs.24998	hypothetical protein MGC10471	SS	9.4
	415169	W42913	Hs.78089	ATPase, vacuolar, 14 kD	ATP-synt_L,SS,TM,CH,Filam	9.4
45	400201			NM_006156: Homo sapiens neural	ubiquitin,SS,TM,Transglut	9.4
	454319	AW247736	Hs.101617	ESTs, Weakly similar to T35227	SS	9.4
	421680	AL031186	Hs.289106	Human DNA sequence from clone	SS,SS,rm,zf-RanBP,rm,GA	9.4
	445143	U29171	Hs.75852	casein kinase 1, delta	pkinaase,SS	9.4
	407507	U73799		gb:Human dynactin mRNA, partia	SS,TM,HCO3_cotransp,CAP_G	9.4
50	450883	NM_001348	Hs.25619	death-associated protein kinas	pkinaase,GTP_EFTU,EFG_C,GT	9.4
	411674	AW861123		gb:RC3-CT0297-120200-014-a05 C	SS	9.3
	414625	AA335738	Hs.76686	glutathione peroxidase 1	GSHPx,SS,ras,HLH	9.3
	456950	AF111170	Hs.306165	Homo sapiens 14q32 Jagged2 gen	SS,TM,DSL	9.3
	445333	BE537641	Hs.44278	hypothetical protein FLJ12538	SS	9.2
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_H	SS,histone,histone	9.1
55	412338	AA151527	Hs.69485	hypothetical protein FLJ12436	SS,TM,TIG,Sema,PSI	9.1
	439963	AW247529	Hs.6793	platelet-activating factor ace	PAF-AH1b,Lipase_GDSL,SS,	9.1
	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN	SS,TM	9.1
	443553	AL040535	Hs.9573	ATP-binding cassette, sub-famil	ABC_tran,SS	9.1
60	448984	AW751955	Hs.22753	hypothetical protein FLJ22318	SS	9.0
	418776	AJ401004	Hs.88411	lymphocyte antigen 117	SS,TNF,TNF	9.0
	418843	AJ251016	Hs.89230	potassium intermediate/small c	TM,CaMBD,SK_channel,TM	9.0
	419244	AJ436567	Hs.89761	ATP synthase, H transporting,	ATP-synt_DE,SS,rm,Ephrin	8.9
	451855	R54913	Hs.175804	ESTs	SS,TM,vwa	8.9
	424826	AF207069	Hs.153357	procollagen-lysine, 2-oxogluta	2OG-Fell_Oxy,Glycos_trans	8.9
65	447374	AF263462	Hs.18376	KIAA1319 protein	SS,Myosin_tail,M	8.9
	430167	Y08976	Hs.234759	FEV protein	Ets,SS,crystall	8.8
	409936	AK001691	Hs.57655	hypothetical protein FLJ10829	SS,TM	8.7
	437926	BE383605	Hs.300818	small GTP-binding protein	SS,TM,TPR	8.7
	430037	BE409649	Hs.227789	mitogen-activated protein kina	pkinaase	8.7
70	424919	BE314461	Hs.153768	U3 snoRNP-associated 55-kDa pr	WD40,SS,KH-domain	8.7
	414534	BE257293	Hs.76366	BCL2-antagonist of cell death	SS,hormone_rec,zf-C4	8.7
	433333	AJ016521	Hs.71816	v-akt murine thymoma viral onc	homeobox,pkinaase,PH,pkina	8.7
	423228	AL137491	Hs.125511	Homo sapiens mRNA: cDNA DKFZp4	SS,TM,sushi	8.7
	419493	AF001212	Hs.90744	proteasome (prosome, macropain	PCL,SS,CDK5_activator	8.7
75	420160	AJ492840		ESTs	SS,TM	8.6
	421871	AK001416	Hs.306122	glycoprotein, synaptic 2	TM,Steroid_dh,SS	8.6
	447827	U73727	Hs.18718	protein tyrosine phosphatase,	Y_phosphatase,fn3,ig,MAM,	8.6
	417183	AJ922189	Hs.288390	hypothetical protein FLJ22795	SS	8.6
80	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-	SS,TM,zf-C2H2	8.5
	458963	AJ701393	Hs.278728	Rad and Gem-related 2 (rat hom	ras,SS,Peptidase_M10,hemo	8.5
	406868	AA505445	Hs.300697	immunoglobulin heavy constant	SS,TM,ig	8.3
	434105	AW952124	Hs.13094	presenilins associated rhombol	TM,Rhomboid,SS,TM	8.3
	421726	AK001237	Hs.319088	hypothetical protein FLJ10375	TM	8.3
	421707	NM_014921	Hs.107054	lectomedin-2	Lathophilin,OLF,7tm_2,Gal	8.2
	453898	AW003512	Hs.232770	arachidonate lipooxygenase 3	SS,TM,lipoxygenase,PLAT,s	8.2

5	456672	AK002016	Hs.114727	Homo sapiens, clone MGC:16327,	SS,PK,PK_C,myosin_head,Rh	8.2
	421592	AF009801	Hs.105941	bagpipe homeobox (Drosophila)	homeobox,SS	8.2
	409829	M33552	Hs.56729	lymphocyte-specific protein 1	Cadherin,SS,Ribosomal_S2	8.1
	444341	A1142027	Hs.146650	ESTs	SS,TM,Repolysin,Pap_M12B	8.0
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	FKBP,TPR,SS	8.0
	436685	W28661	Hs.5288	Homo sapiens mRNA; cDNA DKFZp4	SS,TM,plnase,Activin_rec	8.0
	420932	AW374605	Hs.11607	ESTs, Weakly similar to T21697	SS,bZIP_Maf	8.0
	431493	A1791493	Hs.129873	ESTs, novel cytochrome P450	SS,p450,SS	7.9
10	447598	A1799568	Hs.199630	ESTs	SS,TM	7.9
	415758	BE270465	Hs.78793	protein kinase C, zeta	pkase,DAG_PE-bind,plnase	7.8
	457022	AW377258		gb:MR2-CT0222-261099-003-a10 C	SS,Ribosomal_L7Ae	7.8
	426440	BE382756	Hs.169902	solute carrier family 2 (facil	sugar_tr,SS,TM,sugar_tr	7.8
	432747	NM_014404	Hs.278907	calcium channel, voltage-depen	PMP22_Claudin,SS,TM,PMP22	7.8
15	441084	W24563	Hs.9911	hypothetical protein FLJ11773	SS,TM,hormone_rec,zf-C4	7.8
	424443	A1751281	Hs.284161	hypothetical protein from EURO	SS,TM,SS,TM	7.7
	424198	AB029010	Hs.143026	KIAA1087 protein	SS,TM,Na_Ca_Ex,Catx-beta,	7.6
	430513	AJ012008	Hs.241586	G6C protein	SS,TM,GST_C,abhydrolase	7.6
	417900	BE250127	Hs.82906	CD20 (cell division cycle 20,	WD40,SS,TM,tn3,EGF,tn3,Ig	7.6
20	432891	AF161483	Hs.279761	HSPC134 protein	SS,TM,ubiquitin,Transglut	7.5
	432234	AA531128	Hs.115803	ESTs	SS	7.5
	453485	BE620712	Hs.33026	hypothetical protein PP2447	SS,TM	7.5
	441327	AK001706	Hs.7778	hypothetical protein FLJ10751	SS,TM,7tm_1	7.5
	436540	BE397032	Hs.14468	hypothetical protein MGC14228	SS,TM	7.5
25	418256	AW845318	Hs.12271	I-box and leucine-rich repeat	SS,SS,TM,HSF_DNA-bind	7.5
	457274	AW674193	Hs.227152	-mannan-binding lectin serine p	SS,TM,SS,TM,Claudin,Ig_c	7.5
	437141	BE304917	Hs.31097	hypothetical protein FLJ21478	SS,TM,Glycos_transf_4	7.5
	425428	AL110261	Hs.157211	DKFZP586B0621 protein	C1q,Collagen,SS	7.4
	431934	AB031481	Hs.272214	STG protein	SS	7.4
30	418349	NM_001383	Hs.84183	diphtheria toxin resistance pro	Diphthamide_syn,SS	7.4
	430600	AW950967	Hs.274348	HLA-B associated transcrit-3	ubiquitin,SS,TM,C-patch,a	7.3
	421758	BE397336	Hs.1422	Gardner-Rasheed feline sarcoma	SH2,SH3,plnase	7.3
	412841	A1751157	Hs.101395	hypothetical protein MGC11352	SS,TM	7.3
	418313	BE244231	Hs.84038	CGI-06 protein	SS,wap	7.3
35	429387	AB007867	Hs.278311	plexin B1	Sema,PSI,TIG,SS,TM,TIG,Se	7.3
	418837	U48263	Hs.89040	preprokinectin	Opioids_neuropep,SS	7.2
	423015	U18548	Hs.123034	G protein-coupled receptor 12	TM	7.2
	440188	AK001812	Hs.7036	N-Acetylglucosamine kinase	ROK,SS,TM	7.2
	421975	AW961017	Hs.6459	hypothetical protein FLJ11856	SS,TM,ACAT	7.2
40	423858	AL137326	Hs.133483	Homo sapiens mRNA; cDNA DKFZp4	SS,TM	7.2
	446143	BE245342	Hs.306079	sec51 homolog	secY,SS,TM	7.2
	417704	NM_001747	Hs.82422	capping protein (actin filamen	Gelsolin,SS,Gelsolin	7.2
	440869	NM_014297	Hs.7486	protein expressed in thyroid	lactamase_B,SS,XRCC1_N,BR	7.1
	435099	AC004770	Hs.4756	flap structure-specific endonu	XPG_N,XPG_L5_3_exonuclea	7.1
45	438856	N40027	Hs.7473	ESTs	SS,TM,connexin	7.1
	426268	AF083420	Hs.168913	serine/threonine kinase 24 (St	plnase,plnase	7.1
	418373	AW750770	Hs.84344	CGI-135 protein	SS,TM,PMP22_Claudin,2OG-F	7.1
	445087	AW893449	Hs.12303	suppressor of Ty (S.cerevisiae	S1,SH2,Ribosomal_L23,pln	7.1
	421748	NM_014718	Hs.107809	KIAA0726 gene product	cadherin,TM,TPR	7.1
50	413837	AW163525		lin-cap (telothelin)	SS,Methyltransf_3	7.0
	426691	NM_006201	Hs.171834	PCTAIRE protein kinase 1	plnase,SS,UCH-2,UCH-1,rr	7.0
	409125	R17268	Hs.343567	axonal transport of synaptic v	SS,kinesin,PH,FHA,kinesin	7.0
	424251	AA677466	Hs.143696	coactivator-associated arginin	SS,SNF2_N,helicase_C,brom	7.0
	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD4	Integrin_A,FG-GAP,Rhabd_g	7.0
55	428156	BE269388	Hs.182698	mitochondrial ribosomal protei	SS	7.0
	459255	A1493244	Hs.239500	hypothetical protein MGC13114	SS	7.0
	441323	AA928413	Hs.159089	ESTs, Weakly similar to ALU7_H	SS,Peptidase_C1,zf-C2H2	6.9
	455928	BE170313		gb:QV4-HT0536-040500-193-g02 H	SS	6.9
	420856	BE513294	Hs.205735	HLA class II region expressed	kazal,SS,TM,Ig,plnase	6.9
60	421543	AK000519	Hs.105605	hypothetical protein FLJ20512	TM	6.9
	442258	NM_007275	Hs.8186	lung cancer candidate	SS,TM,Glyco_hydro_56,Glyc	6.9
	445937	AA52943	Hs.321231	UDP-Gal:betaGlcNAc beta 1,4-g	Galactosyl_T_2,SS,TM,ssp_	6.9
	439732	AW629604	Hs.167641	hypothetical protein from EURO	SS,TM,SS,TM,A2M,A2M_N,NTR	6.8
	429542	AF038650	Hs.206713	UDP-Gal:betaGlcNAc beta 1,4-g	Galactosyl_T_2,Ig,SS,TM,A	6.8
65	420190	AJB16209	Hs.95867	hypothetical protein EST00098	SS,dynamin_2,dynamin,PH,G	6.8
	408215	BE614290		syntaxin 10	SS,SS,TM,HLH,TRM,zf-CCCH	6.7
	410277	R88621	Hs.26249	ESTs, Weakly similar to T2D3_H	SS,TM,SS	6.7
	419667	AU077005	Hs.92208	a disintegrin and metalloprote	disintegrin,Repolysin,Pe	6.7
	448877	A1560769		ESTs	SS,TM	6.7
70	425228	NM_005253	Hs.301612	FOS-like antigen 2	bZIP,SS	6.6
	432538	BE258332	Hs.278362	male-enhanced antigen	SS,TM,AAA,Ribosomal_L2	6.6
	421864	BE387198	Hs.108973	dolichyl-phosphate mannosyltra	SS,TM,SS,TM	6.6
	429962	M69113	Hs.226795	glutathione S-transferase pi	GST_C,GST_N,SS,ethand	6.6
	408867	AA157857	Hs.182265	keratin 19	filament,bZIP,SS,filament	6.6
75	426068	AF029778	Hs.166154	jagged 2	DSL,EGF,vwc,granulin,SS,T	6.5
	419344	U94905	Hs.277445	diacylglycerol kinase, zeta (1	ank,DAGKa,DAGKc,DAG_PE-bi	6.5
	424681	AA054400	Hs.151706	KIAA0134 gene product	helicase_C,PRK,SS,TM,7tm_	6.5
	417903	NM_002342	Hs.1116	lymphotoxin beta receptor (TNF	TNFR_c6,SS	6.5
	423876	BE502835	Hs.15463	Homo sapiens, clone IMAGE:2959	SS,ethand	6.4
80	433439	AA431176	Hs.133230	ribosomal protein S15	TM,SS,TM,TPR,ras	6.4
	441379	AW175787	Hs.334841	selenium binding protein 1	SS,RFX_DNA_binding	6.4
	432968	BE614192	Hs.279869	melanoma-associated antigen re	SS,TM,RGS,DIX	6.4
	456863	T16837	Hs.4241	ESTs	fusion_gly,homeobox,TM	6.4
	432269	NM_002447	Hs.2942	macrophage stimulating 1 recep	plnase,Sema,PSI,TIG,AA_E	6.4
	425676	AW410656	Hs.159161	Rho GDP dissociation inhibitor	Rho_GDI,homeobox,SS,Cytd	6.4

5	443420	R06846	Hs.191208	ESTs	SS	6.4
	436322	AL355092	Hs.120243	parvin, gamma	CH,SS,TM,CTF_NFI	6.4
	440088	BE555877	Hs.183232	hypothetical protein FLJ22638	SS,zf-C3HC4,SPRY,zf-B_box	6.4
	447665	BE044245	Hs.30011	hypothetical protein MGC2963	SS,TM	6.3
	431785	AA282385	Hs.268763	Breakpoint cluster region prot	BAF,kazal,TM	6.3
	422714	AB018335	Hs.119387	KIAA0792 gene product	DUF221,SS,TM,TGFb_propept	6.3
	434916	AF161383	Hs.284207	Homo sapiens, Similar to RIKEN	TM	6.3
	414551	AJ815639	Hs.76394	enoyl Coenzyme A hydratase, sh	ECH,Peptidase_U7,SS,TM	6.3
10	413254	U40272	Hs.75253	isocitrate dehydrogenase 3 (NA	isodh,SS	6.3
	458367	AA088470	Hs.83135	Homo sapiens, Similar to RIKEN	SS,IRNA-synt_2d	6.3
	415010	NM_004203	Hs.77783	membrane-associated tyrosine-	pklnase,SS,PMP22_Claudin	6.3
	410076	T05387	Hs.7991	ESTs	SS	6.3
	412940	BE295701	Hs.819	homeo box B7	homeobox,SS,homeobox,home	6.2
	440042	AI073387	Hs.133898	ESTs	SS	6.2
15	414023	BE243628		gb:TCBAP1D1053 Pediatric pro-B	SS	6.2
	414513	AW239400	Hs.76297	G protein-coupled receptor kin	pklnase,RGS,PKINASE_C,SS,	6.2
	446662	NM_013323	Hs.15827	sorting nexin 11	PX,SS	6.2
	409882	AJ243191	Hs.56874	heat shock 27kD protein family	HSP20,SS,TM,zf-C2H2,BTB,E	6.2
20	414576	AK000405	Hs.76480	ubiquitin-like 4	ubiquitin,SS,TM,G6PD,G6PD	6.2
	447507	H59698	Hs.18747	POF7 (processing of precursor,	SS,TM,WD40,vwd,MAM,EPO_TP	6.2
	453447	AW771318	Hs.326586	hypothetical protein MGC11134	SS,TPR	6.1
	435968	AW161481	Hs.111577	integral membrane protein 3	TM	6.1
	424441	X14850	Hs.147097	H2A histone family, member X	histone,CBFD_NFYB_HMF,SS,	6.1
25	434558	AW264102	Hs.39168	ESTs	SS,TM,LRRCT,LRR	6.1
	434202	BE382411	Hs.3764	guanylate kinase 1	Guanylate_kin,CoaE,Viral	6.1
	432183	AW151952	Hs.46679	hypothetical protein FLJ20739	SS	6.0
	444416	AW288085	Hs.11166	hypothetical protein	zf-C3HC4,SpoA,PHD,TM,syna	6.0
	447205	BE617015	Hs.11006	ESTs, Moderately similar to T1	SS,TM,LRRCT,Sema	6.0
30	407704	BE315072	Hs.78768	malignant cell expression-enha	TM,MBOAT,SS,TM	6.0
	453190	AB002354	Hs.32312	KIAA0356 gene product	PH,PHD,RUN,SS	6.0
	439975	AW328081	Hs.6817	inosine triphosphatase (nucleo	Hamp1-like,SS	6.0
	449514	AW970440	Hs.23642	protein predicted by clone Z36	SS,PX,ar,Upocatin,PHD,z	6.0
	432805	X94630	Hs.3107	CD97 antigen	SS,TM,7tm_2,GPS,EGF,SS,TM	6.0
35	414362	AL347934	Hs.75932	N-ethylmaleimide-sensitive fac	NSF,SS,TM	6.0
	417483	BE549343	Hs.82208	acyl-Coenzyme A dehydrogenase,	Acyl-CoA_dh,Acyl-CoA_dh_M	6.0
	427988	AA789333	Hs.181349	hypothetical protein 628	SS,SS	6.0
	423473	H49104	Hs.129888	hypothetical protein FLJ14768	zf-C2H2,SS,rm,ENTH	6.0
	406773	AA812424	Hs.76067	heat shock 27kD protein 1	HSP20,SS	5.9
40	409938	AW974848		gb:EST386752 MAGE resequences,	SS,Adap_comp_sub,GYF	5.9
	424959	NM_005781	Hs.153937	activated p21cdc42Hs kinase	pklnase,SH3	5.9
	453082	H18835	Hs.31608	hypothetical protein FLJ20041	SS,TM,lon_trans	5.9
	452094	AF049105	Hs.27910	centrosomal protein 2	bZIP_5_3_exonuclease,M,SS	5.9
	451524	AK001466	Hs.26516	hypothetical protein FLJ10604	SS,SS,TM,PKINASE,PKINASE_	5.9
45	427438	AW328515	Hs.178011	hypothetical protein FLJ20257	SS,TM	5.9
	439685	AW956781	Hs.293937	ESTs, Weakly similar to FXD2_H	SS,PWWP,TSC22	5.9
	440511	AF132959	Hs.7236	eNOS interacting protein	SS,TM,MAGE,Ribosomal_S17,	5.9
	417334	AA337572	Hs.157240	hypothetical protein MGC4737	SS,TM,lon_trans	5.9
	425976	C75094	Hs.334514	NG22 protein	SS,TM,PKINASE,SH2,SH3,BNR	5.8
50	433173	Z35093	Hs.3196	surfeit 1	SURF1,SS,TM,SURF1,SURF4	5.8
	437891	AW006969	Hs.6311	hypothetical protein FLJ20859	TM,SET	5.8
	410239	AI568350	Hs.61273	hypothetical protein MGC2650	SS,ART,TM	5.8
	458060	R95860	Hs.293629	hypothetical protein MGC3121	SS	5.8
	409591	AA532963	Hs.9100	Homo sapiens cDNA FLJ13100 fis	SS,TM,LM,homeobox	5.8
55	409686	AK000002	Hs.55879	Homo sapiens mRNA; cDNA DKFZp4	SS,ABC_tran,SS,TM	5.8
	450778	U81375	Hs.25450	solute carrier family 29 (nuc	Nucleoside_tran,SS,TM,HSP	5.8
	423612	NM_002067	Hs.1686	guanine nucleotide binding pro	G-alpha,arf,SS,G-alpha	5.8
	422701	NM_014699	Hs.119273	KIAA0296 gene product	zf-C2H2,GST_C,PHD,SS,TM,H	5.8
	412958	BE391579	Hs.75087	Fas-activated serine/threonine	SS,PKINASE	5.8
60	436957	AA902488	Hs.122952	ESTs	SS,DAGKc,DAGKa,RA,DAG_PE-	5.8
	423158	H97991	Hs.193313	Target CAT	MoaA_NifB_PqqE,SS,TM	5.8
	414788	X78342	Hs.77313	cyclin-dependent kinase (CDC2-	pklnase	5.8
	420904	AL036964	Hs.100221	nuclear receptor subfamily 1,	hormone_rec,zf-C4,SS,DNA_	5.7
	410431	BE261320	Hs.158196	transcriptional adaptor 3 (ADA	pklnase	5.7
65	420508	AJ270593	Hs.98428	homeo box B6	homeobox,SS,homeobox,home	5.7
	435593	R88872	Hs.4964	DKFZP586J1624 protein	Herpes_HEPA,SS	5.7
	433064	D79991	Hs.30002	SH3-containing protein SH3GLB2	TM	5.7
	451920	AA224483	Hs.27239	DKFZP586K0524 protein	SS,TM,SS,TM	5.7
	453054	AI878908	Hs.31547	Target CAT	SS	5.7
70	415117	AF120499	Hs.78016	polynucleotide kinase 3'-phosp	Viral_helicase1,SS,Amino_	5.7
	413163	Y00815	Hs.75216	protein tyrosine phosphatase,	fn3,jg,Y_phosphatase,SS,T	5.7
	425246	AI085561	Hs.155321	serum response factor (c-fos s	SRF-TF,flavodoxin,SS,TM,p	5.7
	433271	BE621697	Hs.14317	nuclear protein family A, me	SS,TM	5.7
	448484	BE613340	Hs.334725	Homo sapiens, Similar to RIKEN	TM,SS,TM,Kunitz_BPTI	5.7
75	449139	BE268315	Hs.23111	phenylalanine-IRNA synthetase-	neur,SS,zf-C2H2,DNase_II	5.7
	449181	X96783	Hs.23179	synaptotagmin V	C2,SS,TM,Y_phosphatase,Tr	5.6
	414457	AW514320	Hs.76159	ATPase, H transporting, lysoso	ATP-synt_C,SS,TM,PKINASE	5.6
	424964	AW161271	Hs.153961	ARP1 (actin-related protein 1,	actin,SS	5.6
	415193	AL048891	Hs.12185	hypothetical protein MGC14333	SS,TM,aminotran_1_2,LRR	5.6
80	407754	AA527348	Hs.288967	Homo sapiens cDNA FLJ14105 fis	SS,TM,SS,TM,TSPN,sp_3,SE	5.6
	413049	NM_002151	Hs.823	hepsin (transmembrane protease	trypsin,SS,TM,ATP1G1_PLM_	5.6
	454252	H50258	Hs.63236	ribosomal protein S15a	SS	5.6
	431787	AW972024	Hs.343661	ret finger protein	SS,WD40,PKINASE	5.6
	431607	AB033097	Hs.183669	KIAA1271 protein	SS,TM	5.6
	406782	AA430373		gb:zw20f11.s1 Soares ovary tum	SS	5.6

5	444364	AL137294	Hs.10964	hypothetical protein FLJ22351	SS,TM,pkinase	5.6
	427834	AA506101	Hs.285813	hypothetical protein FLJ11807	SS,TM	5.5
	443759	BE390832	Hs.134729	FXD domain-containing ion tra	SS,TM,ATP1G1_PLM_MAT8,ATP	5.5
	418322	BE019494	Hs.78217	pyrroline-5-carboxylate reduct	PSCR,Octopine_DH_N,SS,thi	5.5
	406673	M34996	Hs.198253	major histocompatibility compl	SS,TM,MHC_II_alpha,lg,SS,	5.5
	415351	U44755	Hs.78403	small nuclear RNA activating c	SS,TM,pkinase	5.5
	411030	BE387193	Hs.67896	7-60 protein	SS,Collagen,Collagen	5.5
	410653	BE383768	Hs.65238	95 kDa retinoblastoma protein	zf-C3HC4,SS,SNF2_N,helica	5.5
10	433012	NM_004045	Hs.279910	ATX1 (antioxidant protein 1, y	HMA,SS,TM	5.5
	437741	BE561610	Hs.5809	putative transmembrane protein	SS,TM,SS,TM,RA,VPS9,SH2	5.5
	421883	X55079	Hs.1437	glucosidase, alpha; acid (Pomp	trefoil,Glyco_hydro_31,SS	5.4
	427361	AW732480	Hs.7678	cellular retinoic acid-binding	SS,TM,aminotran_1_2,LRR	5.4
	411574	BE242842	Hs.6780	protein tyrosine kinase 9-like	collin_ADF,SS,TM	5.4
15	457313	AF047002	Hs.241520	transcriptional coactivator	SS,rm,SS,Cytidylyltransf	5.4
	428345	AI242431	Hs.118282	PAP-1 binding protein	SS,TM	5.4
	434845	BE267057	Hs.325321	hypothetical protein R32184_1	SS,TM,CH,calponin,ARID	5.4
	427162	AB011133	Hs.173864	KIAA0561 protein	SS,pkinase,PDZ,SS,SH2,Rho	5.4
	447402	H54520	Hs.18490	hypothetical protein FLJ20452	SS,TM	5.4
20	433676	AW371389	Hs.250173	hypothetical protein FLJ13158	SS	5.4
	424373	AJ133798	Hs.146219	copine VII	C2,SS	5.4
	423402	BE167615	Hs.141556	Homo sapiens cDNA FLJ12976 fis	SS	5.4
	409983	D50922	Hs.57729	Kelch-like ECH-associated prot	BTB,Kelch,SS,TM	5.4
	450184	W31096	Hs.23767	Homo sapiens, clone IMAGE:3447	SS	5.3
25	431629	AJ077025	Hs.268827	interferon, alpha-inducible pr	pkinase,SH2,SH3	5.3
	430413	AW842182	Hs.241392	small inducible cytokine A5 (R	IL8,SS	5.3
	440333	AJ378424	Hs.288761	hypothetical protein FLJ21749	SS,TM,IP_trans,pkinase,pk	5.3
	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	SS,TM	5.3
	412276	BE262621	Hs.73798	macrophage migration inhibitor	MIF,SS,TM,MIF,sugar_tr	5.3
30	416181	AA174126	Hs.332163	ESTs	SS,TM,GalP_UDP_transf,Gal	5.3
	440609	AI287585	Hs.7301	G protein pathway suppressor 2	SS,Acyl-CoA_dh,Acyl-CoA_d	5.3
	435327	BE301871	Hs.4867	mannosyl (alpha-1,3)-glycopro	SS,HLH,Myc_N_term,Myc-LZ	5.2
	421139	AW553933	Hs.301372	KIAA1552 protein	SS,TM	5.2
	453449	W16752	Hs.32981	sema domain, immunoglobulin do	SS,Sema,lg,PSI,SS,TM,G-el	5.2
35	414411	X54079	Hs.76067	heat shock 27kD protein 1	HSP20,SS	5.2
	440906	AW161556	Hs.240170	hypothetical protein MGC2731	SS,TM,Furin-like,pkinase,	5.2
	421899	AJ011895	Hs.109281	Nef-associated factor 1	Virus_HS,bZIP,G-gamma,Myo	5.2
	439473	AI215529	Hs.144787	ESTs	SS	5.2
	451585	AK001171	Hs.326422	hypothetical protein MGC4549	SS,Metallophos	5.2
40	407191	AA608751	Hs.179516	gbr:ae56h07.s1 Stratagene lung	SS,Peptidase_C1	5.2
	427515	T79526		integral type I protein	EMP24_GP25L,SS	5.2
	405325			C14000786:gq7023514[ab]BAA9	SS	5.2
	434119	AF193844	Hs.3758	COP9 complex subunit 7a	SS	5.1
	413052	BE249841		gbr:600942857F2 NIH_MGC_15 Homo	TM,SS,TM	5.1
45	445109	AF039916	Hs.12330	ectonucleoside triphosphate di	SS,TM,GDA1_CD39,SS,TM,pho	5.1
	409323	H28855	Hs.53447	Homo sapiens mRNA: cDNA DKFZp7	TPR,SS,TM,pkinase,lg	5.1
	438707	L08239		amino acid system N transport	SS,TM,ACAT,MBOAT,SS,TM,TB	5.1
	442599	AF078037	Hs.324051	RelA-associated inhibitor	SH3,ank,SS,TM,HHH,lg	5.1
	420372	AW960049	Hs.293660	Homo sapiens, clone IMAGE:3535	SS	5.1
50	436576	AI458213	Hs.77542	ESTs	SS,TM,7tm_1,DnaJ	5.1
	439012	BE383814	Hs.6455	RuvB (E coli homolg)-like 2	AAA,DnaB,UPF0079,SS,Cys_k	5.1
	418910	Z25821	Hs.89466	Homo sapiens, Similar to dodec	ECH,SS,TM,aminotran_3,ABC	5.1
	414849	AW372721	Hs.291623	ESTs, Weakly similar to unname	TM,pkinase	5.1
	425743	BE396495	Hs.159428	BCL2-associated X protein	Bcl-2,SS,Jenfin,Bcl-2,e	5.1
55	418231	AA326895	Hs.83848	triosephosphate isomerase 1	TM,SS,TM,zf-UBP,UCH-2,UB	5.0
	419238	AW959538	Hs.321214	hypothetical protein DKFZp564D	SS,TM,WH2	5.0
	441917	AI989925	Hs.24891	ESTs, Highly similar to unknow	SS,TM,Ammonium_transp	5.0
	437617	AI026701	Hs.5716	KIAA0310 gene product	SS,zf-C3HC4,Peptidase_M16	5.0
	412867	AJ076861	Hs.74637	testis enhanced gene transcrip	UPF0005,SS,TM	5.0
60	419579	W49529	Hs.296200	hypothetical protein AF053356	MSP_domain,SS,TM,CUB,NTR	5.0
	425824	AI939563	Hs.159589	ESTs, Moderately similar to RE	SS,PHD	5.0
	439414	NM_001183	Hs.6551	ATPase, H transporting, lysoso	SS,SS,TM,GDI,Sema,TIG,PSI	5.0
	436042	AF284422	Hs.119178	cation-chloride cotransporter-	SS,TM,aa_permeases,SS,TM,	5.0
	410775	AB014460	Hs.66198	nth (E.coli endonuclease III)-	HhH-GPD,SS,TM,REJ,PLAT,PK	5.0
65	453350	AI917771	Hs.61790	hypothetical protein FLJ23338	SS,SS,TM,EMP70,PA28_alpha	4.9
	400300	X03363		HER2 receptor tyrosine kinase	pkinase	4.9
	426811	BE259228	Hs.172609	nucleobindin 1	ethand,SS,TM,GFO_IDH_MocA	4.9
	421179	U72664	Hs.148495	proteasome (prosome, macropain	UIM,SS,TM,PMP22_Claudin,P	4.9
	429762	AI346255	Hs.216354	ring finger protein 5	SS,zf-C3HC4,Palm_thioest	4.9
70	419250	AW770185		U5 snRNP-specific protein, 116	SS,TM,7tm_1,BAH,zf-CXXC,D	4.9
	426831	BE296216	Hs.172673	S-adenosylhomocysteine hydroly	AdoHcyase,SS	4.9
	442103	AA333367	Hs.8068	similar to S. cerevisiae Sec5p	SS	4.9
	414820	AA371931	Hs.77422	proteolipid protein 2 (colonic	SS	4.9
	426347	AA454912	Hs.169407	SAC2 (suppressor of actin muta	SS,RasGEF,RA,RasGEFN,hom	4.9
75	423880	BE278111	Hs.134200	DKFZP564C186 protein	UPF0120,SS,TM	4.9
	429545	AI824164		lymphocyte antigen 6 complex,	SS,TM	4.9
	443044	N26522	Hs.8935	quinolinate phosphoribosyltran	ORPase,ORPase_N,SS,TM	4.9
	417080	BE392846	Hs.1063	small nuclear ribonucleoprotei	SS,S10_plectin	4.8
	441455	AJ271671	Hs.7854	zinc-fon regulated transport	Zip,SS,TM,Cytidylyltransf	4.8
80	410182	NM_001983	Hs.59544	excision repair cross-compleme	HHH,SS,SH3,ank	4.8
	456062	AI866286	Hs.71962	ESTs, Weakly similar to B36298	SS	4.8
	439270	BE268278	Hs.28393	hypothetical protein MGC2592	SS,TM,HCO3_cotransp	4.8
	408985	BE267317	Hs.332040	hypothetical protein MGC13010	SS,TM,ACAT,LRR	4.8
	416976	BE243985	Hs.80680	major vault protein	Vault,SS,TM,kinesin,zf-C2	4.8
	436057	AJ004832	Hs.5038	neuropathy target esterase	cNMP_binding,SS,TM,cNMP_b	4.8

5	424501	AI470163	Hs.323342	actin related protein 2/3 comp	SS,Hhh-GPD	4.8
	409214	AW405967	Hs.333388	Homo sapiens, clone IMAGE3957	SS,EF1BD,P5CR	4.8
	432716	AI762864	Hs.205180	ESTs	SS,TM	4.8
	414460	L00727	Hs.898	dystrophia myotonica-protein k	pklnase,SS,WD40	4.8
	443329	BE262943	Hs.9234	hypothetical protein MGC1936	SS,TM,SS,TM,gpdh,gpdh_C	4.7
	426120	AA325243	Hs.166887	copine I	C2,SS,aminotran_5	4.7
	405356			ENSP00000247029:SEBOX	SS,TM,hemopexin,Somatomed	4.7
	437118	AB037857	Hs.300591	CD9 partner 1	TM,Ig,SS,TM	4.7
10	430609	AA302921	Hs.247362	dimethylarginine dimethylamino	SS,TM,GST_C,abhydrolase	4.7
	447131	NM_004585	Hs.17466	retinoic acid receptor respond	SS,TM,plknase	4.7
	428469	BE549205	Hs.184488	flotillin 2	Band_7,Flotillin,TM	4.7
	405189			Target Exon	SS	4.7
	404256			NM_024018:Homo sapiens butyro	SS,TM,SPRY,SPRY,Ig	4.7
15	457955	AI208986	Hs.121647	ESTs	SS,zf-B_box,SPRY,SS,No1_	4.7
	413201	BE275378	Hs.13972	hypothetical protein MGC12972	SS,SH2,RhoGAP,SH3,GILT	4.7
	431115	AB015427	Hs.250493	zinc finger protein 219	zf-C2H2,SS	4.7
	424214	BE408758	Hs.8297	ribonuclease 6 precursor	ribonuclease_T2,SS,ribonu	4.7
	418289	AW403103	Hs.83951	Hermansky-Pudlak syndrome	SS	4.6
20	436730	AA045767	Hs.5300	bladder cancer associated prot	SS	4.6
	444595	BE560662	Hs.11417	Rab acceptor 1 (prenylated)	SS,TM,Ig_chan,ANF_recept	4.6
	433019	AI208513	Hs.279915	translocase of inner mitochond	zf-Tim10_DDP,SS	4.6
	431522	AI625859	Hs.258609	protein tyrosine phosphatase,	fn3,Y_phosphatase,SS,TM	4.6
	400846			sortilin-related receptor, LQD	ldl_recept_a,fn3,ldl_rece	4.6
25	422154	T78045	Hs.168812	ESTs	SS	4.6
	420321	D78761	Hs.96657	hypothetical protein	SS,isp_1,SS	4.6
	439921	AL110209	Hs.6770	LCAT-like lysophospholipase	SS,LACT,SS,TM,aa_permease	4.6
	427122	AW057736	Hs.323910	HER2 receptor tyrosine kinase	plknase,Furin-like,Recep_	4.6
	426899	AL043221	Hs.172825	KJAA1037 protein	WD40,TPR,SS,TM	4.6
30	408116	AA251393	Hs.289052	Homo sapiens, Similar to RIKEN	SS,TM	4.6
	412974	R18978	Hs.75105	emopamil-binding protein (eter	SS,TM,SS,TM,TBC,rm,FtsJ	4.6
	426510	AW861225	Hs.110613	BANP homolog, SMAR1 homolog	TM	4.6
	414702	L22005	Hs.76932	cell division cycle 34	UQ_con,SS,tyrpsin,Ig	4.6
	408135	AA317248	Hs.42957	methyltransferase-like 1	Methyltransf_4,SS,p450,Ge	4.6
35	445637	W58459	Hs.8949	hypothetical protein MGC4172	SS	4.6
	452190	H26735	Hs.91668	Homo sapiens clone PP1498 unkn	SS	4.6
	409680	W31092	Hs.55847	mitochondrial ribosomal protel	SS,TM,synaptobrevin	4.6
	421140	AA298741	Hs.102135	signal sequence receptor, delt	Herpes_UL3,SS,TM,Sema,pki	4.6
	413407	AI356293	Hs.75339	inositol polyphosphate phospho	SH2,SAM,SS,Folate_rec	4.6
40	402463			NM_014624:Homo sapiens S100 ca	efhand,S_100,SS,efhand,S_	4.5
	426402	BE387327	Hs.80475	polymerase (RNA) II (DNA direc	SS,PGAM	4.5
	406939	M34515		gb:Human omega light chain pro	SS,Ig,PH	4.5
	417891	W79410	Hs.82887	protein phosphatase 1, regulat	SS,TFIIS	4.5
	426207	BE390657	Hs.30026	HSPC182 protein	SS	4.5
45	423664	NM_004714	Hs.130988	dual-specificity tyrosine-(Y)-	pklnase,SS,Fibrillarin,CK	4.5
	432562	BE531048	Hs.278422	DKFZP586G1122 protein	zf-C2H2,SS,TM,FG-GAP,inte	4.5
	427391	W60675		hypothetical protein FLJ10350	SS,SS	4.5
	432893	NM_016154	Hs.279771	Homo sapiens clone PP1596 unkn	ras,arf,SS,2OG-Fell_Oxy,2	4.5
50	424954	NM_000546	Hs.1846	tumor protein p53 (L-Fraumeni	P53,SS	4.5
	413815	AL046341	Hs.75562	discolidin domain receptor fami	F8_F8_type_C,plknase,SS,T	4.5
	448963	AA459786	Hs.331247	Homo sapiens, clone IMAGE3610	SS,TM	4.5
	416297	AA157634	Hs.79172	solute carrier family 25 (mito	mito_carr,SS	4.5
	421962	D82061	Hs.288354	FabG (beta-ketoacyl-acyl-car	SS,adh_short,SS,TM,zf-C3H	4.5
	426726	AA488915	Hs.171955	trophinin associated protein (SS	4.5
55	414427	L19711	Hs.76111	dystroglycan 1 (dystrophin-ass	SS,TM	4.5
	435891	AW249394	Hs.5002	copper chaperone for superoxid	sodcu,HMA,SS,TM,spectrin,	4.5
	453997	AW247615	Hs.37003	v-Ha-ras Harvey rat sarcoma vi	ras,SS	4.5
	449029	N28989	Hs.22891	solute carrier family 7 (catio	aa_permeases,SS,TM,bZIP	4.5
	432078	BE314877	Hs.24553	hypothetical protein FLJ12541	SS,TM	4.5
60	409550	T08490	Hs.288969	HSCARG protein	SS,SS,WD40	4.5
	412833	AW960547	Hs.298262	ribosomal protein S19	SS,TM,Ig,ITAM,Ribosomal_S	4.4
	424133	AA335721	Hs.213628	ESTs	SS,TM	4.4
	414787	AL049332	Hs.77311	BTG family, member 3	SS,Anti_proliferat	4.4
	433046	AA229553	Hs.279945	HSPC023 protein	SS	4.4
65	417068	AA451910	Hs.85852	hypothetical protein MGC3169	SS,TM	4.4
	414814	D14697	Hs.77393	farnesyl diphosphate synthase	polyprenyl_synth,SS,TM	4.4
	418267	BE389537	Hs.83919	glucosidase I	Glyco_hydro_63,SS,PH	4.4
	439902	AF174499	Hs.6764	histone deacetylase 6	Hist_deacetyl,zf-UBP,SS,G	4.4
	448847	AI587180	Hs.110906	Homo sapiens, Similar to RIKEN	TM,SS	4.4
70	452160	BE378541		cysteine sulfonic acid decarbo	SS	4.4
	416121	X92762	Hs.79021	atazzin (cardiomyopathy, dia	Acyltransferase,SS,TM,GDI	4.4
	449717	AB040935	Hs.23954	cerebral cell adhesion molecu	SS,SS	4.4
	425069	AA687465	Hs.298184	potassium voltage-gated channe	SS,aldo_ket_red	4.4
	413380	AI904232	Hs.75323	prohibitin	Band_7,SS,Band_7,SH3	4.4
75	452911	AA541537	Hs.112619	metallothionein 1E (functional	SS,SS,TM,Sec1	4.4
	436415	BE265254	Hs.343258	proliferation-associated 2G4,	Peptidase_M24,SS,TM,Pepti	4.4
	428218	AA225065	Hs.198269	Target CAT	SS,Nop	4.4
	447987	BE621544	Hs.157160	hypothetical protein MGC2616	SS,NDK,LRRNT,LRRCT,LRR	4.4
	407230	AA157857	Hs.182265	keratin 19	filament,bZIP,SS,filament	4.3
80	448888	AL137291	Hs.22451	hypothetical protein FLJ10357	SS,PH,Rho,GEF,SS,maseA	4.3
	421178	BE267994	Hs.102419	zinc finger protein	zf-C2H2,SS,TM	4.3
	454031	R35772	Hs.71941	hypothetical protein MGC15677	TM	4.3
	450126	BE018138	Hs.24447	sigma receptor (SR31747 bindin	SS,Ig,fn3	4.3
	446557	U68566	Hs.15318	HS1 binding protein	SS,TM,MIP,UBA	4.3
	413781	J05272	Hs.850	IMP (inosine monophosphate) de	IMPDH_C,IMPDH_N,CBS,NPD,S	4.3

5	433251	AB040955	Hs.322735	KIAA1522 protein	SS,SS,zf-C3HC4,SPRY	4.3
	420531	AJ652069	Hs.98614	ribosome binding protein 1 (do	bZIP,SS	4.3
	432179	X75208	Hs.2913	EphB3	EPH_bld,fn3,pkinase,SAM	4.3
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA)	Neur_chan_LBD,Neur_chan_m	4.3
	426626	AI124572	Hs.323879	Inhibitor of kappa light polyp	zf-C2H2,SS	4.3
	432956	AL037895	Hs.279861	CGI-31 protein	thioredo,SS,TM	4.3
	428970	BE276891	Hs.194691	retinoic acid induced 3	7tm_3,SS,TM	4.3
	428953	AA306610	Hs.348183	tumor necrosis factor receptor	TNFR_c6,SS	4.2
10	401128			C12000644.gij5729785[ref]NP_00	SS	4.2
	446899	NM_005397	Hs.16426	podocalyxin-like	SS,TM,SS,TM	4.2
	407151	H25836	Hs.301527	ESTs, Moderately similar to un	SS,TNF	4.2
	426613	U96132	Hs.171280	hydroxyacyl-Coenzyme A dehydro	adh_short,SS	4.2
	408616	R51604	Hs.300842	KIAA1608 protein	SS,DENN,DENN	4.2
15	446616	R65964	Hs.334873	ESTs, Weakly similar to ALU8_H	SS,Zn_carbOpept	4.2
	414467	AW903820	Hs.85752	copine II	SS	4.2
	455857	T70192		gb:yc18d03.s1 Stratagene lung	SS,TM,Isodh	4.2
	401751			RAN binding protein 3	SS,Orexin,SH2,STAT	4.2
	400563			Target Exon	SS,Pep_M12B_propep	4.2
20	430237	AI272144	Hs.236522	DKFZP434P108 protein	abhydrolase,TM	4.2
	406101			C11000273.gij12656107[gb]AAK0	SS,TM,7tm_1	4.2
	421661	BE281303	Hs.299148	hypothetical protein FLJ21801	SS,VHP	4.2
	444590	AA457456		hypothetical protein FLJ20435	SS	4.2
	408187	AF034373	Hs.43509	ataxin 2 related protein	SS	4.2
25	437696	ZB3844	Hs.5790	hypothetical protein dJ37E16.5	SS,Hydrolase,SS,Gal-bind_	4.2
	400278			JENSP00000243264:Dolichyl-dipho	SS,TM	4.2
	407394	AF005081		gb:Homo sapiens skin-specific	SS	4.2
	447407	BE387301	Hs.18528	Sjogren's syndrome nuclear aut	SS,HLH,ras,GSHPx	4.2
	410237	AI750589	Hs.61258	argininosuccinate lyase	lyase_1,SS	4.1
30	415410	AF037332	Hs.278569	sorting nexin 17	PX,fn3,pkinase,SAM,EPH_lb	4.1
	457757	AA434109	Hs.12271	f-box and leucine-rich repeat	SS,F-box,SS,TM,HSF_DNA-bl	4.1
	446388	AA292979	Hs.7788	NPD007 protein	SS,TM	4.1
	412825	AW167439	Hs.190651	Homo sapiens cDNA FLJ13625 fis	SS	4.1
	439737	AI751438	Hs.41271	Homo sapiens mRNA full length	SS,C1q,Collagen	4.1
35	422256	M64673	Hs.1499	heat shock transcription facto	NA,SS,TM,F-box	4.1
	441184	AB023180	Hs.7724	KIAA0963 protein	helicase_C,SS,RNA_pol_H	4.1
	401727			Target Exon	A_deamin,SS	4.1
	411142	NM_014256	Hs.69009	transmembrane protein 3	Galactosyl_T,SS,Ribosomal	4.1
	458176	AI961519	Hs.140309	Homo sapiens, clone IMAGE:3677	SS,pkinase,pkinase_C	4.1
40	432178	BE265369	Hs.272814	hypothetical protein DKFZp434E	SS,serine_carbpept	4.1
	421537	BE383488	Hs.105547	neural proliferation, differen	SS,TM,Glyco_hydro_47	4.1
	421380	D31833	Hs.1372	arginine vasopressin receptor	7tm_1	4.1
	422702	AJ011373	Hs.119285	chromosome 9 open reading fram	SS,TM,SS,TM	4.1
	434142	U47927	Hs.3759	ubiquitin specific protease 5	zf-UBP,UCH-2,UBA,UCH-1,SS	4.1
45	423696	Z92546		Sushi domain (SCR repeat) cont	SS,TPR,vwd,sushi,Somatome	4.1
	427407	BE268649	Hs.177766	ADP-ribosyltransferase (NAD; p	BRCT,PARP,zf-PARP,PARP_re	4.1
	413749	AI929320	Hs.75516	tyrosine kinase 2	pkinase,SS,TM,jg	4.1
	411927	BE274009	Hs.772	glycogen synthase 1 (muscle)	Glycos_transf_1,SS	4.1
	433320	D60647	Hs.250879	ESTs, Highly similar to CTXN R	SS,TM,rm	4.1
50	433890	AF103801	Hs.16361	hypothetical protein	DAO,SS	4.1
	425603	AW410601	Hs.30026	HSPC182 protein	SS	4.1
	444496	BE302472	Hs.11314	DKFZP564N1363 protein	SS,GKAP,Band_41	4.1
	422556	NM_006245	Hs.118244	protein phosphatase 2, regulat	B56,SS,TM,Atrophin-1,Exo_	4.1
	447347	AA570056	Hs.122730	ESTs, Moderately similar to Ki	TM,SS	4.1
55	428284	AA535762	Hs.183435	NM_004545:Homo sapiens NADH de	SS,TM,Josephin,UIM,Joseph	4.1
	426551	AA381268	Hs.323947	ESTs	SS,sushi	4.0
	417782	T10149	Hs.4243	hypothetical protein FLJ12650	SS,TM	4.0
	443639	BE269042	Hs.9661	proteasome (prosome, macropain	proteasome,SS,TM,LACT,try	4.0
60	410039	AF207989	Hs.58014	Homo sapiens, Similar to G pro	SS,TM,7tm_3,SS,TM	4.0
	452715	Z21093	Hs.30352	ribosomal protein S6 kinase, 5	pkinase	4.0
	442549	AI751601	Hs.8375	TNF receptor-associated factor	zf-C3HC4,MATH,zf-TRAF,SS,	4.0
	430603	AA148164	Hs.247280	HBV associated factor	SS,zf-C3HC4,zf-RanBP,pkin	4.0
	427239	BE270447		ubiquitin carrier protein	UQ_con,SS,TM	4.0
	402665			Target Exon	SS,TM,jg,DSpc	4.0
65	413818	BE161405	Hs.79	hypothetical protein MGC15429	SS,KH-domain,WD40,Ribosom	4.0
	406919	M88359		gb:Homo sapiens DNA-binding pr	SS,rm	4.0
	412656	AF006011	Hs.74375	dishevelled 1 (homologous to D	SS,PDZ,DEP,DIX,Dishevelle	4.0
	437546	AW074836	Hs.173984	T-box 1	SS,TM,T-box,GTP_CDC,LRRC	4.0
70	419489	AW411280	Hs.90693	replication initiation region	zf-C2H2,LIM,TM	4.0
	410043	D30612	Hs.58167	zinc finger protein 282	zf-C2H2,KRAB,SS,zf-C2H2,K	4.0
	430067	U79458	Hs.231840	VW domain binding protein 2	GRAM,SS	4.0
	408449	NM_004408	Hs.166161	dynamitin 1	PH,GED,dynamitin,dynamitin_2,	4.0
	448099	BE621839	Hs.61976	Homo sapiens cDNA FLJ12947 fis	SS	4.0
	436656	N35568	Hs.5245	hypothetical protein FLJ20643	SS,TM,sugar_tr,PID	4.0
75	424512	X53002	Hs.149846	integrin, beta 5	integrin_B,EGF,SS,TM	4.0
	440346	AI923985	Hs.59621	ESTs, Weakly similar to A40815	SS,TM,jg,pkinase	3.9
	420065	AW140093	Hs.129926	ESTs	SS,TM	3.9
	426636	BE242634	Hs.2055	ubiquitin-activating enzyme E1	ThiF,UBACT,SS,pkinase,UCH	3.9
80	421579	NM_002975	Hs.105927	stem cell growth factor; lymph	lectin_c,SS,TM	3.9
	427498	NM_003926	Hs.178728	methyl-CpG binding domain prot	SS,HLH	3.9
	457820	AA341497	Hs.31408	RAR (RAS like GTPASE)	SS,TM,Rhomboid	3.9
	439998	BE559554	Hs.61790	hypothetical protein FLJ23338	SS,SS,TM,EMP70,PA28_alpha	3.9
	438662	AA223599	Hs.6351	cleavage and polyadenylation s	zf-CCHC,zf-CCCH,thumatin	3.9
	414303	NM_004427	Hs.165263	early development regulator 2	SAM,SS	3.9
	435406	F26698	Hs.4884	calcium/calmodulin-dependent p	pkinase,SS,hexokinase,hex	3.9

414168	AW783296	Hs.103845	ESTs, Moderately similar to I5	SS	3.9
451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp5	SS	3.9
418181	U37012	Hs.83727	cleavage and polyadenylation s	CPSF_A,SS,TM	3.9
402793			Target Exon	SS,TM,cyclin,cyclin_C	3.9
5	418581	AA287788	Insulin receptor tyrosine kina	SS,SiK3	3.9
412621	L40397	Hs.74137	transmembrane trafficking prot	EMP24_GP25L,SS,TM	3.9
420631	AW976530	Hs.28355	hypothetical protein FLJ22402	SS,TM	3.9
438483	AW966735	Hs.321635	ESTs, Weakly similar to A46302	SS,TM,IP_trans	3.9
431472	AK001023	Hs.256549	nucleotide binding protein 2 (fer4_NIH,ParA,APS_kinase	3.9
10	447800	AL080092	DKFZP564N1362 protein	SS,TM,SS,TM	3.8
436686	AW450205	Hs.305890	BCL2-like 1	TM,Bcl-2,BH4	3.8
408815	AW957974	Hs.25485	hypothetical protein FLJ22341	SS,TM	3.8
441196	BE397802	Hs.7744	NM_007103*-Homo sapiens NADH d	Complex1_51K,SNF2_N,helic	3.8
433030	AW068857	Hs.279929	gp25L2 protein	SS,TM,EMP24_GP25L,SS,TM,G	3.8
408721	BE515274	Hs.47082	polymerase (RNA) II (DNA direc	RNA_POL_M_15KD,SS,COX7a	3.8
435049	AL122067	Hs.4746	hypothetical protein FLJ21324	SS,pkB	3.8
431347	AI133461	Hs.251664	Insulin-like growth factor 2 (SS,Insulin,Insulin	3.8
450835	BE262773	Hs.25584	hypothetical protein FLJ10767	AriGap,SS,vwa,TSPN,fn3,Co	3.8
20	414134	X50188	mitogen-activated protein kina	pkkinase,SS,pkinase,T-box	3.8
418090	U57059	Hs.83429	tumor necrosis factor (ligand)	TNF,SS	3.8
448832	AW245212	Hs.22199	ECSIT	SS,rm	3.8
447256	AW593008	Hs.6126	hypothetical protein dJ1141E15	SS,TM,SS,TM	3.8
448107	D45853	Hs.20313	protein tyrosine kinase 2 beta	Focal_AT,pkinase,SS,Pepti	3.8
25	426433	L38969	thrombospondin 3	TSPN,isp_3,SS,TM,SEA,TSPN	3.8
431626	AL035681	Hs.265327	hypothetical protein DKFZp761l	SS	3.8
430956	AI183529	Hs.2708	glutathione peroxidase 4 (phos	GSHPx,SS,TM,ABC_tran	3.8
450998	BE387614	Hs.25797	splicing factor 3b, subunit 4,	SS,TM,sugar_br,histone	3.8
434899	BE613631	Hs.283565	FOS-like antigen-1	bZIP,SS,bZIP,cofilin_ADF,	3.8
30	444734	NM_001360	7-dehydrocholesterol reductase	ERG4_ERG24,SS,TM	3.8
411090	BE165650	Hs.339697	VPS28 protein	SS,TM,CPSF_A	3.8
452135	AA92175	Hs.21446	KIAA1716 protein	SS,SDX,POZ,DEP,Dlshevelle	3.8
421339	AA070224	Hs.103561	SRp25 nuclear protein	SS	3.7
406535			Target Exon	SS,TM,Ribosomal_S19e,Ig,I	3.7
35	447281	AA017018	hypothetical protein FLJ20446	SS,SS,Teklin,PwI,PAZ	3.7
433126	AB021262	Hs.99816	beta-catenin-interacting prote	SS,TM	3.7
425215	AF030291	Hs.155165	zinc finger protein-like 1	PHD,SS,TM,DnaJ,ERG4_ERG24	3.7
420536	AL117455	Hs.275438	histone deacetylase 7A	Hist_deacetyl,SS,Hist_dea	3.7
417998	AW957420		gb:EST379495 MAGE resequences,	SS,TM	3.7
40	430890	X54232	glypican 1	Glypican,SS	3.7
427863	AF189712	Hs.181002	MLL septin-like fusion	SS,GTP_CDC,SS,TM	3.7
448606	BE613362		Homo sapiens ubiquitin conjuga	SS,TM	3.7
421961	AB032993	Hs.109929	likely homolog of rat GRIP-ass	TM,K_tetrajon_trans,HLH,	3.7
410293	AK000047	Hs.61960	hypothetical protein	K_tetra,SS	3.7
425233	Z17861	Hs.155218	E1B-55kDa-associated protein 5	SPRY,SAP,SS,TM,SPRY,SAP,p	3.7
423683	BE388699	Hs.4188	hypothetical protein MGC10812	SS,Peptidase_C15,TGF-beta	3.7
415697	AI365603	Hs.78605	DKFZP566I1024 protein	SS,cpn60_TCP1	3.7
415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3	SS	3.7
418052	AA350659	Hs.83347	angio-associated, migratory ce	WD40,Bacterial_PQQ,TM,UPF	3.7
444706	AK000398	Hs.11747	hypothetical protein FLJ20391	SS,SS,TM	3.7
50	407381	AA420659	ESTs, Weakly similar to ALUC_H	SS,TM	3.7
423432	BE252996	Hs.44067	ESTs	TM	3.7
444982	AK002182	Hs.12211	GDP-fucose transporter 1	SS,TM,DUF6,SS,TM	3.7
407777	AA161071	Hs.71465	squalene epoxidase	SS,TM,Monoxygenase	3.7
422715	AA332178	Hs.119403	hexosaminidase A (alpha polype	Glyco_hydro_20,Glyco_hydr	3.7
55	422609	Z46023	sialidase 1 (lysosomal sialida	SS,TM,BNR,SS,TM,SET,HSP70	3.7
414732	AW410976	Hs.77152	minichromosome maintenance def	MCM,RIP,SS,zf-C2H2,KRAB	3.7
452579	AA131657	Hs.23830	ESTs	SS,CN_hydrolase	3.7
419032	W81330	Hs.58643	ESTs, Highly similar to JAK3B	SS,pkinase,SH2,Insulin,pk	3.6
411165	NM_000169	Hs.69089	galactosidase, alpha	Malfliase,Ribosomal_L44,z	3.6
444000	AI095034	Hs.135528	ESTs	SS,HLH	3.6
441174	BE312775	Hs.294005	Homo sapiens, clone IMAGE:3050	SS,TM	3.6
429491	NM_012111	Hs.204041	chromosome 14 open reading fra	SS	3.6
438433	AB018274	Hs.6214	KIAA0731 protein	SS	3.6
425162	BE514851	Hs.154886	choline kinase-like	Carn_acyltransf,Choline_k	3.6
65	429671	BE378335	proteasome (prosome, macropain	AAA,NB-ARC,TM	3.6
421018	AI569028	Hs.129888	hypothetical protein FLJ14768	zf-C2H2,SS,rm,ENTH	3.6
433604	NM_013442	Hs.3439	stomatol-like 2	Band_7,SS,TM,AAA,cdc48_N,	3.6
451544	AK000429	Hs.26570	hypothetical protein FLJ20422	SS,TM,COX3,SS,TM,SRF-TF	3.6
444369	AV649296	Hs.282793	ESTs	SS	3.6
406660	X65371	Hs.172550	polypyrimidine tract binding p	rm,beta-lactamase,SS,try	3.6
456503	AW977779	Hs.194613	ESTs	SS,TM,bromodomain,abhydro	3.6
451711	AK000461	Hs.26890	cat eye syndrome chromosome re	SS,SS,TM,A_deaminase	3.6
425394	AA356730	Hs.323949	kangal 1 (suppression of tumor	SS,TM,transmembrane4	3.6
428011	BE387514	Hs.181418	KIAA0152 gene product	Acyl-CoA_th,SS,elfhand	3.6
75	407627	AI419020	chromosome 6 open reading fram	SS	3.6
436437	F12200	Hs.5811	chromosome 21 open reading fra	SS,Syja_N,Exo_endo_phos	3.6
419418	X75621	Hs.90303	tuberous sclerosis 2	Rap_GAP,Tuberin,Peptidase	3.6
440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN	SS	3.6
448136	AA036680	Hs.20447	protein kinase related to S. c	pkinase,PBD	3.6
435977	AL138079	Hs.5012	brain-specific membrane-anchor	SS,TM,SS,TM,ubiquitin,Rib	3.6
419095	AA234009	Hs.188715	ESTs	pkinase,PH,pkinase_C	3.6
447267	AL360143	Hs.17936	DKFZP434H132 protein	SS	3.6
418054	NM_002318	Hs.83354	lysyl oxidase-like 2	SS	3.6
444354	AA847582	Hs.10927	hypothetical protein R33729_1	SRCLR,lysyl_oxidase,SS,TM,	3.6

5	429098	AF030249	Hs.196176	enoyl Coenzyme A hydratase 1,	ECH,Herpes_V23,SS,Gal-bin	3.6
	430622	BE616971	Hs.247478	Homo sapiens, Similar to DNA s	G-patch,SS,TM,ubiquitin,a	3.6
	440675	AW005064	Hs.47883	ESTs, Weakly similar to KCC1_H	pklnase	3.6
	409678	NM_005632	Hs.55836	small optic lobes (Drosophila)	TM,Peptidase_C2	3.6
	413097	BE383876	Hs.75196	ankyrin repeat-containing prot	ank,SET,SS,TM,plkinase,SH2	3.6
	427579	AA366143	Hs.179669	hypothetical protein FLJ20637	HECT,SS,HECT	3.6
	409154	U72882	Hs.50842	interferon-induced protein 35	SS,ras,Ribosomal_L27e,KOW	3.5
	448528	BE613248	Hs.172084	Homo sapiens, clone IMAGE:3627	SS,PD,SH2	3.5
10	444426	AL121105	Hs.11170	RNA binding motif protein 14	rm,SS,spectrin,PH,rm,so	3.5
	409297	R34662	Hs.53066	hsp70-interacting protein	SS	3.5
	441138	T56785	Hs.10101	hypothetical protein FLJ12875	SS	3.5
	435169	AF148509	Hs.278881	mannosidase, alpha, class 1B,	TM,Glyco_hydro_47	3.5
	422575	AK000646	Hs.118552	hypothetical protein FLJ20539	TM,SS,TM,SRGR,Glyco_trans	3.5
15	403325			C2000428*glj7705383[re]NP_05	SS	3.5
	437895	AB014568	Hs.5898	KIAA0668 protein	TM,UL21,Lipoprotein_6,GBP	3.5
	449030	AF365582	Hs.57100	Homo sapiens mRNA for FLJ00016	SS,Synuclein	3.5
	426542	AF190746	Hs.170310	cat eye syndrome chromosome re	A_deaminase,SS,TM,Hydrola	3.5
	439873	BE159253	Hs.300638	ESTs	SS	3.5
20	428950	BE311879	Hs.194673	phosphoprotein enriched in ast	DED,SS,TM,Calsequestrin	3.5
	421564	AB007864	Hs.105850	KIAA0404 protein	SS	3.5
	441094	U33819	Hs.7647	MYC-associated zinc finger pro	SS,zf-C2H2,LIM,PHD,TFIS,	3.5
	450007	BE270693	Hs.24301	polymerase (RNA) II (DNA direc	NA,SS	3.5
	422898	AL043101	Hs.127401	DKFZP434A163 protein; selectiv	SS,TM	3.5
25	444914	AA046947	Hs.12142	WD repeat domain 13	WD40,SS,TBC,rm	3.5
	420178	D50550	Hs.95659	Jethal giant larvae (Drosophil	WD40,SS,TM	3.5
	418984	AA421401		ribosomal protein L18	SS,TM	3.5
	414166	AW888941	Hs.75789	N-myc downstream regulated	Ndr,abhydrolase,SS	3.5
	409944	BE297925	Hs.57687	four and a half LIM domains 3	LIM,SS	3.5
30	421458	NM_003654	Hs.104576	carbohydrate (keratan sulfate	SS	3.5
	423599	AI805664	Hs.31731	peroxiredoxin 5	Ahp-C-TSA,SS,hormone_rec,z	3.5
	427715	BE245274	Hs.180428	KIAA1181 protein	TM,SS,TM,KOW	3.5
	405496			Target Exon	SS,tubulin,SS	3.5
	417911	AA333387	Hs.82916	chaperonin containing TCP1, su	cpn60_TCP1,SS,cpn60_TCP1	3.5
35	433620	AA604520	Hs.269468	ESTs, Moderately similar to AL	SS,UCH-2,UCH-1	3.5
	430053	AF052155	Hs.227949	SEC13 (S. cerevisiae)-like 1	WD40,SS,TM,E1-E2_ATPase,C	3.5
	458687	AW024815	Hs.170088	GLUT4 enhancer factor	SS	3.5
	424679	AL117477	Hs.119960	DKFZP727G051 protein	chromo,SS	3.5
	417360	AW651703	Hs.82023	hypothetical protein similar t	SS,TM,GDA1_CD39,GDA1_CD39	3.5
40	439641	AI251317	Hs.33184	ESTs	SS,TM,GYF,actin,PA	3.5
	426437	BE076537	Hs.169895	ubiquitin-conjugating enzyme E	UQ_con,SS,TM,Armadillo_se	3.5
	427117	BE258946	Hs.173611	Target CAT	complex1_49Kd,SS,TM,ITAM,	3.4
	422051	AW327546	Hs.111024	solute carrier family 25 (mito	SS,mito_carr,SS,mito_carr	3.4
	422759	AA316582	Hs.224571	ESTs	SS	3.4
45	417230	U40998	Hs.81728	unc119 (C.elegans) homolog	SS,glycolytic_enzy	3.4
	450158	AK001999	Hs.24545	hypothetical protein FLJ11137	SS,zf-C2H2,SCAN,TFIS,SS	3.4
	425421	L11669	Hs.157145	tetracycline transporter-like	SS,TM,SS,TM	3.4
	415515	F11327	Hs.167406	gb:HSC2VD101 normalized infant	SS	3.4
50	427868	AI360119.comp	Hs.181013	phosphoglycerate mutase 1 (bra	PGAM,SS,TM,kdh	3.4
	413503	BE410228	Hs.75410	heat shock 70kD protein 5 (glu	SS,HSP70,homeobox,Hydanto	3.4
	413014	AW250533	Hs.75139	partner of RAC1 (arlaplin 2)	SS,hemopexin,Filamin,NHL,	3.4
	457655	AA622968	Hs.71574	hypothetical protein FLJ14926	SS,P5CR,EF1B	3.4
	419432	AK001459	Hs.90375	hypothetical protein FLJ10597	PEP-utilizers,PEP-utilize	3.4
55	421066	AI076725	Hs.101408	branched chain aminotransferas	aminotran_4,TM	3.4
	428038	AW134758	Hs.192477	ESTs	SS,Exonuclease,zf-C2H2	3.4
	430352	AW750535	Hs.50742	Homo sapiens cDNA: FLJ23331 fi	TM	3.4
	432647	AI807481	Hs.278581	fibroblast growth factor recep	lg,plkinase,SS,TM,lg,plkina	3.4
	421310	AW630087	Hs.103315	trinucleotide repeat containin	TM,zf-C2H2,SS,PHD	3.4
60	420999	AA338903	Hs.100915	peroxisomal biogenesis factor	SS	3.4
	409561	U58048	Hs.183138	procollagen (type III) N-endop	SS,TM	3.4
	419727	AW160798	Hs.92700	DKFZP564O243 protein	Herpes_env,SS,TM,Peptidas	3.4
	421267	BE314724	Hs.103081	ribosomal protein S6 kinase, 7	plkinase,plkinase_C,SS	3.4
	411501	AB002368	Hs.70500	KIAA0370 protein	SS,TM,SS,TM	3.4
	448741	BE614567	Hs.18574	hypothetical protein MGC5469	SS	3.4
65	407103	AA424881	Hs.256301	hypothetical protein MGC13170	SS,TM,tryptsin	3.4
	422808	AA449014	Hs.121025	chromosome 11 open reading fra	SS,TM,tryptsin,CUB,ubiquit	3.4
	448173	N95657	Hs.6820	ESTs, Moderately similar to YO	SS	3.4
	416535	H61851		gb:yr80e10.r1 Soares fetal liv	SS,TM,homeobox,LIM	3.4
	406656	M16714	Hs.181392	major histocompatibility compl	MHC_I,lg,SS,TM	3.4
70	435669	AI867781	Hs.31819	HT014	SS,abhydrolase_2	3.4
	411077	AW977263	Hs.68257	general transcription factor I	SS,TM,TGF-beta	3.4
	427062	AW327785	Hs.173421	KIAA1564 protein	SS,Peptidase_M24	3.4
	421890	AW959488	Hs.21732	ESTs	SS,zf-C3HC4,SPRY	3.4
	412968	AW500508	Hs.75102	alanine-tRNA synthetase	DHHA1,SS,IRNA-synt_2c,DHH	3.4
75	439496	BE616501	Hs.32343	Homo sapiens, Similar to RIKEN	SS	3.4
	433659	AK001301	Hs.3487	hypothetical protein FLJ10439	WD40,SS,TM,Syntaxin,Synta	3.3
	447578	AA912347	Hs.136585	ESTs, Weakly similar to JC5314	SS	3.3
	441722	AW960504	Hs.173103	FE65-LIKE 2	SS,TM	3.3
80	452345	AA293279	Hs.29173	hypothetical protein FLJ20515	DSPc,SS,jmj,C,F-box	3.3
	451714	AK000344	Hs.26898	hypothetical protein FLJ20337	SS,TBC,FHA,zf-C3HC4	3.3
	410633	BE546789	Hs.346742	hypothetical protein MGC3260	SS,TM	3.3
	410609	BE298441	Hs.287361	ADP-ribosylation factor relate	arf,ras,SS,arf,Statmin	3.3
	414775	AA992036	Hs.172702	ESTs, Weakly similar to (defi	SS,PCI	3.3
	428495	NM_013279	Hs.184640	hypothetical protein MGC10781	SS,TM,XPG_N,XPG_I,5_3_exo	3.3
	429215	NM_005341	Hs.2364	GLI-Kruppel family member HKR3	zf-C2H2,BTB,TP2,K_tetra,S	3.3

5	446618	AL110307	Hs.15591	COP9 subunit 6 (MOV34 homolog,	Mov34,SS,zf-C2H2,SCAN	3.3
	444868	BE560471	Hs.12101	hypothetical protein	SS,PCI	3.3
	430041	AW247237	Hs.227835	KIAA1049 protein	SS,TM,7tm_1,tubulin	3.3
	416950	ALD49798	Hs.80552	dermatoponin	SS	3.3
	431203	AW248421	Hs.250758	proteasome (prosome, macropain	AAA,Sigma54_activat,SS,TP	3.3
	432714	Y12059	Hs.278875	bromodomain-containing 4	bromodomain,SS,TM,SNF2_N,	3.3
	415674	BE394784	Hs.78596	proteasome (prosome, macropain	SS,proteasome,SS,TM,Cadhe	3.3
	426152	BE299180	Hs.167246	P450 (cytochrome) oxidoreducta	flavodoxin,FAD_binding,SS	3.3
10	418440	NM_006936	Hs.85119	SMT3 (suppressor of mit two 3,	ubiquitin,SS,UQ_con	3.3
	410545	U32324	Hs.64310	Interleukin 11 receptor, alpha	ig,fn3,SS,TM,GalP_UDP_tra	3.3
	409428	M33680	Hs.54457	CD81 antigen (target of antipr	transmembrane4,cyclin,SS,	3.3
	443121	Z19267	Hs.9006	VAMP (vesicle-associated membr	TM,MSP_domain	3.3
	453856	AA804769	Hs.19447	PDZ-LIM protein mystique	LIM,SS,SH3,Sorb	3.3
15	430137	NM_005456	Hs.234249	mitogen-activated protein kina	SS,SH3,PID,SS,PID	3.3
	446427	AW295863	Hs.119632	ESTs	SS	3.3
	400747			Target Exon	fn3,lg	3.3
	445580	AF167572	Hs.12912	skb1 (S. pombe) homolog	SS,SS	3.3
	452568	AA805634	Hs.300870	Homo sapiens mRNA; cDNA DKFZp5	SS,rm,Ephrin,ptkinase,ATP	3.3
20	418558	AW082266	Hs.86131	Fas (TNFRSF6)-associated via d	death,DED,SS,TM	3.3
	401655			Target Exon	SS	3.3
	429460	D56263	Hs.203238	phosphodiesterase 1B, calmodul	PDEase,SS,PDEase	3.3
	416448	L13210	Hs.79339	lectin, galactoside-binding, s	SRCR,SS,TM	3.3
	433038	AF192559	Hs.279939	mitochondrial carrier homolog	TM,mito_car,TM	3.3
25	440251	AW796016	Hs.332012	'Homo sapiens, clone IMAGE:3687	SS,TM,SS,TM,IRK	3.3
	412922	M60721	Hs.74870	J12.0 (Drosophila)-like homeo b	SS,homeobox,SS	3.3
	432941	W04803	Hs.278851	hypothetical protein FLJ10241	SS,RNase_PH,RNase_PH_C	3.3
	441244	BE612935	Hs.184052	PP1201 protein	SS,TM,WD40	3.3
	438175	AI376727	Hs.122110	ESTs	SS,TM,trypsin,kringle,fn2	3.3
30	423024	AA593731	Hs.325823	ESTs, Moderately similar to AL	SS,TM,CD36,CD36	3.3
	430120	AW675298	Hs.233694	hypothetical protein FLJ11350	SS	3.3
	419571	AW674962	Hs.91146	protein kinase D2	pklnase,DAG_PE-bind,PH,DC	3.3
	413019	BE281604	Hs.75140	low density lipoprotein-relate	SS	3.3
	400299	X07730	Hs.171995	kallikrein 3, (prostate specif	trypsin,SS,trypsin,trypsi	3.3
35	433519	BE263901		ESTs, Weakly similar to S37431	SS,TM	3.2
	434702	AL039734	Hs.4099	narditysin (N-arginine dibasic	Peptidase_M16,HCO3_cotran	3.2
	422242	AJ251760	Hs.273385	guanine nucleotide binding pro	G-alpha,arf,SS,G-alpha	3.2
	430480	AL079399	Hs.241543	DKFZP586F1524 protein	SS,TM,hemopexin,Somatomed	3.2
	452438	BE514230	Hs.29595	JM4 protein	SS,TM,KOW,HLH	3.2
40	456939	AA431633	Hs.163867	NM_002488-Homo sapiens NADH d	SS,IRNA-synt_2b,WHEP-TRS,	3.2
	421009	ALD49709	Hs.343357	Human DNA sequence from clone	TM	3.2
	411969	X12458	Hs.72980	Protein P3	SBF,SS,TM,G6PD,G6PD_C,hex	3.2
	409197	N54706	Hs.303025	chromosome 11 open reading fra	SS	3.2
	417896	AA379770	Hs.82890	defender against cell death 1	DAD,SS,TM	3.2
45	418026	BE379727	Hs.83213	fatty acid binding protein 4,	lipocalin,SS,lipocalin	3.2
	409057	AA702305	Hs.180060	ESTs	SS,TGfb_propeptide,TGF-be	3.2
	437869	W91976	Hs.290834	ESTs	SS,TM,SH3,zf-C3HC4	3.2
	413211	AW967107	Hs.109274	hypothetical protein MGC4365	SS,TM	3.2
	425080	AI393498		Inositol 1,4,5-trisphosphate re	SS,CITF_NFI	3.2
50	445363	NM_005993	Hs.12570	tubulin-specific chaperone d	ATP-synt_B,HEAT_PBS,SS,TM	3.2
	421943	BE616520	Hs.343912	Homo sapiens, Similar to RIKEN	SS,TM,SS,TM	3.2
	443337	Y07604	Hs.8235	non-metastatic cells 4, protei	NDK,SS,adh_short,NDK	3.2
	418885	D17530	Hs.89434	drebrin 1	cofilin_ADF,SS,cofilin_AD	3.2
	411817	BE302900	Hs.72241	mitogen-activated protein kina	pklnase,SS	3.2
55	413891	BE271020		tumor suppressor deleted in or	SS,TM	3.2
	449455	T60748	Hs.278408	hypothetical protein	TM	3.2
	419193	D29643	Hs.34789	dolichyl-diphosphodiglyceride	SS,TM,DDOST_48kD,VP7,SS,T	3.2
	405701	AA780613	Hs.62954	ferritin, heavy polypeptide 1	SS,TM,UDPGT	3.2
	436467	AW450278	Hs.91681	ESTs, Weakly similar to DCHUO	SS,IRNA-synt_1b,IRNA_bind	3.2
60	446334	U52427	Hs.14839	polymerase (RNA) II (DNA direc	S1,SS	3.2
	410270	AF279142	Hs.195727	tumor endothelial marker 1 pre	SS,TM,EGF,lectin_c,sushl,	3.2
	445411	AL137255	Hs.12646	hypothetical protein FLJ22693	SS,hormone_rec,zf-CCCH	3.2
	458018	AI199575	Hs.37716	ESTs	SS,TM,Oxysterol_BP	3.2
	426530	U24578	Hs.278625	complement component 4A	SS,A2M,NTR,A2M_N,prenyltr	3.2
65	445604	T08568	Hs.12956	Tax interaction protein 1	PDZ,SS,TM,P2X_receptor,FG	3.2
	443402	U77846		elastin (supravascular aortic	SS,PDZ_LIM,ptkinase	3.2
	432416	BE410937	Hs.2985	emerin (Emery-Dreifuss muscula	LEM,SS,Ribosomal_L10e,Acy	3.2
	429662	AI929701	Hs.211586	phosphoinositide-3-kinase, reg	SH2,SH3,RhoGAP,SS,GILT,SH	3.2
70	429150	AF120103	Hs.197366	smoothened (Drosophila) homolo	SS,TM,Fz,Fritzzled,7tm_2,S	3.2
	427729	AB033100	Hs.300646	KIAA1274 protein (similar to m	SS	3.2
	418151	AA664238.comp	Hs.83583	actin related protein 2/3 comp	RhoGEF,REV,PH,SS,TM,Ribos	3.2
	448250	NM_016034	Hs.20776	mitochondrial ribosomal protei	Ribosomal_S2,SS,lipocalin	3.2
	431158	AW859138	Hs.136280	Homo sapiens cDNA: FLJ22288 ti	SS,Exonuclease	3.2
	414292	BE388407	Hs.75875	ubiquitin-conjugating enzyme E	UQ_con,SS,TM,SAM_PNT	3.2
75	406307			Target Exon	SS,TM,7tm_2,SS,TM,7tm_2,G	3.2
	423325	R55565	Hs.347286	hypothetical protein FLJ22427	SS,TM,Supr,ubiquitin,TBC	3.2
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis vir	NA,SS	3.1
	419069	AA233801		ESTs, Weakly similar to CA13_H	SS	3.1
80	431717	BE396150	Hs.6945	mitochondrial ribosomal protei	SS,TM	3.1
	448381	D61580	Hs.21036	Homo sapiens mRNA; cDNA DKFZp4	RhoGAP,SS,TM,SET,zf-CXXC,	3.1
	419394	AB011124	Hs.90232	KIAA0552 gene product	SS,lg	3.1
	436240	BE388673	Hs.5086	hypothetical protein MGC10433	SS,TM,Ets,COX6B,transmemb	3.1
	413900	AW409747	Hs.75612	stress-induced-phosphoprotein	TPR,SS,TM,DnaJ	3.1
	417920	S47833	Hs.82927	adenosine monophosphate deamin	A_deaminase,SS,G-alpha,GS	3.1
	421819	NM_013403	Hs.108665	zhedin	WD40,ptkinase,ptkinase	3.1

5	426362	BE267158	Hs.169474	DKFZP586J0119 protein	IF-2B,SS,PP2C	3.1
	408917	AW249025	Hs.7768	fibroblast growth factor (acid	SS,bZIP,cofilin_ADF,EGF	3.1
	443099	AJ372836	Hs.8003	hypothetical protein FLJ13868	TM	3.1
	427022	AW245839	Hs.173255	small nuclear ribonucleoprotein	rm,SS,rm,SH3,ras,2OG-Fa	3.1
	452711	AW967047	Hs.293224	ESTs, Weakly similar to T00375	SS	3.1
	407236	W79485	Hs.173980	nuclear matrix protein NMP200	WD40,SS,TM,PTR2,7tm_1	3.1
	452537	AW247390	Hs.77735	hypothetical protein FLJ11618	SS,SNF2_N,helicase_C	3.1
	452139	AA099969	Hs.16331	Homo sapiens cDNA: FLJ21482 fi	SS	3.1
10	447629	AF034790	Hs.19105	translocase of inner mitochond	Tim17,SS,TM,pkinase,OTU	3.1
	401097			C12000858:gij7363437/refNP_0	SS,TM,7tm_1,SS	3.1
	452736	CO1164	Hs.4232	Homo sapiens PAC clone RP1-130	SS,SS,TM,TBC,Supr,ubiquit	3.1
	435507	AI143579	Hs.26510	vacuolar protein sorting 33B (SS,Sec1,Sec1	3.1
	424934	U75370	Hs.153880	polymerase (RNA) mitochondrial	PPR,SS,TM,cNMP_binding,RN	3.1
15	413245	BE244334	Hs.75249	ADP-ribosylation factor-like 6	SS,TM,kazal,Ribosomal_S8,	3.1
	409858	NM_006586	Hs.56828	trinucleotide repeat containin	SS,SS,TM,B56	3.1
	424582	AF026849	Hs.150922	BCS1 (yeast homolog)-like	AAA,SS,PI-PLC-X,PI,PI-PLC	3.1
	431677	AK000496	Hs.306989	hypothetical protein FLJ20489	SS	3.1
	417947	AA323563	Hs.325309	hypothetical protein FLJ14595	SS,TM,PTPA	3.1
20	409283	NM_004860	Hs.52788	fragile X mental retardation,	KH-domain,SS,TM,HMG_box	3.1
	412813	AF086947	Hs.74617	dynactin 1 (p150, Glued (Droso	CAP_GLY,SS	3.1
	456535	AA305079	Hs.1342	cytochrome c oxidase subunit V	COX5B,SS,p450,actin	3.1
	432482	L19267	Hs.275924	dystrophin myotonic-containin	WD40,SS,pkinase,pkinase	3.1
	437256	AL137404	Hs.97871	Homo sapiens, clone IMAGE:3845	TM,SS	3.1
25	440191	AJ990417		tubulin, beta 5	SS,formiminotr,prenyltran	3.0
	407972	AA827639	Hs.18587	JKIAA1588 protein	SS,TM	3.0
	420890	AA434058	Hs.100071	6-phosphogluconolactonase	Glucosamine_Iso,SS	3.0
	440060	AJ696387	Hs.126451	ESTs, Weakly similar to A46302	SS	3.0
	452222	AW806287	Hs.21432	SEX gene	SS,TM,Sema,TIG,PSI,GDI	3.0
30	401772			NM_014520:Homo sapiens MYB bin	SS	3.0
	453754	AW972580	Hs.172753	ESTs	SS,TM,ras,Ribosomal_S19,T	3.0
	423865	H05202	Hs.133968	FGF receptor activating protei	SS,TM	3.0
	450982	BE535647	Hs.25723	Sjogren's syndrome/scleroderma	SS,TM	3.0
	441954	AJ744935	Hs.8047	Fanconi anemia, complementatio	TPR,SS,TM,AAA,cdc48_N,Ban	3.0
35	412787	D87452	Hs.74579	KIAA0263 gene product	zf-CCCH,SS,TM,NTP_transfe	3.0
	422034	AC006486	Hs.333069	Ets2 repressor factor	Ets,SS,pkinase,PAF-AH_Ib	3.0
	450788	AJ738410		ESTs	SS,TM	3.0
	452511	BE408178	Hs.285165	Homo sapiens cDNA FLJ20845 fis	SS,thioredo,P5CR	3.0
40	414380	BE391815	Hs.75981	ubiquitin specific protease 14	UCH-2,UCH-1,ubiquitin,SS	3.0
	407597	AA043925	Hs.339352	Homo sapiens brother of CDO (B	SS,TM,SS,TM	3.0
	434955	BE276128	Hs.284286	mitochondrial ribosomal protel	SS	3.0
	435632	AF220049	Hs.43549	uncharacterized hematopoietic	SS,UQ_con	3.0
	432465	D56165	Hs.275163	non-metastatic cells 2, protel	NDK,SS,NDK	3.0
	430526	AF181862	Hs.242407	G protein-coupled receptor, fa	7tm_3,homeobox,SS,TM	3.0
45	453412	AJ003290		gb:AJ003290 Selected chromosom	pkinase	3.0
	446456	BE613933	Hs.15106	chromosome 14 open reading fra	UPF0143,SS	3.0
	433180	AB038651	Hs.31854	K562 cell-derived leucine-zipp	TM,Acetyltransf,TM,Acetyl	3.0
	447322	BE617649	Hs.77690	RAB5B, member RAS oncogene fam	SS,oxidored_molyb,heme_1,	3.0
	422268	N25485	Hs.330310	maternal G10 transcript	G10,SS,WD40	3.0
50	419578	AF064853	Hs.91299	guanine nucleotide binding pro	WD40,SS,EPO_TPO	3.0
	446929	AA076132	Hs.9460	Homo sapiens mRNA: cDNA DKFZp5	SS,TM,WD40	3.0

TABLE 21B:

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

55	Pkey	CAT Number	Accession
	408215	10478_1	BE614290 AA307674 N35629 AA338538 AI193603 AA781096 AI680061 AI613258 AW276647 BE221263 AI348910 AI985031 AI090078 AI359617 AA666391 AI160210 AI446461 AI355345 AI343638 AI343640 AI275091 M78746 AW262795 AW250002 AA503756 AI934519 AW272086 N26520 AA626639
60	409938	116091_1	AW974648 AA652153 AA649671 AA078582
	411674	1253746_1	AW861123 AW861125 AW856717 AW861116 AW856706 AW856788 AW856774 AW856787 AW856780 AW856782 AW856789 AW856772 AW856784 AW856786 AW856776 AW856635 AW856767
65	413052	1347214_1	BE249841 BE062657 BE062771 BE062636 BE062813 BE062699 BE062895 BE062747 BE062719 BE293541
	413837	139363_1	AW163525 AW163255 AW163385 AI929359 BE278279 AA132590 AW157329 AA584408 AW157252 AI692198 AW003514 T24436 AI765658 AW157459 AI810740 AI659582 AI969924 AI929284 AI340993 AI349083 AW299522 AW664650 AW299513 AA132529 AI340991 AI912836 AI341293 AI650609 AA279
70	413891	139759_1	BE271020 AI763358 AI925430 AI806151 AW003726 T15590 AA649945 AW129911 AI570748 T57492 AA828002 AW237602 AW003539 AI139045 AI950958 BE042625 AW778973 AI287859 AI983931 AW515101 AW150029 AI358496 AI621173 AA846016 AI470921 AW169748 AI991000 AW513748 AJ04058
	414023	1410860_1	BE243628 BE246081 BE247016 BE241984 BE241534 BE246091 BE245679 BE243620 BE245998 BE242329 BE241417 BE241457 BE242522 BE241989 BE241464
	416535	1599332_1	H61851 H74099 T67099
75	417998	171375_1	AW967420 AA210915 AA236991 AA210916
	418984	181094_1	AA421401 T49326 AA330666 AA328941 W63573 AA758023 AA976306 H52254 AA877107 BE207784 AW664584 AI924890 AA458586 AI422142 AI891097 AI811174 R69866 T49327 AA233722 AA631138 AA910314 AI379416 AI129321 AA861574 AA635649 AI339443 AW009533 AA677036 AA948287 AA62
	419069	181650_3	AA233801 BE383487 AA913939 AI632681 AI813277 AI373652 AW134802 AI863574 AW305364 AI858557 AI670746 AI015036 AI935384 AI935317 AA138668 AW204971 AI765223 AA884146 AA973341 AA234082
80	419250	183289_2	AW770185 AW296271 H11254 AW403510 AI032786 AA767046 AI376115 AI582209 AA460965 AI868663 AI016900 R05715 AI127382 AI660953 AI023844 H00465 AW959578 AA815039 AW292253 R05714 AA815462 AA235654 AA461274 YW24933 AA300091 H00515 AI492840 AI287657 AA255989 AI698206 AI468558
	420160	191054_1	AA531607 AI565370 AI376907 AI811618 AW138145 AW139465 AA421658 AA293069 AW118141 AI214980 AW663502 AI343486 AI553789 AA650416 AI498947
	421572	204022_1	

423696 23112_1 Z92546 AA330586 AI570568 AW341487 AI827050 AW298668 AI792189 AI015693 AI733599 AI572251 AI672488 AW193262 AI244716 AI864375
AI206100 AA912444 AI269365 AI640254 AW772466 AI867336 AA627604 H16914 AA358477 AA338009

425080 246559_1 AI393498 RA2314 AI088818 AI696468 AI418641 AA573152 F08817 AI910796 AW338984 R39024 AA729145 BE245956 AI093722 AA541730
F09835 AI242755 AA350447 AA865667 T93903 AW081029 AA493711 AA650030 N35995 N21491 T57002 Z25379 AI906851
BE270447 AW405921 BE207288 BE207170 D56355 BE263223 BE408171 BE262243 BE392439 BE292738 BE261776 BE314300 BE267719
BE268715 BE513876 BE295291 BE297066 AA210923 BE407519 H51344 BE622905 AW248281 AW250313 T19021 AA355115 AA316879
BE269633 BE621936 AA290724

427391 27815_1 W60675 AK001212 AA155752 AA878366 AA090872 AB033013 AW249107 AA031890 AA112820 AW366388 N55156 AA326756 AW952294
AA180820 C03570 C04358 W60676 AW248674 AA034989 AA044781 AA074274 H26212 AI800572 AI127583 AI951785 AA856557 AI571746
H23835 AI589543 AI215670

428092 286920_1 AW879141 AA421182 AI734104 AI733923 AA430600
429545 305902_1 AI824164 AI676005 AW129612 AI825903 AA773987 AI823645 AI823860 AA456229 AI824295 AA454622 AI264049 AI090237 AI669787 AI804012
AI306153 W96164 AI298273 AW884073 AW883986
AW968343 AA468507 AI478223 AW513008 AI762122 AI554512 AA862642 AA468976
BE263901 AA596086 AI190276 AI094806 AI831250 AI572658 AW204652 AI660600 AI922941 R49621

430168 313927_1 L08239 BE618914 AW385394 AW385398 AW385401 AI922683 AA907337 AA160504 AA928142 AA601969 AA010594 BE618528 AA160591
433519 368801_2 AI990417 AI304400 AI193071 AI742483 AW003408 AW131556 AI400201 AI656740 AI309186 AW665173 AW204722 AI215122 AI200785
438707 46360_1 BE467373 AI147599 AI215120 AI076110 AI803429 AI262491 AI808243 AI281007 AW135212 AW205103 AI754349 AI004801 AI051273 AW768918
440191 48804_3 AW103289 AI4

443402 5681_1 U77846 AA479373 AA346348 AA348194 M26867 AA728901 AA715367 AA377787 R64236 AI752721 R77311 AA339685 BE074254 AW938712
AW068444 AA330624 AA347098 AA327507 AW391973 AA495763 AA479278 AW605018 T19644 AI204484 AW834745 AW081309 AW090002
AI095659 AI131556 AI56

444590 6116_1 AA457456 AA907921 AI567715 AA579472 T64216 AA373128 F35533 AA722113 T64403 AA653738 F28806 AA595689 AA047537 AA022499
AW440532 F36782 AI554180 AI183767 AI806052 AA160379 AA481678 AI185031 AI148988 AI74482 AA868833 AI674395 AA481440 AI914985
AI698771 AAA4

445625 64558_1 BE246743 AA436942 AW024744 AW242177 AA975476 AW385185 R07536 R73462 AV654529 T57442 AI399986 R50073 R48743 AI769689
AI833005 AA317806 AI678000 AW189963 AI986207 AW471273 R73463 AI335104 AI590161 AI69257 AI954604 H21954 T25141 AA856793
R50074 AI708253 AI2

448606 77159_1 BE613362 AA447862 H72036 AA393654 AI681334 AW139128 AA932579 AI302241 AI936800 AW950628 AI492148 C06192 AA336107 AA808008
AW615212 BE297403 BE298978 AI187207 AA928695 AI620631 AA938128 AI346527 AI040261 AA808401 AW130326 AI440313 AA868693
AI653329 AI33246

448677 775217_1 AI560769 AI87497 AW151454
450788 846840_1 AI738410 AW016905 AI971725
452160 901991_1 BE378541 AI863051
453412 966264_1 AJ003290 AJ003288 AW276947
455857 1376021_1 T70192 BE147698
455928 1383899_1 BE170313 BE158339 BE158290
457022 274445_1 AW377258 BE067468 BE067511 BE067515 BE067467 BE067514 AA397442

TABLE 21C:

Pkey: Unique number corresponding to an Eos probaset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495

Strand: Indicates DNA strand from which exons were predicted

NL_position: Indicates nucleotide positions of predicted exons

Pkey	Ref	Strand	NL_position
400460	8389428	Plus	35559-36295
400563	9844011	Plus	81941-82434
400747	7329330	Minus	71249-71441
400846	9188605	Plus	39310-39474
401097	9965518	Minus	60356-61096
401128	8699792	Plus	37349-37885
401655	9099093	Plus	79556-80132
401727	8134856	Plus	54342-54482
401751	9828651	Plus	139165-139322
401772	9966243	Plus	183917-184042
402365	9454515	Minus	70928-71185
402463	9796896	Minus	8818-8952
402665	8077033	Minus	11824-12090,14290-14544
402793	6136940	Minus	69012-69165
402916	7406502	Minus	361-474,541-687
403028	7670577	Minus	114150-114272
403325	8440025	Minus	109763-109926
404258	9367203	Plus	146931-147796
405189	7229907	Minus	168236-168795
405325	6094661	Minus	25818-26380
405358	2155224	Plus	36116-36276
405496	8468968	Plus	147706-148062
406101	9124019	Plus	125325-125831
406307	8576099	Plus	95473-95585,98900-99180
406535	7711477	Plus	83135-83362

Table 22A lists about 811 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 20A, except that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 4.0, the "average" ovarian cancer level was set to the 96th percentile value amongst various ovarian cancer specimens, the "average" normal adult tissue level was set to the 75th percentile value amongst various non-malignant tissues, the "average" ovarian cancer value was greater than or equal to 80 units, and the predicted protein contained a structural domain that is indicative of enzymatic function or of transducing an intracellular signal, or of being modulatable by small molecules (e.g., kinase, peptidase, phosphatase, or ion_transporter). Predicted protein domains are noted.

TABLE 22A:

Pkey: Unique Eos probaset Identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 Protein Dom.: Predicted protein domain
 R1: Ratio of tumor to normal body tissue

5	Pkey	ExAccn	UniGene ID	Unigene Title	Protein Dom.	R1
	407223	H98850		gb:yy03b12s1 Soares melanocyt		58.9
	430281	A1878842	Hs.237924	CGI-69 protein	mito_carr	46.7
10	410418	D31382	Hs.63325	transmembrane protease, serine	ldl_recept_a, trypsin	41.0
	431773	BE409442	Hs.268557	pleckstrin homology-like domai	PH	37.1
	438424	A912498	Hs.25895	hypothetical protein FLJ14996		35.3
	418969	W33191	Hs.28907	hypothetical protein FLJ20258	SH3	35.2
	453028	AB006532	Hs.31442	RecQ protein-like 4	DEAD, helicase_C	28.2
15	407722	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin	pfkB	28.2
	451721	NM_006946	Hs.26915	spectrin, beta, non-erythrocyt	spectrin, PH, CH	27.9
	416819	U77735	Hs.80205	pim-2 oncogene	pk kinase	27.9
	430397	A924533	Hs.105607	bicarbonate transporter relate	HCO3_cotransp	27.7
	450334	AF035959	Hs.24879	phosphatidic acid phosphatase	PAP2	26.7
20	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	lipoxygenase, PLAT	25.3
	424420	BE814743	Hs.146688	prostaglandin E synthase	MAPEG	25.1
	412674	X04106	Hs.74451	calpain 4, small subunit (30k)	efhand	24.4
	430023	AA158243	Hs.227729	FK506-binding protein 2 (13kD)	FKBP	24.3
	444672	Z95636	Hs.11669	laminin, alpha 5	laminin_EGF, laminin_G, EGF	24.0
25	413726	AJ278465	Hs.75510	annexin A11	annexin	23.1
	438951	U51336	Hs.6453	inositol 1,3,4-triphosphate 5'	oxidoreductase	23.0
	429099	BE439952	Hs.196177	phosphorylase kinase, gamma 2	pk kinase	23.0
	431765	AF124249	Hs.268541	novel SH2-containing protein 1	SH2	22.4
	422645	L40027	Hs.118890	glycogen synthase kinase 3 alp	pk kinase	22.4
	413438	AF238083	Hs.68061	sphingosine kinase 1	DAGKc	22.3
30	422639	A929377	Hs.173724	creatine kinase, brain	ATP_gua_Ptrans, ATP_gua_Pi	21.5
	429869	AJ907018	Hs.15977	Target CAT		21.3
	418891	NM_002419	Hs.89449	mitogen-activated protein kina	SH3, pk kinase, pyridoxal_deC	21.1
	419138	U48508	Hs.89631	ryanodine receptor 1 (skeletal	RYRDR, JTPR, RyR, SPRY, ion_tr	21.0
	432666	BE395875	Hs.279609	mitochondrial carrier homolog	mito_carr	20.9
35	452875	BE275760	Hs.30928	DNA segment on chromosome 19 (Euk_porph	20.8
	426997	BE820738	Hs.173125	peptidylprolyl isomerase F (cy	pro_isomerase	20.8
	402916			ENSP00000202587: Bicarbonate t	HCO3_cotransp	20.8
	425760	D17629	Hs.159479	galactosamine (N-acetyl)-6-sul	Sulfatase	20.7
40	400419	AF084545		Target	EGF, ig, lectin_c, sushi, XII	20.0
	419444	NM_002496	Hs.90443	Target CAT		19.5
	459133	U40343	Hs.29656	cyclin-dependent kinase inhibi	ank	19.2
	447595	AW379130	Hs.18953	phosphodiesterase 9A	PDEase	19.2
	422708	AB017430	Hs.119324	kinesin-like 4	kinesin, homeobox	19.0
45	414837	U24266	Hs.77448	aldehyde dehydrogenase 4 fami	aldehyde	18.8
	429712	AW245825	Hs.211914	ENSP00000233627: NADH-ubiquino	oxdoreductase	18.5
	425848	BE24709	Hs.159637	valyl-tRNA synthetase 2	GST_C, GST_N, Tropomyosin	18.4
	451643	M64437	Hs.234799	breakpoint cluster region	RhoGEF, RhoGAP, PH, C2	18.1
	447859	AK002194	Hs.19851	peroxisomal biogenesis factor		17.5
50	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	DAG_FE-bind, RhoGAP	17.3
	421612	AF161254	Hs.106196	8D6 antigen	ldl_recept_a	17.1
	421363	NM_001381	Hs.103854	docking protein 1, 62kD (downs	PH, IRS	16.9
	442739	NM_007274	Hs.8679	cytosolic acyl coenzyme A thio	Acyl-CoA_hydro	16.8
	420568	F09247	Hs.247735	procadherin alpha 10	cadherin	16.8
55	421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054	asp	16.8
	425424	NM_004954	Hs.157199	ELKL motif kinase	pk kinase, KA1, UBA	16.7
	446329	NM_013272	Hs.14805	solute carrier family 21 (orga	kazal, OATP_N, OATP_C	16.5
	406620	M81105	Hs.146550	myosin, heavy polypeptide 9, n	myosin_head, Myosin_tail, I	16.4
	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4	PX, SH3, OPR	16.3
60	429183	AB014604	Hs.197955	KIAA0704 protein	PH, Oxysterol_BP	16.2
	444664	N26362	Hs.11615	map kinase phosphatase-like pr	DSPc, Rhodanese	16.2
	427640	AF058293	Hs.180015	D-dopachrome tautomerase	MIF, late_protein_L2	16.2
	425123	AW205274	Hs.154695	phosphomannomutase 2	PMM	16.0
	416006	AA324251	Hs.78950	branched chain keto acid dehyd	E1_dehydrog	15.8
65	412942	AL120344	Hs.75074	mitogen-activated protein kina	pk kinase	15.8
	423366	Z80345	Hs.127610	acyl-Coenzyme A dehydrogenase,	Acyl-CoA_dh, Acyl-CoA_dh_M	15.7
	426391	AW161050	Hs.168611	second mitochondria-derived ac		15.7
	424568	AF005418	Hs.150595	cytochrome P450, subfamily XXV	p450	15.5
	420029	BE258876	Hs.94446	polyamine-modulated factor 1	aldo_ket_red	15.5
70	433573	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G	7tm_2, EGF, cadherin, Jamini	15.4
	407619	AL050341	Hs.37165	collagen, type IX, alpha 2	Collagen	15.3
	427326	AJ287878		gb:xy23f06.x1 NC1_CGAP_Lym6 Ho	7tm_1	15.2
	442620	C00138	Hs.8535	Homo sapiens mRNA for KIAA1668		15.1
	458130	AA115811	Hs.6838	ras homolog gene family, membe	ras, arf	15.0
75	449336	AA938293	Hs.60088	hypothetical protein MGC11314		15.0
	409230	AA852431	Hs.51299	NM_021074: Homo sapiens NADH de	complex1_24kD	14.7
	423801	NM_015071	Hs.132942	GTPase regulator associated wi	RhoGAP, SH3, PH	14.0
	419639	AK001502	Hs.91753	hypothetical protein		13.6
	419298	AA853479	Hs.89890	pyruvate carboxylase	CPSase_L_chain, PYC_QADA_H	13.6
80	426108	AA622037	Hs.166468	programmed cell death 5	DUF122	13.5
	448133	AA723157	Hs.73769	folate receptor 1 (adult)	Folate_rec	13.5
	418736	T18979	Hs.87908	Snf2-related CBP activator pro	helicase_C, AT_hook	13.5
	436543	NM_002212	Hs.5215	integrin beta 4 binding protei	elF6	13.3
	431515	NM_012152	Hs.258583	endothelial differentiation, I	7tm_1	13.3
	429469	M64590	Hs.27	glycine dehydrogenase (decarbo	GDC-P	13.2

431462	AW583572	Hs.256311	granin-like neuroendocrine pep		13.2
444855	BE408261	Hs.12084	Tu translation elongation fact	GTP_EFTU,GTP_EFTU_D3,GTP_	13.2
423464	NM_016240	Hs.128856	CSR1 protein	Collagen	13.1
450787	AB006190	Hs.25475	aquaporin 7	MIP	13.0
428539	AW410063	Hs.184877	solute carrier family 25 (mito	mito_carr	13.0
436014	AF281134	Hs.283741	exosome component Rrp46	RNase_PH,RNase_PH_C	12.9
416866	AA297358	Hs.80324	serine/threonine protein phosph	Metallophos	12.9
433857	AK000596	Hs.3618	hippocalcin-like 1	efhand	12.9
411408	U76666	Hs.69949	calcium channel, voltage-depen	ion_trans	12.8
432329	NM_002962	Hs.2960	S100 calcium-binding protein A	S_100,efhand	12.7
447887	AA114050	Hs.19949	caspase 8, apoptosis-related c	ICE_p20,DED,ICE_p10	12.7
427448	BE246449	Hs.2157	Wiskott-Aldrich syndrome (ecze	WH1,P8D,WH2	12.7
428820	AA436187	Hs.172631	integrin, alpha M (complement	FG-GAP	12.7
446603	NM_014835	Hs.15519	oxysterol-binding protein-rela	Oxysterol_BP	12.6
422633	X56832	Hs.118804	enolase 3, (beta, muscle)	enolase	12.6
446839	BE091926	Hs.16244	mitotic spindle coiled-coil re	Tropotin	12.6
414757	U46922	Hs.77252	fragile histidine triad gene	HIT	12.5
428593	AW207440	Hs.185973	degenerative spermatocyte (hom		12.5
432370	AA308334	Hs.274424	N-acetylneuraminic acid phosph	Antifreeze,NeuB	12.5
401542			C15001413*gi10645199[ref]NP_		12.4
428782	X12830	Hs.193400	Interleukin 6 receptor	fn3,jg	12.3
425999	AW513051	Hs.332981	ESTs, Weakly similar to I38022	FAD_binding_2	12.3
422301	AJ752163	Hs.114599	collagen, type VIII, alpha 1	C1q,Collagen	12.2
410720	AF035154	Hs.65756	regulator of G-protein signal	RGS,G-gamma,DEP	12.2
407143	C14076	Hs.332329	EST		12.1
421321	NM_005309	Hs.103502	glutamic-pyruvate transaminase	aminotran_1_2	12.1
425251	Z22521	Hs.155342	protein kinase C, delta	pkinase,DAG_PE-bind,pkina	12.0
431354	BE046958	Hs.251673	DNA (cytosine-5)-methyltransf	PWWP,PHD	12.0
420421	AF281133	Hs.343589	exosome component Rrp41	RNase_PH,RNase_PH_C	12.0
416714	AF283770	Hs.79630	CD79A antigen (immunoglobulin-	ig,ITAM,Zn_plus	12.0
427338	NM_005658	Hs.21134	TNF receptor-associated factor	MATH	12.0
409799	D11928	Hs.76845	phosphoserine phosphatase-like	Hydrolase	11.9
436319	H90727	Hs.5123	inorganic pyrophosphatase	Pyrophosphatase	11.9
400748			NM_022122:Homo sapiens matrix		11.9
428948	BE514362		FK506-binding protein 3 (25kD)	FKBP,PIPSK	11.8
401215			C12000457*gi7512178[pir]T30	trypsin	11.7
401281			DKFZP586N2124 protein		11.7
427397	AJ929685	Hs.177656	calmodulin 1 (phosphorylase ki	efhand,RmaAD	11.7
453496	AA442103	Hs.33084	solute carrier family 2 (facil	sugar_tr	11.7
409508	AF231023	Hs.55173	cadherin, EGF LAG seven-pass G	7tm_2,cdherin,GPS,lamini	11.7
424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	enolase	11.7
447495	AW401864	Hs.18720	programmed cell death 8 (apopt	pyr_redox	11.6
426928	AF037062	Hs.172914	retinol dehydrogenase 5 (11-ci	adh_short	11.6
405371			NM_005569:Homo sapiens LIM do	pkinase,LIM,PDZ	11.5
416282	R86664	Hs.167257	brain link protein-1	Xlink	11.4
452295	BE379936	Hs.28866	programmed cell death 10		11.4
430390	AB023186	Hs.241161	KIAA0969 protein	PH	11.4
430594	AK000790	Hs.246885	hypothetical protein FLJ20783	PH	11.2
443814	BE281240	Hs.9857	carbonyl reductase		11.2
440242	AW295871		glucose transporter protein 10		11.1
447365	BE383676	Hs.334	Rho guanine nucleotide exchang	SH3,PH,RhoGEF	11.1
400843			NM_003105:Homo sapiens sortil	ldl_recept_a,fn3,ldl_rece	11.1
422418	AK001383	Hs.116385	hypothetical protein FLJ10521	RhoGEF	11.0
400232			NM_001895:Homo sapiens casein	pkinase	10.9
426828	NM_000020	Hs.172670	activin A receptor type II-lik	pkinase,Activin_rec	10.9
431157	AJ823969	Hs.132678	ESTs	MAPEG	10.8
422616	BE300330	Hs.118725	selenophosphate synthetase 2	AIRS,AIRS_C	10.8
406779	AA412048	Hs.279574	CGI-39 protein; cell death-reg		10.8
400389	AL135841		olfactory receptor, family 2,	7tm_1	10.8
402207			Target Exon	A2M_N,A2M	10.8
435615	Y15065	Hs.4975	potassium voltage-gated channe	ion_trans,KCNQ1_channel	10.8
452434	D30934	Hs.29549	C-type lectin-like receptor-1	lectin_c	10.7
402053			C11001722*gi11436283[ref]XP_		10.7
418641	BE243136	Hs.86947	a disintegrin and metalloprote	disintegrin,Reprolysin,Pe	10.6
431512	BE270734	Hs.2795	lactate dehydrogenase A	ldh,ldh_C	10.6
403213			NM_019595:Homo sapiens interse	SH3,efhand,C2,PH,RhoGEF	10.6
412158	BE241740	Hs.785	integrin, alpha 2b (platelet g	FG-GAP,Integrin_A	10.6
423673	BE003054	Hs.1695	matrix metalloproteinase 12 (m	Peptidase_M10,hemopexin	10.6
403949			C10000813*gi5453992[ref]NP_0		10.6
457670	AF119666	Hs.23449	insulin receptor tyrosine kina	SH3	10.5
418416	U11700	Hs.84999	ATPase, Cu transporting, beta	E1-E2_ATPase,HMA,Hydrolas	10.4
419594	AA013051	Hs.91417	topoisomerase (DNA) II binding	BRCT	10.4
422765	AW409701	Hs.1578	baculoviral IAP repeat-contain	BIR,TK	10.4
453023	AW028733	Hs.31439	serine protease inhibitor, Kun	Kunitz_BPTI	10.4
425694	U51333	Hs.159237	hexokinase 3 (white cell)	hexokinase,hexokinase2	10.4
438800	AB037108	Hs.6418	seven transmembrane domain orp		10.3
402478			Target Exon	Carn_acyltransf	10.3
444202	AL031685	Hs.12785	KIAA0939 protein	Na_H_Exchange,ABC2_membr	10.3
425597	U28694	Hs.158324	chemokine (C-C motif) receptor	7tm_1	10.3
413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E	UQ_con	10.2
415200	AL040328	Hs.78202	SWI/SNF related, matrix associ	SNF2_N,helicase_C,bromodo	10.2
414874	D26351	Hs.77515	inositol 1,4,5-triphosphate re	RYDR,ITPR,ion_trans,MiR	10.2
423524	AF055989	Hs.127338	potassium voltage-gated channe	ion_trans,K_tetra,themat	10.2
457558	AF083955	Hs.279852	G protein-coupled receptor	7tm_1,globin	10.2

	445629	AI245701	Hs.193326	fibroblast growth factor recep		10.1
	434314	BE392921	Hs.3797	RAB26, member RAS oncogene fam	ras,arf	10.1
	402497			C1001261*:gij2695979[emb]CAA70		10.1
5	449853	AF006823	Hs.24040	potassium channel, subfamily K	ion_trans	10.0
	427672	AA356615	Hs.336916	death-associated protein 6		10.0
	412048	AW866863	Hs.73090	nuclear factor of kappa light	RHD,TIG,ank,death	10.0
	410079	U94362	Hs.58589	glycogenin 2	Glyco_transf_8	10.0
	420319	AW406289	Hs.96593	hypothetical protein	ras,arf	10.0
10	420332	NM_001756	Hs.1305	serine (or cysteine) proteinase	serpin	9.9
	405474			NM_001093*:Homo sapiens acetyl	CPSase_L_chain,biotin_lip	9.9
	401507			C15000810*:gij11131272[sp]P793		9.9
	431434	BE267696	Hs.254105	enolase 1, (alpha)	enolase	9.9
	447232	AW499834	Hs.327	interleukin 10 receptor, alpha		9.8
15	432343	NM_002960	Hs.2861	S100 calcium-binding protein A	S_100	9.8
	408931	AA251936	Hs.334648	poly(A) polymerase alpha	NTP_transf_2	9.8
	421542	AA411607	Hs.118964	ESTs, Weakly similar to KIAA11		9.8
	430323	U40714	Hs.239307	tyrosyl-tRNA synthetase	DUF101	9.8
	412270	AC005262	Hs.73797	guanine nucleotide binding pro	G-alpha,arf	9.7
20	424649	BE242035	Hs.151461	embryonic ectoderm development	WD40	9.7
	400772			NM_003105*:Homo sapiens sortil	lcl_recept_a,fn3,lcl_rece	9.7
	450493	M93718	Hs.166373	nitric oxide synthase 3 (endot	flavodoxin,FAD_binding,NO	9.7
	401510			NM_017434:Homo sapiens dual ox	efhand,Ferri_reduct	9.7
	404596			Target Exon		9.7
25	451367	AA923729	Hs.26322	cell cycle related kinase	pkinase	9.7
	417810	D28419	Hs.82609	hydroxymethylbilane synthase	Porphobil_deam	9.6
	432855	AF017988	Hs.279565	secreted frizzled-related prot	Fz,NTR	9.6
	424263	M77640	Hs.1757	L1 cell adhesion molecule (hyd	fn3,Ig,IRK	9.6
	430398	AF105202	Hs.241376	potassium voltage-gated channe	ion_trans,KCNQ1_channel	9.6
30	424339	BE257148		endoglycan	MCM	9.6
	429257	AW163799	Hs.198365	2,3-bisphosphoglycerate mutase	PGAM	9.6
	407065	Y10141		ghb:Hsapiens DAT1 gene, partia	SNF	9.6
	433938	AF161536	Hs.284292	ubiquinol-cytochrome c reducta		9.6
	409649	AA159216	Hs.55505	hypothetical protein FLJ20442	Y_phosphatase,DSPc	9.6
35	404968			C4001170:gij6863176[gb]AAF3040		9.5
	400833			C11000690:gij3748443[gb]AAC639	7tm_1	9.5
	410191	AI609645		NM_021075*:Homo sapiens NADH d		9.5
	444633	AF111713	Hs.286218	junctional adhesion molecule 1	Ig	9.4
	427747	AW411425	Hs.180655	serine/threonine kinase 12	pkinase	9.4
40	415169	W42913	Hs.78089	ATPase, vacuolar, 14 kD	ATP-synt_LF	9.4
	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis	CARD	9.4
	422328	X60459	Hs.1513	interferon (alpha, beta and om		9.4
	445143	U29171	Hs.75852	casein kinase 1, delta	pkinase	9.4
	450883	NM_001348	Hs.25619	death-associated protein kinas	pkinase	9.4
45	414625	AA335738	Hs.76688	glutathione peroxidase 1	GSHPx	9.3
	401935			Target Exon	PH	9.3
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	PALP,CBS	9.3
	425242	D13635	Hs.155287	KIAA0010 gene product	HECT,IQ	9.3
	400404	AF161221		kallikrein 14	trypsin	9.2
50	422332	AI693251	Hs.8248	Target CAT	fer2,molybdopterin,bac_dn	9.2
	431534	AL137531	Hs.258890	Homo sapiens mRNA; cDNA DKFZp4		9.2
	402823			C1002456*:gij9530918[emb]CAC05		9.1
	404527			peptide YY, 2 (seminalplasmin)	GDA1_CD39	9.1
	439963	AW247529	Hs.6793	platelet-activating factor ace	PAF-AH_b,Lipase_GDSL	9.1
55	412970	AB026436	Hs.177534	dual specificity phosphatase 1	Rhodanese,DSPc	9.1
	443553	AL040535	Hs.9573	ATP-binding cassette, sub-famI	ABC_tran	9.1
	400933			NM_004347:Homo sapiens caspase	ICE_p20,ICE_p10,CARD	9.0
	403268			NM_002210*:Homo sapiens Integr	FG-GAP	9.0
	446673	NM_016361	Hs.15871	LPAP for lysophosphatidic acid	acid_phosphat	9.0
60	422531	AW967280	Hs.293894	ESTs, Weakly similar to HERC2	pkinase	9.0
	421658	X84048	Hs.301760	frequenin (Drosophila) homolog	efhand	9.0
	401885			Target Exon	kinesin	9.0
	402651			NM_000721*:Homo sapiens calci	ion_trans	9.0
	457432	NM_005136	Hs.268538	potassium voltage-gated channe	ISK_Channel	9.0
65	433146	AB033002	Hs.21413	solute carrier family 12, (pot		9.0
	420090	AA220238	Hs.94986	ribonuclease P (38kD)	Ribosomal_L7Ae	9.0
	425281	AA444390	Hs.155482	hydroxyacyl glutathione hydrol	lactamase_B	9.0
	410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	SNF2_N,helicase_C	9.0
	407988	U32659	Hs.41724	interleukin 17 (cytotoxic T-ly		9.0
70	431131	N84730	Hs.250616	isocitrate dehydrogenase 3 (NA	Isodh	9.0
	422802	NM_004278	Hs.27008	phosphatidylinositol glycan, c	DUF158	9.0
	447958	AW796524	Hs.68644	Homo sapiens microsomal signal		9.0
	438080	AA777381	Hs.291530	ESTs, Weakly similar to ALUC_H		9.0
	418843	AJ251016	Hs.89230	potassium intermediate/small c	CaMBD,SK_channel	9.0
75	419244	AI436567	Hs.89761	ATP synthase, H transporting,	ATP-synt_DE	8.9
	404676			Target Exon		8.9
	428744	BE267033	Hs.192853	ubiquitin-conjugating enzyme E	UQ_con	8.9
	421474	U76362	Hs.104637	solute carrier family 1 (gluta	SDF	8.9
	419056	M89597	Hs.89575	CD79B antigen (immunoglobulin-	IgJTAM	8.9
80	424825	AF207069	Hs.153357	procollagen-lysine, 2-oxogluta	2OG-Fell_Oxy,Glycos_trans	8.9
	444628	U01120	Hs.242	glucose-6-phosphatase, catalyt	PAP2	8.9
	404199			ENSP00000211797*:Helicase SK02	RasGAP,PH	8.9
	428826	AL048842	Hs.194019	atractin	lectin_c,CUB,Kelch,PSLEG	8.9
	410681	AW246890	Hs.65425	calbindin 1, (28kD)	efhand	8.8
	415056	AB004662	Hs.77867	adenosine A1 receptor	7tm_1	8.8

400471			Target Exon		8.8
406591			NM_003888*:Homo sapiens retina	aldedh	8.8
425427	A1652662	Hs.157205	branched chain aminotransferase	aminotran_4	8.8
410839	NM_006849	Hs.66581	protein disulfide isomerase	thioredo_rho_GDI,gnIR	8.7
430037	BE409649	Hs.227789	mitogen-activated protein kinase	kinase	8.7
450848	A1677994	Hs.428	fms-related tyrosine kinase 3	flk3_lig	8.7
414534	BE257293	Hs.76386	BCL2-antagonist of cell death		8.7
401454			NM_014226*:Homo sapiens renal	kinase	8.7
408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (mus	PGAM	8.7
433333	A1016521	Hs.71816	v-akt murine thymoma viral onc	homeobox,kinase,PH,ptina	8.7
430432	AB037758	Hs.241419	KIAA1337 protein	Patched	8.7
406128			NM_002920*:Homo sapiens regula	Oest_recep,zf-C4,hormone_	8.7
419493	AF001212	Hs.90744	proteasome (prosome, macropain	PCI	8.7
439569	AW602166	Hs.222399	CEGP1 protein	CUB,EGF	8.6
401134			C12001198:gl[3183183]sp[Q92142	biotpterin_H	8.6
442286	W31847	Hs.50335	cytochrome P450 monooxygenase		8.6
428376	AF119665	Hs.184011	pyrophosphatase (inorganic)	Pyrophosphatase	8.6
433494	AB029396		beta-1,3-glucuronyltransferase	Glyco_tranf_43	8.6
427001	NM_006482	Hs.173135	dual-specificity tyrosine-(Y)-	kinase	8.6
437278	AA748017	Hs.290145	ESTs	cnMP_binding	8.6
414463	T69078	Hs.76177	alpha-1-microglobulin/bikunin	lipocalin,Kunitz_BPTI	8.6
421871	AK001416	Hs.306122	glycoprotein, synaptic 2	Steroid_dh	8.6
447827	U73727	Hs.19718	protein tyrosine phosphatase,	Y_phosphatase,fn3,lg,MAM	8.6
403379			Target Exon	DNA_pol_A	8.6
446872	X97058	Hs.16362	pyrimidinergic receptor P2Y, G	7tm_1	8.6
432857	NM_016103	Hs.279582	GTP-binding protein Sara	arf,ras	8.5
420970	AA305079	Hs.1342	cytochrome c oxidase subunit V	COX5B	8.5
427221	L15409	Hs.174007	von Hippel-Lindau syndrome	VHL	8.5
402209			Target Exon	A2M_N,A2M	8.5
400518			C10002057*:gl[3211705]g[AA2C1		8.5
425606	U52112	Hs.158331	renin-binding protein		8.5
437965	AA843222	Hs.193534	ESTs, Moderately similar to AL	RasGEF	8.5
433392	AF038535	Hs.127588	synaptotagmin VII	C2	8.5
402191			NM_021733*:Homo sapiens testis		8.5
459563	A1701393	Hs.278728	Rad and Gem-related 2 (rat hom	ras	8.5
431857	W19144	Hs.271742	ADP-ribosyltransferase (NAD; p	PARP,PARP_reg	8.5
457579	AB030816	Hs.36761	HRAS-like suppressor		8.5
409656	NM_005133	Hs.288626	RCE1, prenyl protein protease	Abi	8.5
456373	BE247706	Hs.89751	membrane-spanning 4-domains, s		8.4
432499	BE276633		RAB6B, member RAS oncogene fam	ras,arf	8.4
400565			Target Exon		8.4
401960			Target Exon	Branch	8.3
432545	X52466	Hs.3041	uracil-DNA glycosylase 2	cyclin	8.3
445303	AW362198	Hs.12503	Interleukin 15 receptor, alpha	sushi	8.3
404528			peptide YY, 2 (seminalplasmin)	GDA1_CD39	8.3
428542	D79989		KIAA0167 gene product	ank,PH,ArfGap,ras	8.3
406868	AA505445	Hs.300697	immunoglobulin heavy constant		8.3
405473			NM_001093*:Homo sapiens acetyl	CPSase_L_chain,biotin_lip	8.3
408601	U47928	Hs.86122	protein A	7tm_1	8.3
415008	NM_002777	Hs.928	proteinase 3 (serine proteinase	trypsin	8.3
430258	AU076644	Hs.236963	protein phosphatase 2A, regula		8.3
436483	AJ272063	Hs.283010	vanilloid receptor subtype 1	ank,ion_trans	8.3
459302	NM_002314	Hs.35566	LIM domain kinase 1		8.3
437844	AA748575	Hs.136748	lectin-like NK cell receptor	lectin_c	8.3
421707	NM_014921	Hs.107054	lectormedin-2	Latrophilin,OLF,7tm_2,Gal	8.2
414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/m	COesterase	8.2
453898	AW003512	Hs.232770	arachidonate lipoygenase 3		8.2
424053	AF057036	Hs.138520	collagen-like tail subunit (sl	Collagen	8.2
457398	BE258532	Hs.251871	CTP synthase	GATase	8.2
421504	AW402997	Hs.105052	adaptor protein with pleckstri	SH2,PH	8.1
406495			Target Exon	SRCR	8.1
453610	AW368882	Hs.33818	RecQ protein-like 5	DEAD,helicase_C	8.1
424880	NM_000328	Hs.153614	retinitis pigmentosa GTPase re	RCC1	8.1
423847	U16997	Hs.133314	RAR-related orphan receptor C	hormone_rec,zf-C4	8.1
409629	M33552	Hs.56729	lymphocyte-specific protein 1	Caldesmon	8.1
401180			eukaryotic translation elongat	lon_trans,IQ	8.1
452072	BE258857	Hs.27744	RAB3A, member RAS oncogene fam	ras,arf	8.1
426484	AA379658	Hs.272759	KIAA1457 protein	IP_trans	8.1
402453			C1002496:gl[7363439]ref[NP_039	7tm_1	8.1
457310	W28363	Hs.239752	nuclear receptor subfamily 2,		8.1
422069	AJ010063	Hs.343603	titin-cap (teletonin)	globin,cNMP_binding,ptina	8.1
400275			NM_006513*:Homo sapiens seryl-	NA	8.0
434357	AW732284	Hs.3828	mevalonate (diphospho) decarbo	GHMP_kinases	8.0
430299	W28673	Hs.106747	serine carboxypeptidase 1 prec		8.0
413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	FKBP,TPR	8.0
402393			ENSP00000085284*:CDNA FLJ20404	RhoGEF,PH	8.0
429252	NM_004658	Hs.198312	RAS protein activator like 1 (C2,PH,RasGAP,BTK	8.0
456181	L36463	Hs.1030	ras inhibitor	RA,SH2,VPS9	7.9
431493	A1791493	Hs.129873	ESTs, novel cytochrome P450	p450	7.9
451558	NM_001089	Hs.26630	ATP-binding cassette, sub-fami	ABC_tran,SRP54	7.8
415758	BE270465	Hs.78793	protein kinase C, zeta	kinase,DAG_PE-bind,ptina	7.8
419270	NM_005232	Hs.89839	EphA1	EPH_bnd,kinase,SAM,fn3	7.8
422837	U25441	Hs.121478	dopamine receptor D3	7tm_1	7.8
401118			Target Exon	kinase	7.8

5	426440	BE382756	Hs.169902	solute carrier family 2 (facil	sugar_tr	7.8
	418635	L11329	Hs.1183	dual specificity phosphatase 2	DSPc,Rhodanese,Y_phosphat	7.8
	432747	NM_014404	Hs.278907	calcium channel, voltage-depen	PMP22_Claudin	7.8
	403672			C4001244:gl 539933 pir A61275	tubulin	7.8
	437806	A1424921	Hs.122487	ESTs, Weakly similar to A54854	RasGAP	7.7
	456890	U48213	Hs.155402	D site of albumin promoter (al	DAGKc,bZIP	7.7
	424107	AB014606	Hs.139648	kinesin family member 1C	kinesin,FHA	7.7
	452695	AW780199	Hs.30327	mitogen-activated protein kina		7.7
10	433262	A571225	Hs.284171	KIAA1535 protein	cNMP_binding,ion_trans	7.7
	424198	AB029010	Hs.143026	KIAA1087 protein	Na_Ca_Ex,Cabr-beta	7.6
	406496			Target Exon	SROR	7.6
	425423	NM_005897	Hs.157180	Intracisternal A particle-prom	BTB,Kelch	7.6
	402211			KIAA0430 gene product	ion_trans,K_tetra	7.6
15	408710	Y10256	Hs.47007	mitogen-activated protein kina	pkinase,SAM_decarbox	7.5
	457615	W56321	Hs.111460	calcium/calmodulin-dependent p	pkinase	7.5
	402760			NM_021797:Homo sapiens eosino	Glyco_hydro_18,CBM_14	7.5
	425428	AL110261	Hs.157211	DKFZP58680621 protein	C1q,Collagen	7.4
	423579	NM_004121	Hs.1675	gamma-glutamyltransferase-like	G_glu_transpept	7.4
20	413104	L42374	Hs.75199	protein phosphatase 2, regulat	B56	7.4
	419660	BE280337	Hs.194693	solute carrier family 7 (calio	aa_permeases	7.4
	424774	BE244179	Hs.153022	TATA box binding protein (TBP)		7.4
	402632			Target Exon	Fz,kringle,Ig	7.4
	444159	AF116846	Hs.10431	dead ringer (Drosophila)-like	ARID,SNF	7.4
25	405714			ENSP00000221137:Olfactory rece	7tm_1	7.3
	442732	AA257161	Hs.8658	hypothetical protein DKFZp434E	EGF,laminin_EGF,Xlink,S_m	7.3
	421758	BE397336	Hs.1422	Gardner-Rasheed feline sarcoma	SH2,SH3,pkinase	7.3
	415995	NM_004573		phospholipase C, beta 2	PI-PLC-X,PI-PLC-Y,C2	7.3
	405137			Target Exon		7.3
30	402460			C1001261:gl 2695979 emb CAA70		7.3
	431398	BE616547	Hs.2785	keratin 17	filament	7.3
	429592	AB029041	Hs.209646	KIAA1118 protein	Troponin	7.3
	429225	BE250337	Hs.198273	Target CAT		7.2
	423015	U18548	Hs.123034	G protein-coupled receptor 12		7.2
35	454373	NM_005133	Hs.288626	RCE1, pranyl protein protease	Abi	7.2
	440188	AK001812	Hs.7036	N-Acetylglucosamine kinase	ROK	7.2
	432920	U37689	Hs.3128	polymerase (RNA) II (DNA direc		7.2
	446143	BE245342	Hs.306079	sec61 homolog	secY	7.2
	422201	NM_001505	Hs.113207	G protein-coupled receptor 30	7tm_1	7.2
40	440869	NM_014297	Hs.7486	protein expressed in thyroid	lactamase_B	7.1
	435099	AC004770	Hs.4756	flap structure-specific endonu	XPG_N,XPG_L,5_3_exonuclea	7.1
	437161	AA054477	Hs.25391	ESTs		7.1
	429683	AF148213	Hs.211604	a disintegrin-like and metallo	tsp_1,Reprolysin,Pep_M12B	7.1
45	426268	AF083420	Hs.168913	serine/threonine kinase 24 (St	pkinase	7.1
	445087	AW893449	Hs.12303	suppressor of Ty (S.cerevisiae	S1,SH2,Ribosomal_L23,pkin	7.1
	416377	AA179930	Hs.293857	caspase recruitment domain pro		7.1
	421748	NM_014718	Hs.107809	KIAA0726 gene product	cadherin	7.1
	426691	NM_006201	Hs.171834	PCTAIRE protein kinase 1	pkinase	7.0
	428599	AB033078	Hs.186613	sphingosine-1-phosphate lyase	pyridoxal_deC	7.0
50	411898	BE409714	Hs.44856	hypothetical protein FLJ12116		7.0
	427010	AW138332		muscle RAS oncogene homolog	ras	7.0
	457305	BE268048	Hs.236494	RAB10, member RAS oncogene fam	ras,arf	7.0
	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD4	integrin_A,FG-GAP,Rhadd_g	7.0
55	457764	AW028284	Hs.4815	nuclx (nucleoside diphosphata	NUDX	6.9
	435575	AF213457	Hs.44234	triggering receptor expressed	Ig	6.9
	456488	AW015098	Hs.301946	ESTs, Weakly similar to T30857		6.9
	428761	AF236119	Hs.193076	GRB2-related adaptor protein 2	SH2,SH3	6.9
	430396	D49742	Hs.241363	hyaluronan-binding protein 2	trypsin,kringle,EGF	6.9
60	422066	AW249275	Hs.343521	malate dehydrogenase 2, NAD (m	klh,lth_C,adh_short,Semla	6.9
	445937	AI452943	Hs.321231	UDP-GalbetaGlcNAc beta 1,4- g	Galactosyl_T_2	6.9
	457499	AA953015	Hs.274370	hypothetical protein FLJ20260	PH	6.8
	400845			NM_003105:Homo sapiens sortil	ldl_recept_a,fn3,ldl_rece	6.8
	416931	D45371	Hs.80485	adipose most abundant gene tra	C1q,Collagen	6.8
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistan	dynamln_Z,dynamln,GED	6.8
65	432990	AL036071	Hs.279899	tumor necrosis factor receptor	TNFR_c6	6.8
	458128	W32474	Hs.301746	RAP2A, member of RAS oncogene	ras,ar ldh	6.8
	429542	AF038660	Hs.206713	UDP-GalbetaGlcNAc beta 1,4- g	Galactosyl_T_2,Ig	6.8
	401488			Target Exon	Glyco_hydro_1	6.7
	456243	AI345001	Hs.82380	menage a trois 1 (CAK assembly	zf-C3HC4	6.7
70	424321	W74048	Hs.1765	lymphocyte-specific protein ty	SH2,SH3,pkinase	6.7
	405187			NM_014272:Homo sapiens a disin	Reprolysin,tsp_1,Pep_M12B	6.7
	413055	AV655701	Hs.75183	cytochrome P450, subfamily IIE	p450	6.7
	448496	BE379077	Hs.130849	ESTs, Weakly similar to I38022	NADHdh_2	6.7
	419667	AU077005	Hs.92208	a disintegrin and metalloprote	disintegrin,Reprolysin,Pe	6.7
75	417103	Z33905	Hs.81218	hypothetical protein MGC3597	TPR_zf-C3HC4,PHD	6.7
	407687	AK002011	Hs.37558	hypothetical protein FLJ11149	FAD_Synth	6.7
	456469	NM_005109	Hs.95220	oxidative-stress responsive 1	zf-C2H2,pkinase	6.7
	449546	W86248	Hs.58819	ESTs	hexokinase	6.6
	428926	NM_001702	Hs.194654	brain-specific angiogenesis in	7tm_2,sp_1,GPS,HRM	6.6
80	404953			C1002000:gl 12735712 ref XP_0		6.6
	449401	AL135401	Hs.23557	serologically defined colon ca	pro_isomerase	6.6
	429962	M69113	Hs.226795	glutathione S-transferase pi	GST_C,GST_N	6.6
	421547	AA489908	Hs.1399	proteasome (prosome, macropain	Cathrin_Ig_ch,proteasome	6.6
	430035	NM_003463	Hs.227777	protein tyrosine phosphatase I	Y_phosphatase,DSPc	6.6
	406867	AA157857	Hs.182265	keratin 19	filament,bZIP	6.6

	404946		Target Exon	3Beta_HSD	6.5
	435213	AA092510	non-kinase Cdc42 effector prot		6.5
	411201	T74588	ESTs, Weakly similar to C3HU c	A2M_N,A2M	6.5
5	415344	U94905	diacylglycerol kinase, zeta (1	ank,DAGKa,DAGKc,DAG_PE-b	6.5
	426194	T50872	thromboxane A synthase 1 (plat	p450	6.5
	424681	AA054400	KIAA0134 gene product	helicase_C,PRK	6.5
	417903	NM_002342	lymphotoxin beta receptor (TNF	TNFR_c6	6.5
	408905	AV655783	Target CAT		6.5
10	438646	AI973076	matrix metalloproteinase 28		6.5
	431530	XG1615	leukemia inhibitory factor rec	fn3	6.5
	428883	AA436959	ATPase, (Na)/K transporting, b	Na_K-ATPase	6.5
	404757		Target Exon		6.4
	406370		Interleukin 11	trypsin	6.4
15	443611	NM_014397	NIMA (never in mitosis gene a)	pkinase	6.4
	424008	R02740	putative chemokine receptor; G	7tm_1	6.4
	444912	AW247380	putative prostate cancer suscep	lactamase_B	6.4
	454460	XG6945	fibroblast growth factor recep	lg,pkinase	6.4
	432269	NM_002447	macrophage stimulating 1 recep	pkinase,Sema,PSI,TIG,AA_E	6.4
20	458718	AI359478	ESTs		6.4
	405282		Target Exon	Cache	6.4
	447245	AK001713	hypothetical protein FLJ10851	E1_dehydrog	6.3
	442297	NM_006202	phosphodiesterase 4A, cAMP-spe	PDEase	6.3
	400894		C11000129:g 9938014 ref NP_06	7tm_1	6.3
25	440446	NM_013385	pleckstrin homology, Sec7 and	PH,Sec7	6.3
	430866	L36149	chemokine (C motif) XC recepto	7tm_1	6.3
	451394	NM_003595	tyrosylprotein sulfotransferase	Sulfotransfer	6.3
	436523	BE612990	single-strand selective monofu		6.3
	422714	AB018335	KIAA0792 gene product	DUF221	6.3
30	408924	AW295608	homeodomain-interacting protei		6.3
	414551	AB15539	enoyl Coenzyme A hydratase, sh	ECH,Peptidase_U7	6.3
	413254	U40272	isocitrate dehydrogenase 3 (NA	isodh	6.3
	415010	NM_004203	membrane-associated tyrosine-	pkinase	6.3
	449761	AB009698	solute carrier family 22 (orga	sugar_tr	6.3
35	432221	M21191	aldolase A, fructose-bisphosph	glycolytic_enz,Adeno_E3	6.3
	414513	AW239400	G protein-coupled receptor kin	pkinase,RGS,pkinase_C	6.2
	458516	BE010749	ESTs		6.2
	417985	AA187545	crystallin, zeta (quinone redu	adh_zinc	6.2
	447507	H59696	POP7 (processing of precursor,		6.2
40	418322	AA284166	cyclin-dependent kinase inhibi	Y_phosphatase,DSPc	6.2
	428443	BE618106	CDC10 (cell division cycle 10,	GTP_CDC,M	6.2
	432329	AC003965	protease, serine, 26	trypsin	6.2
	408903	BE244377	farnesyl-diphosphate farnesyl	SQS_PSY,dsm,z-alpha	6.2
	426176	AB000462	SH3-domain binding protein 2	PH,SH2	6.1
45	421395	D90084	pyruvate dehydrogenase (lipoam	E1_dehydrog	6.1
	430517	S80071	solute carrier family 6 (neuro	SNF	6.1
	435906	AI686379	SAR1 protein	arf,ras	6.1
	402758		C1001899:g 12722636 ref XP_0	Glyco_hydro_18	6.1
	434202	BE382411	guanylate kinase 1	Guanylate_kin,CoaE,Viral_	6.1
50	402115		NM_021624:Homo sapiens histam	7tm_1	6.1
	407601	AC002300	sodium channel, nonvoltage-gat	ASC	6.1
	404679		Target Exon		6.0
	450739	AI732707	ESTs, Weakly similar to ALU7_H	V1R	6.0
	439888	AB040949	pancreas-enriched phospholipid	C2,PI-PLC-Y,PI-PLC-X,RasG	6.0
55	415742	BE410243	thimet oligopeptidase 1	Peptidase_M3	6.0
	453190	AB002354	KIAA0356 gene product	PH,PHD,RUN	6.0
	439975	AW328081	inosine triphosphatase (nucleo	Ham1p_ljke	6.0
	412800	AW950852	polymerase (DNA directed), del	homeobox	6.0
	432805	X94630	CD97 antigen	7tm_2,GPS,EGF	6.0
60	418964	T74640	gbvyc57c12.r1 Stratagene liver	A2M_N,A2M	6.0
	417483	BE549343	acyl-Coenzyme A dehydrogenase,	Acyl-CoA_dh,Acyl-CoA_dh_M	6.0
	419755	H18444	BAI1-associated protein 3	C2	6.0
	457276	AF235097	Homo sapiens chromosome X map		6.0
	423908	AJ006422	centaurin-alpha	PH,AriGap	6.0
65	432118	N98718	gbvyc65g02.r1 Soares_multiple		5.9
	427334	R44789	Homo sapiens, Similar to trans		5.9
	424959	NM_005781	activated p21cdc42Hs kinase	pkinase,SH3	5.9
	453082	H18835	hypothetical protein FLJ20041	ion_trans	5.9
	421168	AF182277	cytochrome P450, subfamily IIB	p450	5.9
70	422287	F16365	cytochrome c oxidase subunit V	COX7a,Phage_G	5.9
	401736		C16000492:g 3127193 gb AAD05	AMP-binding	5.9
	434755	AA648502	ESTs		5.9
	414962	AF273304	XPMC2 protein	Exonuclease	5.8
	407338	AA773213	gb:ab66f10.s1 Stratagene lung	lg	5.8
75	448426	BE018315	tankyrase, TRF1-interacting an		5.8
	409686	AK000002	Homo sapiens mRNA; cDNA DKFZp4	ABC_tran	5.8
	450778	U81375	solute carrier family 29 (nucl	Nucleoside_tran	5.8
	423612	NM_002067	guanine nucleotide binding pro	G-alpha,arf	5.8
	430845	AF024690	G protein-coupled receptor 43	7tm_1	5.8
80	424741	AF051941	nucleoside diphosphate kinase	NDK	5.8
	412958	BE391579	Fas-activated serine/threonine		5.8
	415701	NM_003878	gamma-glutamyl hydrolase (conj	GATase	5.8
	423158	H97991	Target CAT	MoaA_NiB_PqqE	5.8
	414788	X78342	cyclin-dependent kinase (CDC2-	pkinase	5.8
	412915	AW087727	NM_004541:Homo sapiens NADH de		5.7

5	420904	AL035964	Hs.100221	nuclear receptor subfamily 1,	hormone_rec,zf-C4	5.7
	415503	U36601	Hs.78473	N-deacetylase/N-sulfotransfera	Sulfotransfer	5.7
	433074	AL045019	Hs.323462	Homo sapiens cDNA FLJ11214 fis	DEAD,helicase_C,dsmr,Vira	5.7
	409124	AW292809	Hs.50727	N-acetylglucosaminidase, alpha		5.7
	428270	BE501549	Hs.107040	ESTs		5.7
	435114	AA775483	Hs.288936	mitochondrial ribosomal protei	ODC_AZ	5.7
	425211	M18667	Hs.1867	progastricin (pepsinogen C)	asp	5.7
	453054	AJ878908	Hs.31547	Target CAT		5.7
10	420730	NM_002691	Hs.99890	polymerase (DNA directed), del	ICL	5.7
	415117	AF120499	Hs.78016	polynucleotide kinase 3'-phosp	Viral_helicase1	5.7
	400985			Target Exon		5.7
	413163	Y00815	Hs.75216	protein tyrosine phosphatase,	fn3,ig_Y_phosphatase	5.7
	413858	NM_001610	Hs.75589	acid phosphatase 2, lysosomal	acid_phosphat	5.7
15	457308	AJ416988	Hs.238272	inositol 1,4,5-triphosphate re	ion_trans,RYDR_ITPR,MIR	5.7
	400551			C10001991*gi16624920[emb]CAB8	SRCR	5.7
	433472	AJ541246	Hs.3343	phosphoglycerate dehydrogenase	2-Hacid_DH,2-Hacid_DH_C,M	5.7
	409531	BE384319	Hs.54702	xylosylprotein beta1,4-galacto	Galactosyl_T_2	5.7
	449139	BE258315	Hs.23111	phenylalanine-tRNA synthetase-	neur	5.7
	450207	T87615	Hs.14716	ESTs		5.7
20	400266			NM_002858*Homo sapiens ATP-bi	ABC_tran	5.6
	430713	AA351647	Hs.2642	eukaryotic translation elongat	GTP_EFTU,GTP_EFTU_D3,GTP_	5.6
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (TPR	5.6
	405683			Target Exon		5.6
25	449181	X96783	Hs.23179	synaptotagmin V	C2	5.6
	414457	AW514320	Hs.76159	ATPase, H transporting, lysoso	ATP-synLC	5.6
	415193	AL048891	Hs.12185	hypothetical protein MGC14333		5.6
	434883	AW381538	Hs.18807	hypothetical protein MGC12959		5.6
	433135	AA443873	Hs.110477	dolichyl-phosphate mannosyltra		5.6
30	413049	NM_002151	Hs.823	hepsin (transmembrane protease	trypsin	5.6
	420899	NM_001629	Hs.100194	arachidonate 5-lipoxygenase-ac	MAPEG	5.6
	423397	NM_001838	Hs.1652	chemokine (C-C motif) receptor	7tm_1	5.5
	443759	BE390832	Hs.134729	FXD domain-containing ion tra		5.5
	454112	NM_000885	Hs.40034	integrin, alpha 4 (antigen CD4	integrin_A,FG-GAP	5.5
35	405594			NM_021949:Homo sapiens ATPase,	E1-E2_ATPase,Hydrolase	5.5
	416322	BE019494	Hs.79217	pyrroline-5-carboxylate reduct	P5CR,Octopine_DH_N	5.5
	446755	AW451473	Hs.16134	serine/threonine kinase 10	pk kinase,TYA	5.5
	411030	BE387193	Hs.67896	7-60 protein		5.5
	431498	AK001777	Hs.258551	aspartyl aminopeptidase	Peptidase_M18	5.5
40	433012	NM_004045	Hs.279910	ATX1 (antioxidant protein 1, y	HMA	5.5
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	pk kinase,POLO_box	5.5
	424572	M19650	Hs.92909	2,3'-cyclic nucleotide 3' pho		5.5
	406617			Target Exon		5.5
	421883	X55079	Hs.1437	glucosidase, alpha; acid (Pomp	efhand,Ferric_reduct	5.5
45	419525	T79257	Hs.1259	astialglycoprotein receptor 2	trefoil,Glyco_hydro_31	5.4
	448093	AW977382	Hs.15898	2,4-dienoyl CoA reductase 2, p	lectin_c	5.4
	411574	BE242842	Hs.6780	protein tyrosine kinase 9-like	adh_short	5.4
	406432			CD1E antigen, a polypeptide	cofilin_ADF	5.4
	428921	Z43809	Hs.194638	polymerase (RNA) II (DNA direc	Sulfotransfer	5.4
50	430337	M36707	Hs.239600	calmodulin-like 3		5.4
	427182	AB011133	Hs.173864	KIAA0561 protein	efhand	5.4
	414216	D86970	Hs.75822	TGFB1-induced anti-apoptotic f	pk kinase,PDZ	5.4
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase,	oxidored_q4,myosin_head,b	5.4
	424373	AJ133798	Hs.146219	copine VII	lipoxygenase,PLAT	5.4
55	449405	AA001350		gbzh83h05.r1 Soares_fetal_liv	C2	5.4
	409983	D50922	Hs.57729	Kelch-like ECH-associated prot	mito_carr	5.4
	455818	A1733747	Hs.71174	interleukin 21 receptor	BTB,Kelch	5.4
	424357	AW861058	Hs.44856	hypothetical protein FLJ12116		5.4
	423606	AB011094	Hs.129892	KIAA0522 protein		5.4
60	423211	BE083080	Hs.274323	similar to stacyltransferase 7	PH,bZIP,IQ,Sec7	5.3
	450080	AB037831	Hs.24372	ESTs, Weakly similar to dJ207H	Glyco_transf_29	5.3
	423778	Y09267	Hs.132821	flavin containing monooxygenas	DEAD,GSPIL_E	5.3
	402338			Target Exon	FMO-like,pyr_redox	5.3
	412276	BE262621	Hs.73798	macrophage migration inhibitor	p450	5.3
65	437967	BE277414	Hs.5947	mel transforming oncogene (der	MIF	5.3
	424766	BE388855	Hs.152978	proteaseome (prosome, macropai	ras,arf	5.3
	447766	NM_016011	Hs.19513	CGI-63 protein	PA28_alpha,PA28_beta	5.3
	453660	X98507	Hs.286228	myosin IC	adh_zinc	5.3
	435327	BE301871	Hs.4867	mannosyl (alpha-1,3)-glycopro	myosin_head,IQ	5.2
70	432336	NM_002759	Hs.274382	protein kinase, Interferon-ind	HLH,Myr_N_term,Myr-LZ	5.2
	445139	AB037848	Hs.12365	synaptotagmin XIII	dsmr,pkinase	5.2
	429214	AB012722	Hs.198256	kinesin-like 3	C2	5.2
	432462	AK000013	Hs.274701	thymidine kinase 2, mitochondr	kinesin	5.2
	424387	A1739312	Hs.284163	ANKHZN protein	dNK	5.2
	405697			gb:Human homeobox-like mRNA		5.2
75	450321	Y16521	Hs.24812	CDP-diacylglycerol synthase (p	Cytidylyltrans,Adeno_VII	5.1
	412939	AW411491	Hs.75069	eukaryotic translation elongat	SHMT	5.1
	445109	AF039916	Hs.12330	ectonucleoside triphosphate di	GDA1_CD39	5.1
	419073	AW372170	Hs.183918	Homo sapiens cDNA FLJ12797 fis	lg,bsp_1,ZU5	5.1
80	409958	NM_001523	Hs.57697	hyaluronan synthase 1	Glycos_transf_2	5.1
	442599	AF078037	Hs.324051	RelA-associated inhibitor	SH3,ank	5.1
	424305	BE386095	Hs.112272	histone deacetylase 8	Hist_deacetyl	5.1
	427247	AW504221	Hs.174103	integrin, alpha L (antigen CD1	vwa,integrin_A,FG-GAP	5.1
	429061	Y14039	Hs.195175	CASP8 and FADD-like apoptosis	DED,ICE_p20	5.1
	420849	X52221	Hs.99987	excision repair cross-compleme		5.1

5	453337	R73417	Hs.25391	gbjy92g12.r1 Soares breast 2N	GSPII_III	5.1
	418910	Z25821	Hs.89466	Homo sapiens, Similar to dodec	ECH	5.1
	425771	BE561776	Hs.159494	Bruton agammaglobulinemia tyro	SH2,SH3,kinase,PH,BTK	5.1
	405202			NM_021734*:Homo sapiens deoxyn	mito_carr	5.1
	451452	BE560065	Hs.28433	dolichyl-phosphate (UDP-N-acet	Glycos_transf_4	5.0
	418231	AA326885	Hs.83848	triosephosphate isomerase 1	TIM	5.0
	425165	NM_014434	Hs.154899	Target CAT		5.0
	407876	NM_004519	Hs.40866	potassium voltage-gated channe	ion_trans,KCNQ1_channel	5.0
10	417831	H16423	Hs.82685	CD47 antigen (Rh-related antig	tg	5.0
	404716			NM_007313*:Homo sapiens v-abl	SH2,SH3,kinase	5.0
	405020			Target Exon	7tm_1	5.0
	426236	NM_004798	Hs.168212	kinesin family member 3B	kinesin	5.0
	433178	AB038269	Hs.253706	cysteinyl leukotriene CysLT2 r	7tm_1	5.0
15	422340	AW296219	Hs.115325	RAB7, member RAS oncogene faml	arf,ras	5.0
	439414	NM_001183	Hs.6551	ATPase, H transporting, lysoso		5.0
	425846	AA102174	Hs.159629	myosin IXB	myosin_head,DAG_PE-bind,I	5.0
	413599	AJ005239	Hs.75438	quinoid dihydropteridine reduc	adh_short	5.0
	424168	L29277	Hs.321677	signal transducer and activato	SH2,STAT,STAT_bind,STAT_p	5.0
20	436042	AF284422	Hs.119178	cation-chloride cotransporter-	aa_permeases	5.0
	410775	AB014460	Hs.66196	nth (E.coli endonuclease III)-	HhH-GPD	5.0
	428734	BE303044	Hs.192023	eukaryotic translation initial	WD40	5.0
	420340	NM_000734	Hs.97087	CD32 antigen, zeta polypeptide	ITAM	4.9
	433075	NM_002959		sortilin 1	BNR	4.9
25	400300	X03363		HER2 receptor tyrosine kinase	pkinase	4.9
	426811	BE259228	Hs.172609	nucleophdin 1	efhand	4.9
	401577			NM_000761:Homo sapiens cytochr	p450	4.9
	409637	AA323948	Hs.55407	Homo sapiens mRNA; cDNA DKFZp4	Collagen	4.9
	426831	BE296216	Hs.172673	S-adenosylhomocysteine hydrola	AdoHcyase	4.9
30	430904	U65402	Hs.248124	G protein-coupled receptor 31	7tm_1	4.9
	423552	AF107028	Hs.129783	sodium channel, voltage-gated,	Ig,Adeno_E3_CR2	4.9
	421487	AF027406	Hs.104865	serine/threonine kinase 23	pkinase	4.9
	402183			NM_004491*:Homo sapiens glucoc	FF	4.9
	456748	AW137749	Hs.125902	ubiquitin specific protease 2	UCH-1,UCH-2	4.9
35	424771	BE397151	Hs.153003	serine/threonine kinase 16	pkinase	4.9
	406441			Target Exon	Aa_trans	4.9
	437053	AJ077018	Hs.3235	keralin 4	filament,bZIP,Tropomyosin	4.9
	443044	N28522	Hs.8935	quinolinate phosphoribosyltran	QRPTase,QRPTase_N	4.9
	431204	F28841	Hs.250760	cytochrome c oxidase subunit V	dUTPase,COX6A,ras,ATP-syn	4.9
40	456417	L36331	Hs.91296	integrin, alpha 8	integrin_A,FG-GAP	4.8
	436735	L48489		mannosyl (beta-1,4)-glycoprot		4.8
	441455	AJ271671	Hs.7854	zincron regulated transport	Zip	4.8
	446948	BE409053	Hs.299629	peroxisomal long-chain acyl-co		4.8
	451564	AJ076698	Hs.132760	hypothetical protein MGC15729	sugar_tr,Condensation	4.8
45	403771			NM_003061:Homo sapiens slit (D	EGF,laminin_G,LRR,LRRNT,L	4.8
	403248			ESTs, Weakly similar to I78885	SLT	4.8
	410214	L29555	Hs.301698	sialyltransferase 4A (beta-gal	Glyco_transf_29	4.8
	407047	X65965		gbHLsapiens SOD-2 gene for ma	sodfe	4.8
	422668	AF199364	Hs.119120	E3 ubiquitin ligase SMURF1	C2,VWV,HECT	4.8
50	436057	AJ004832	Hs.5038	neuropathy target esterase	cNMP_binding	4.8
	431262	NM_006672	Hs.251395	solute carrier family 22 (orga	sugar_tr	4.8
	406625	Y13647	Hs.119597	stearyl-CoA desaturase (delta	FA_desaturase	4.8
	428659	U66579	Hs.188859	G protein-coupled receptor 20		4.8
	432716	AJ762964	Hs.205180	ESTs		4.8
55	414460	L00727	Hs.898	dystrophin myotonic-protein k	pkinase	4.8
	400287	S39329	Hs.181350	kallikrein 2, prostatic	trypsin	4.8
	428948	D42046	Hs.194665	DNA2 (DNA replication helicase	UvrD-helicase,Viral_helic	4.7
	420028	AB014680	Hs.8786	carbohydrate (N-acetylglucosam	Sulfoltransfer	4.7
	402912			Target Exon	pkinase	4.7
60	443329	BE262943	Hs.9234	hypothetical protein MGC1936		4.7
	426120	AA325243	Hs.166887	copine 1	C2	4.7
	430609	AA302921	Hs.247362	dimethylarginine dimethylamino		4.7
	451320	AW118072		diacylglycerol kinase, zeta (1	zf-C2H2,BAR,SH3	4.7
65	447131	NM_004585	Hs.17466	retinoic acid receptor respons		4.7
	431222	X58777	Hs.273790	zona pellucida glycoprotein 3A	zona_pellucida	4.7
	406458			C14000133*:gij1082739[pair]C44	proteasome	4.7
	427804	AL049654	Hs.180871	protein kinase C, alpha bindin	PDZ	4.7
	450748	AJ733093	Hs.247686	ESTs	7tm_1	4.7
	422937	U03270	Hs.122511	centrin, EF-hand protein, 1	efhand	4.7
70	407978	AW385129	Hs.41717	phosphodiesterase 1A, calmodul	PDEase	4.7
	428773	BE256238	Hs.193163	bridging integrator 1	SH3,BAR	4.7
	456444	AA884517	Hs.31856	ESTs, Weakly similar to KIAA14		4.7
	405574			Target Exon	pkinase	4.7
	442414	BE408758	Hs.8297	ribonuclease 6 precursor	ribonuclease_T2	4.7
75	418289	AW403103	Hs.83951	Hermansky-Pudlak syndrome		4.6
	421601	AJ660190	Hs.106070	cyclin-dependent kinase inhibi	CDI	4.6
	422795	AB033109	Hs.120866	KIAA1283 protein	kazal,A2M,A2M_N	4.6
	433019	AJ208513	Hs.279915	translocase of inner mitochond	zf-Tim10_DDP	4.6
	431522	AJ625859	Hs.258609	protein tyrosine phosphatase,	fn3,Y_phosphatase	4.6
80	400846			sortilin-related receptor, L/D	ldl_recept_a,fn3,ldl_rece	4.6
	456881	AW028302	Hs.155079	protein phosphatase 2, regulat	B56	4.6
	418172	X61157	Hs.83636	adrenergic, beta, receptor kin	pkinase,PH,RGS	4.6
	408433	AW162931	Hs.45002	ras-related C3 botulinum toxin	ras	4.6
	439921	AL110209	Hs.6770	LCAT-like lysophospholipase	LACT	4.6
	427122	AW057738	Hs.323910	HER2 receptor tyrosine kinase	pkinase,Furin-like,Recep_	4.6

5	427945	AW137156	Hs.181202	hypothetical protein FLJ10038	Collagen	4.6
	451777	U09210	Hs.459	solute carrier family 18 (vesl)	sugar_tr	4.6
	429938	BE296804	Hs.226377	phosphate cytidylyltransferase	Cytidylyltransf,COX5C	4.6
	412974	R18978	Hs.75105	emopamil-binding protein (ster		4.6
	414702	L22005	Hs.76932	cell division cycle 34	UQ_con	4.6
	425795	AJ000479	Hs.159543	endothelial differentiation, G	7tm_1	4.6
	422454	U49070	Hs.161362	protein (peptidyl-prolyl cis/t	Rotamase,WW	4.6
10	408135	AA317248	Hs.42957	methyltransferase-like 1	Methyltransf_4	4.6
	457388	AF035300	Hs.264157	cadherin-like 22	cadherin,Cadherin_C_term	4.6
	421140	AA288741	Hs.102135	signal sequence receptor, delt	Herpes_UL3	4.6
	434834	AF156774	Hs.324020	1-acylglycerol-3-phosphate O-a	Acyltransferase	4.6
	413407	AJ356293	Hs.75339	inositol polyphosphate phospho	SH2,SAM	4.6
	402463			NM_014624:Homo sapiens S100 ca	efhand,S_100	4.5
15	417891	W79410	Hs.82887	protein phosphatase 1, regulat		4.5
	421681	AA384922	Hs.195175	CASP8 and FADD-like apoptosis	ICE_p20,DED	4.5
	426516	BE262660	Hs.170197	glutamic-oxaloacetic transamin	aminotran_1_2	4.5
	418963	BE304571	Hs.89529	aldo-keto reductase family 1,	aldo_ket_red	4.5
	423664	NM_004714	Hs.130988	dual-specificity tyrosine-(Y)-	pkinase	4.5
20	427681	AB018263	Hs.180338	tumor necrosis factor receptor	TNFR_c6,death,PH,Xlink,Rh	4.5
	432893	NM_016154	Hs.279771	Homo sapiens clone PP1596 unkn	ras,arf	4.5
	413815	AL046341	Hs.75562	discoidin domain receptor fami	F5_F8_type_C,pkinase	4.5
	405546			NM_018833*:Homo sapiens transp	ABC_membrane,ABC_tran	4.5
	416297	AA157634	Hs.79172	solute carrier family 25 (mito	mito_carr	4.5
25	421962	D82061	Hs.288354	FabG (beta-ketoacyl-acyl-car	adh_short	4.5
	415341	R00602		gb:ye74c04.r1 Soares fetal liv	pkinase	4.5
	456668	W81526	Hs.118329	ESTs, Moderately similar to GA	Neur_chan_LBD,Neur_chan_m	4.5
	456652	AW327546	Hs.111024	solute carrier family 25 (mito	mito_carr	4.5
30	407863	AA317089	Hs.597	glutamic-oxaloacetic transamin	aminotran_1_2	4.5
	435891	AW249394	Hs.5002	copper chaperone for superoxid	sodcu,HMA	4.5
	453997	AW247615	Hs.37003	v-Ha-ras Harvey rat sarcoma vi	ras	4.5
	449029	N28989	Hs.22891	solute carrier family 7 (catio	aa_permeases	4.5
	424829	NM_002507	Hs.1827	nerve growth factor receptor (death,TNFR_c6	4.5
35	429362	T25833	Hs.200478	ubiquitin-conjugating enzyme E	UQ_con	4.5
	429133	N31854	Hs.197116	solute carrier family 7 (catio	aa_permeases	4.5
	426079	D31220	Hs.166168	peter pan (Drosophila) homolog	7tm_1	4.4
	414814	D14697	Hs.77393	farnesyl diphosphate synthase	polyprenyl_syn1	4.4
	433261	AB040967	Hs.112034	KIAA1534 protein	PH,Oxysterol_BP	4.4
	402915			ENSP00000202587*:Bicarbonate t	HCO3_cotransp	4.4
40	418267	BE389537	Hs.83919	glucosidase I	Glyco_hydro_63	4.4
	430716	BE387257	Hs.247831	Homo sapiens, Similar to myosi	efhand	4.4
	420874	X66357	Hs.336478	cyclin-dependent kinase 3	pkinase	4.4
	439902	AF174499	Hs.6764	histone deacetylase 6	Hist_deacetyl,zf-UBP	4.4
	400223			Eos Control	Skp1	4.4
45	450611	NM_004405	Hs.419	distal-less homeo box 2	homeobox	4.4
	412965	L06419	Hs.75093	procollagen-lysine, 2-oxogluta	2OG-Fell_Oxy	4.4
	435564	AF210652	Hs.16614	5(3)-deoxyribonucleotidase (dN		4.4
	416121	X92762	Hs.79021	tafazzin (cardiomyopathy, dila	Acyltransferase	4.4
50	423323	AJ951628	Hs.127007	potassium channel, subfamily K	ion_trans	4.4
	448191	NM_005881	Hs.20644	branched chain alpha-ketoacid	HATPase_c	4.4
	456217	BE253181	Hs.81687	non-metastatic cells 3, protel	NDK,Arterl_glycop	4.4
	436415	BE265254	Hs.343258	proliferation-associated 2G4,	Peptidase_M24	4.4
	429218	AA225065	Hs.198269	Target CAT		4.4
	407433	AF209923		gh:Homo sapiens orphan G-prote	7tm_3	4.4
55	425955	T96509	Hs.248549	ESTs, Moderately similar to S6		4.4
	407230	AA157857	Hs.182265	keratin 19	filament,bZIP	4.3
	410197	NM_005518	Hs.59889	3-hydroxy-3-methylglutaryl-Co	HMG_CoA_synt	4.3
	416409	R61573	Hs.79300	ubiquitin-conjugating enzyme E	UQ_con	4.3
60	447957	NM_014821	Hs.20126	KIAA0317 gene product	Filamin,HECT	4.3
	421771	NM_001224	Hs.108131	caspase 2, apoptosis-related c	ICE_p20,CARD,ICE_p10	4.3
	448886	AL137291	Hs.22451	hypothetical protein FLJ10357	PH,RhoGEF	4.3
	414821	M63835	Hs.77424	Fc fragment of IgG, high affin	Ig	4.3
	431096	AA324358	Hs.249227	Homo sapiens DNA, cosmid clone		4.3
	429692	NM_003803	Hs.2504	myomesin 1 (skelemin) (185kD)	Ig,fn3	4.3
65	450126	BE018138	Hs.24447	sigma receptor (SR31747 bindin		4.3
	413781	J05272	Hs.850	IMP (inosine monophosphate) de	IMPDH_C,IMPDH_N,CBS,NPD	4.3
	406530			NM_005546*:Homo sapiens IL2-in	SH2,SH3,pkinase,PH,BTK	4.3
	428363	AK000284	Hs.183860	hypothetical protein FLJ20277	GNT4	4.3
70	413954	AL037111	Hs.75641	galactose-1-phosphate uridylyl	GalP_UDP_transf,GalP_UDP_	4.3
	432179	X75208	Hs.2913	EphB3	EPH_bdf,fn3,pkinase,SAM	4.3
	456529	AF014643	Hs.100072	connexin46.6	connexin	4.3
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA)	Neur_chan_LBD,Neur_chan_m	4.3
	426626	AJ124572	Hs.323879	Inhibitor of kappa light polyp	zf-C2H2	4.3
	432956	AL037895	Hs.279861	CGI-31 protein	thiorel	4.3
75	428970	BE276891	Hs.194691	retinoic acid induced 3	7tm_3	4.3
	428953	AA306610	Hs.348183	tumor necrosis factor receptor	TNFR_c6	4.2
	423922	AK001663	Hs.135458	muscle-specific beta 1 integr		4.2
	426513	U96132	Hs.171280	hydroxyacyl-Coenzyme A dehydro	adh_short	4.2
	426566	AF131836	Hs.170453	tropomodulin	Tropomodulin,pkinase	4.2
80	425179	AJ224442	Hs.155020	putative methyltransferase		4.2
	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)		4.2
	459298	R86701		gb:ym85d09.r1 Soares adult bra		4.2
	404879			NM_030807:Homo sapiens glucose		4.2
	400836			Target Exon	Apolipoprotein	4.2
	430940	ZZ5470	Hs.248145	melanocortin 5 receptor		4.2

400563			Target Exon	Pep_M12B_propep	4.2
430237	A1272144	Hs.236522	DKFZP434P106 protein	abhydrolase	4.2
425175	AF020202	Hs.155001	UNC13 (C. elegans)-like	DAG_PE-blind,C2	4.2
409067	BE260459	Hs.50267	putative GTP-binding protein s	ras	4.2
419982	AA252544	Hs.55610	solute carrier family 30 (zinc		4.2
428394	AU076472	Hs.184141	glutaryl-Coenzyme A dehydrogen	Acyl-CoA_dh,Acyl-CoA_dh_M	4.2
437698	Z83844	Hs.5790	hypothetical protein dJ37E16.5	Hydrolase	4.2
454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 famil	aldehyd	4.2
410237	A1750589	Hs.61258	argininosuccinate lyase	lyase_1	4.1
451478	NM_012331	Hs.26458	methionine sulfoxide reductase	PMSR	4.1
415410	AF037332	Hs.278569	sorting nexin 17	PX,fn3,kinase,SAM,EPH_b	4.1
406538			Target Exon	trypsin	4.1
424349	AF141289	Hs.145550	solute carrier family 7 (catio	sa_permeases	4.1
441164	AB023180	Hs.7724	KIAA0963 protein	helicase_C	4.1
421318	U63973	Hs.103501	rhodopsin kinase	kinase,kinase_C,RGS	4.1
439340	AB032436	Hs.6535	brain-specific Na-dependant in	sugar_tr,BT1	4.1
417447	N73703	Hs.293267	ESTs	Glyco_hydro_31	4.1
409693	AA010233	Hs.55921	glutamyL-prolyL-tRNA synthetas	WHEP-TRS,GST_C,HGTP_antic	4.1
403655			NM_003071:Homo sapiens SWI/SNF	SNF2_N,helicase_C,zf-C3HC	4.1
411142	NM_014256	Hs.69009	transmembrane protein 3	Galactosyl_T	4.1
437016	AU076916	Hs.5398	guanine monophosphate synthetas	GMP_synth_C,GATase	4.1
422699	BE410590	Hs.119257	ems1 sequence (mammary tumor a	SH3,HS1_rep	4.1
427202	BE272922	Hs.173936	interleukin 10 receptor, beta	Tissue_fac	4.1
421380	D31833	Hs.1372	arginine vasopressin receptor	7tm_1	4.1
434142	U47827	Hs.3759	ubiquitin specific protease 5	zf-UBP,UCH-2,UBA,UCH-1	4.1
427407	BE268649	Hs.177766	ADP-ribosyltransferase (NAD; p	BRCT,PARP,zf-PARP,PARP_re	4.1
413749	A1929320	Hs.75516	tyrosine kinase 2	kinase	4.1
411927	BE274009	Hs.772	glycogen synthase 1 (muscle)	Glycos_transf_1	4.1
419726	U50330	Hs.1274	bone morphogenetic protein 1	EGF,CUB,Asiactin	4.1
423814	AF105020	Hs.132989	putative protein O-mannosyltra	PMT,MIR	4.1
451355	NM_004197	Hs.444	serine/threonine kinase 19		4.1
422556	NM_006245	Hs.118244	protein phosphatase 2, regulat	B56	4.1
428284	AA535762	Hs.183435	NM_004545:Homo sapiens NADH de		4.1
431968	AF117222	Hs.272261	UDP-Gal4betaGlcNAc beta 1,3-ga	Galactosyl_T	4.0
443639	BE269042	Hs.9661	proteasome (prosome, macropain	proteasome	4.0
410039	AF207989	Hs.58014	Homo sapiens, Similar to G pro	7tm_3	4.0
431066	AF026273	Hs.249175	interleukin-1 receptor-associa	kinase,death	4.0
452715	Z21093	Hs.30352	ribosomal protein S6 kinase, 5	kinase	4.0
403692			NM_007037:Homo sapiens a disl	Reprolysin,tsp_1,Pep_M12B	4.0
442549	A1751601	Hs.8375	TNF receptor-associated factor	zf-C3HC4,MATH,zf-TRAF	4.0
427239	BE270447		ubiquitin carrier protein	UQ_con	4.0
451125	AA015779	Hs.226923	ESTs	Y_phosphatase	4.0
425081	X74794	Hs.154443	minichromosome maintenance def	MCM	4.0
402171			Target Exon	C2	4.0
402665			Target Exon		4.0
420148	U34227	Hs.95361	myosin VIIA (Usher syndrome 1B	myosin_head,IQ,MyTH4,SH3,	4.0
412187	U68487	Hs.73739	5-hydroxytryptamine (serotonin	7tm_1	4.0
412656	AF006011	Hs.74375	dishevelled 1 (homologous to D	PDZ,DEP,DIX,Dishevelled	4.0
425786	U35234	Hs.159534	protein tyrosine phosphatase,	fn3,Ig_Y_phosphatase,DSFc	4.0
424288	AW137198	Hs.278682	Phosphatidylglycerophosphate S		4.0
452230	AW135360	Hs.224170	ESTs	kinase	4.0
408449	NM_004408	Hs.166181	dynamin 1	PH,GED,dynamin,dynamin_2	4.0
423883	AF250238	Hs.134514	ATP-binding cassette, sub-fam1	ABC_tran,pholoRC,SRP54,Ca	4.0
422676	D28481	Hs.1570	histamine receptor H1	7tm_1	4.0
458639	BE247683	Hs.14811	dual specificity phosphatase 1	DSPc	4.0
400726			C13000717-gil129376[sp]P26196	DEAD,helicase_C	4.0
405370			NM_005569:Homo sapiens LIM do	kinase,LIM,PDZ	4.0
413654	AA331881	Hs.75454	peroxiredoxin 3	AhpC-TSA	4.0
423917	NM_014125	Hs.241517	PRO0327 protein		4.0
448362	AA641767	Hs.21015	hypothetical protein DKFZp564L	sugar_tr	4.0
424512	X53002	Hs.149846	Integrin, beta 5	Integrin_B,EGF	4.0

TABLE 22B:

Pkey: Unique Eos probaset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey	CAT Number	Accession
410191	11824_1	A1609645 A1818201 AA948024 A1278970 AA688086 AA858279 F21973 W95840 AW969644 X99726 AA431579 AA970887 A1885085 A1767835 BE566516 AA725824 A1000871 AW242322 AW007204 W68289 AA431450 AW466973 BE222544 AA483454 A1968050 W95975 A1381017 AA775726 A1040976 AA89
415341	1534442_1	R00602 Z42921 F06132
415995	1564_1	NM_004573 M95678 BE242666 AW504110 AW408049 AW402206 AA774879 AW630959 A1439623 A1933994 AW751282 AW374413 AA578823 H18054 AA310466 F12578 T74300 AA353176 AW950138 AW950600 AA912021 A1524064 AW183098 A1416986 AW769231 A1767111 AA293723 AA22290 AA465038 A
418964	1809680_1	T74640 T74649
424339	23827_1	BE257148 BE312111 AF219137 NM_015720 BE313658 BE382652 BE252205 BE251553 F12128 T66208 BE255806 BE254484 AA324163 H07952 AL134164 A1867802 A1204971 A1282924 AW192547 A1652760 A1266471 A1083778
427010	27436_1	AW138332 AW207450 AW138931 AW136963 NM_012219 AF043938 AA931386 A1084600 AA975999 BE551105 AA450260 A1080368 AA324154 AF022080 BE009901 A118847 W44458 A1765270 AA453121 A1148638 A1373696 AA324153 BE174809 AA350765
427239	27647_1	BE270447 AW409921 BE207288 BE207170 D56355 BE263223 BE408171 BE262243 BE392439 BE292738 BE261776 BE314300 BE267719 BE268715 BE513876 BE295291 BE297066 AA210923 BE407519 H51344 BE622905 AW248281 AW250313 T19021 AA355115 AA316879 BE269633 BE621936 AA290724
427328	277229_1	A1287878 A1804160 AA400787

428542 29266_1 D79989 NM_014770 U81031 AA352392 AA984512 H38328 AL120358 AL134787 AL134589 AI637763 AI671506 AA526909 AI651627 AW243560
AA939069

428948 29737_1 BE514362 AI879343 BE272870 BE616390 AW163444 AW161588 AW378754 AW238803 BE267205 BE047746 BE207213 BE312782 BE266301
BE266413 BE278348 BE280885 BE278833 BE281417 BE407788 BE378176 BE392818 AW377597 BE395951 BE393978 AW327483 BE394175
BE385795 BE275663 BE3

432118 341702_-1 N98718

432499 34857_1 BE276633 NM_016577 AF166492 BE276152 AF091031 AA908607 U66623 AI570393 AA682567 AW593957 AI148105 AW002431 AI637463
AI767195 AA339439 R13005 R23431 AW961068 AA233819 AA224118 R19818 AI890314 Z46184

433075 35820_1 NM_002959 X98248 AA233278 AAB46376 AI470560 AI470533 BE327147 AW291971 AA017125 AI198417 AI365213 AI168442 AI337018
AI475049 H85459 AA969895 AAB88000 AA418326 AA418378 N71981 AL043634 AA426361 AA418275 AA232975 AL036861 BE277220 BE387505
N99710 AW375004 A

433494 3679_1 AB029396 T04934 R21715 R19005 H11563 H14256 R46605 Z40857 BE218899 AI457785 BE550988 AI693847 AA961017 H40944 M78617
H38447 N80090 BE549719 BE550952 AW005546 AI332686 AI928848 N49234 R44075 AI694943 AI858538 AI290722 BE550759 R43116 H40212
H40089 AA018091

434755 392764_1 AA648502 AAB14365 AW976711 AA746117

436735 425_1 L48489 AL022312 D13789 AI761974 AW173260 AW271715 AAB37437 AI075278 AI357012 AI953032 AI571173 H44868 AA743691 H47026
AA837368 AAB29826 AA713585 AW502618 AW500856 AW501353 AW499765 AA339125 H19141 H29645 R18883 AW450375 AA326081
AW406015 BE263659 NS2684 A

440242 489536_1 AW295871 AI005144 AA909877 T52634 AI239684 AAB75959 BE171353 AI767633 AW510907 AI742007

449405 80651_1 AA001350 AA203114 H83070 R00660

450739 844917_1 AI732707 AI742120

451320 86576_1 AW118072 AI631982 T15734 AA224195 AI701458 W20198 F26326 AA890570 N90552 AW071907 AI671352 AI375892 T03517 R88265 AI124088
AA224388 AI084316 AI354686 T33652 AI140719 AI720211 T03490 AI372637 T15415 AW205836 AA630384 T03515 T33230 AA017131 AA443303
T33623

459298 983107_1 R86701 R84600 AL157655_

TABLE 22C:

Key: Unique number corresponding to an Eos probe set

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495

Strand: Indicates DNA strand from which exons were predicted

NL_position: Indicates nucleotide positions of predicted exons

Key	Ref	Strand	NL_position
400471	9931670	Minus	105629-105760
400518	9796703	Plus	37240-37774
400551	9801071	Minus	40629-40934
400563	9844011	Plus	81941-82434
400565	9863505	Minus	93178-93429
400728	8118950	Plus	51524-51786
400748	8119063	Plus	84237-84398
400772	8131629	Minus	34896-35021,41078-41197
400833	8705148	Minus	187599-188138
400836	8954179	Plus	677-1188
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,10634-10789,15254-15403,23827-23958
400845	9188605	Plus	34428-34612
400846	9188605	Plus	39310-39474
400894	9958307	Minus	84607-85554
400933	7651935	Minus	105330-105503
400985	8085497	Minus	5856-6006,6236-6402
401118	9966714	Minus	111939-112126
401134	7210005	Plus	51210-51406
401180	9438648	Minus	150981-152128
401215	9858408	Plus	103739-103919
401281	9800073	Minus	13622-15130
401454	9186923	Minus	114659-114832
401488	7341775	Plus	54523-54686,55364-55451,55737-55846,58047-58175,58261-58356
401507	7534110	Plus	71055-71259
401510	7622346	Minus	46835-47128
401542	8072607	Minus	87695-87840
401577	9280797	Minus	139377-139674,141195-141281,142217-142340
401736	3219338	Plus	1771-1894
401885	8140731	Plus	148234-148321,150365-150559
401935	3808091	Plus	46329-46473
401960	3249127	Minus	87589-88081
402053	8083229	Plus	62703-63179
402115	8547592	Minus	101750-102018
402171	8575908	Minus	79357-79514,83258-83476
402183	7658390	Minus	100618-104298
402191	8576073	Minus	69410-69583
402207	8576119	Plus	41683-41851
402209	8576119	Minus	53315-53472
402211	7689783	Minus	67414-68229
402338	6957691	Minus	36915-37250
402393	9929688	Plus	19813-20084,20163-20263
402453	7534025	Plus	41-631
402460	9796884	Minus	108901-109254,110246-110581,113613-113960
402463	9796896	Minus	8818-8952
402478	9797301	Minus	106204-106535
402497	9797775	Plus	98984-99452
402632	9931268	Plus	101166-101419
402651	7960391	Plus	174215-174380
402665	8077033	Minus	11824-12090,14290-14544
402758	9213869	Plus	87638-87924

5	402760	9213869	Plus	136829-136952,137336-137521
	402823	8217451	Plus	57916-58170,58475-58759,58580-59867
	402912	7263904	Plus	145965-146257,150876-151368
	402915	7406502	Minus	140-276
	402916	7406502	Minus	361-474,541-687
	403213	7630897	Minus	162572-162739,164442-164540
	403248	7656833	Minus	167439-167606
	403268	7230852	Minus	73632-73962
10	403379	9438244	Minus	117348-117560
	403655	8736093	Plus	65668-65859
	403672	7283286	Minus	96600-96881,96951-97280,97393-97594
	403692	7387384	Minus	93803-93938
	403771	7770492	Plus	112901-113045
15	403949	7711872	Minus	1731-1941
	404189	6010176	Minus	1669-2740
	404527	8152087	Plus	127737-127796,128080-128210,129888-130054,132545-132869
	404528	8152087	Plus	135325-135486
	404596	9958262	Minus	104807-105043
20	404676	9797204	Minus	56167-56342,58066-58189,58891-59048,60452-60628
	404679	9797204	Plus	125964-126092,126691-127011,127774-127893
	404716	9838068	Minus	123145-123417
	404757	7706327	Plus	100933-101083,101580-101782
	404879	5103013	Plus	78346-78473,78693-78893
25	404946	7382189	Plus	134445-134750
	404953	7387324	Plus	16588-17031
	404968	6899755	Plus	39287-39606
	405020	7137674	Plus	106606-107309
	405137	8570507	Plus	158969-159423
30	405187	7229826	Plus	117025-117170,118567-118736
	405202	7230116	Plus	40209-40429
	405282	3810573	Minus	10482-10689
	405370	2078469	Minus	38980-39111
	405371	2078469	Minus	47657-47766,48461-48596
35	405473	8439781	Plus	153074-153343,154501-154598,156879-156999,158863-159051,159910-160053,161109-161229,163035-163131,165163-165259,165868-166003,167375-167552,169252-169364,171127-171281
	405474	8439781	Plus	172005-172175
	405546	1054740	Plus	124010-124183
	405574	3820491	Minus	33200-33646
40	405594	6960456	Plus	161628-161734,162823-163014,164439-164652
	405683	4508157	Minus	21701-21844
	405697	4309923	Minus	56765-57010,57696-58016
	405714	4156179	Minus	42789-43553
	406128	9159110	Plus	50425-50876
45	406370	9256130	Plus	125320-125482
	406432	9256504	Plus	3804-3930,4026-4120,4929-5109
	406441	9280715	Plus	26200-26458
	406458	9756020	Plus	145874-146911
	406495	7711328	Minus	174661-174978
50	406496	7711328	Minus	178947-179264,181779-182087
	406530	7711474	Minus	11703-11860,14711-14829,14920-14984,16232-16448,16916-17087
	406538	7711478	Plus	35196-35367,38229-38476,40080-40216,43522-43840
	406591	8224230	Minus	2117-2257,2436-2540
	406617	8439858	Plus	36430-36552

Table 23A lists about 779 genes up-regulated in ovarian cancer compared to non-malignant adult ovaries. These were selected as for Table 20A, except that the ratio of "average" ovarian cancer to "average" normal ovaries was greater than or equal to 4.0, the "average" ovarian cancer level was set to the 93rd percentile value amongst various ovarian cancer specimens, the "average" normal adult tissue level was set to the 93rd percentile value amongst various non-malignant adult ovaries, the "average" ovarian cancer value was greater than or equal to 200 units.

TABLE 23A:

Key: Unique Eos probeset identifier number

Ex. Accn: Exemplar Accession number, Genbank accession number

UG ID: UniGene number

Title: UniGene gene title

Protein Dom.: Predicted protein domain

R1: Ratio of tumor to normal ovaries

Key	Ex. Accn	UG ID	Title	Protein Dom.	R1
421296	NM_002666	Hs.103253	perilipin	perilipin,SS	37.8
437897	AA770561	Hs.146170	hypothetical protein FLJ22969	SS,TM,zf-DHHC	29.2
453028	AB006532	Hs.31442	RecQ protein-like 4	DEAD,helicase_C,Fork_head	27.6
441021	AW578716	Hs.7644	H1 histone family, member 2		27.2
422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS	SS,TM,pkinase_in3,lg	26.5
454017	AW023617	Hs.347130	hypothetical protein FLJ22709	SS,TM,myosin_head,RA,DAG_	25.9
438424	AI912498	Hs.25895	hypothetical protein FLJ14996	SS,TM	25.8
435017	AA336522	Hs.12854	angiotensin II, type I recepto		25.0
409518	BE384836	Hs.3454	KIAA1821 protein	SS	23.3
410418	D31382	Hs.63325	transmembrane protease, serine	SS,TM,ld_recepLa,trypsi	22.8
439924	AI985897	Hs.125293	ESTs	SS	22.7
446374	AA329256	Hs.24756	ESTs, Moderately similar to al		22.6
431773	BE409442	Hs.268557	pleckstrin homology-like domai	PH,SS,LIM,Troponin	21.4
420839	AI792682	Hs.282960	hypothetical protein MGC10870	SS,DS,UPF0139,Glyco_hydro	21.4
413436	AF238083	Hs.68061	sphingosine kinase 1	DAGKc	21.2

424420	BE614743	Hs.146688	prostaglandin E synthase	MAPEG,SS,TM,MAPEG	20.7
422845	L40027	Hs.118890	glycogen synthase kinase 3 alp	kinase,SS,Ets	20.7
436725	BE045223	Hs.136912	hypothetical protein MGC10796		20.4
422098	H03117	Hs.111497	similar to mouse neuronal prot	TM	20.2
428556	AW139399	Hs.98988	ESTs	SS,kinase,PMP22_Claudin	20.1
434098	AA977835	Hs.127274	ESTs	SS	20.0
423767	H18283	Hs.132753	F-box only protein 2	F-box,SS,F-box,HORMA	19.9
423852	AF052122	Hs.130712	Homo sapiens clone 23929 mRNA	ABC1,SS,PID,PID	19.8
422179	AF091619	Hs.112657	dynein, axonemal, intermediate	WD40,SS	19.3
441356	BE384361	Hs.182685	ESTs, Weakly similar to JC5024	SS,TM,ank	18.5
418969	W33191	Hs.28907	hypothetical protein FLJ20258	SH3,SH3	17.2
432631	H08379	Hs.165563	hypothetical protein DKFZp434N	TM,DnaJ,UBA,ArlGap,homeob	17.2
439108	AW163034	Hs.6467	synaptogyrin 3	Synaptogyrin,SS,TM,PDZ,WD	17.2
451643	M64437	Hs.234799	breakpoint cluster region	RhoGEF,RhoGAP,PH,C2	17.2
434518	M54955	Hs.37372	Homo sapiens DNA binding pepti	SS	16.9
413244	AW955951	Hs.159265	kruppel-related zinc finger pr	SS,TM,BTB,Pep_M12B_propep	16.3
456642	AW451623	Hs.109752	putative c-Myc-responsive		16.2
421612	AF161254	Hs.106196	8D6 antigen	Idl_recept_a,SS,TM	16.0
456177	NM_012391	Hs.79414	prostate epithelium-specific E	Ets,SAM_PNT	15.7
409261	BE315042	Hs.19210	hypothetical protein MGC11308		15.6
414837	U24266	Hs.77448	aldehyde dehydrogenase 4 famil	aldedh	15.6
401278			Target Exon	Band_41	15.4
444804	A084452	Hs.22158	hypothetical protein FLJ21988	SS	15.4
406620	M81105	Hs.146550	myosin, heavy polypeptide 9, n	myosin_head,Myosin_tail,I	15.1
421495	A0583067	Hs.149152	ESTs, Weakly similar to RHOP M		15.0
416893	AA455588	Hs.62406	hypothetical protein FLJ22573	SS,rm,SS	15.0
442620	C00138	Hs.8535	Homo sapiens mRNA for KIAA1668	SS,RNA_pol_K	14.9
406901	M14624	Hs.78950	gb:Human 4-beta-galactosyltran		14.8
416008	AA324251	Hs.80205	branched chain keto acid dehyd	E1_dehydrog	14.6
455557	AW995839	Hs.301394	gb:QV4-BN0044-110200-108-h07 B	Metallophos	14.4
416819	U77735	Hs.80205	plm-2 oncogene	kinase,SS,TM,OTU,K_tetra	14.3
444441	AW613841	Hs.301394	hypothetical protein MGC3101		14.0
406918	M88357	Hs.6479	gb:Homo sapiens DNA-binding pr	zf-C2H2,SS	14.0
407605	W03512	Hs.18079	hypothetical protein MGC13272	SS,Sema,kinase,TIG,PSI,e	13.6
447304	Z98883	Hs.18079	phosphatidylinositol glycan, c	SS,Peptidase_C2	13.6
402365			Target Exon	SS,SS,TM,Ig	13.4
407767	W15398	Hs.38628	hypothetical protein	SS,zf-CCCH	13.3
432931	AF174487	Hs.293753	Bcl-2-related ovarian killer p		12.7
439233	AA831893	Hs.292767	hypothetical protein FLJ23109	zf-C3HC4,TM,Sulfate_trans	12.7
423801	NM_015071	Hs.132942	GTPase regulator associated w/	RhoGAP,SH3,PH	12.6
430397	A0924533	Hs.105607	bicarbonate transporter relate	HCO3_cotransp,SS,TM	12.6
411570	BE144584	Hs.314341	ESTs		12.5
400206			Eos Control	SS,SS,Glyco_transf_43,COLF	12.3
457941	A004525	Hs.14587	ESTs, Weakly similar to AF1518	SS,TM,SS,TM	12.2
412674	X04106	Hs.74451	calpain 4, small subunit (30K)	efhand,SS,CAP_GLY	12.0
400460			C11002253*gi129091 sp P23267	SS,TM,SCAN,zf-C2H2,KRAB	12.0
417595	AA424317	Hs.6259	KIAA1698 protein	SS,TM,Glyco_hydro_31,Glyc	11.6
428758	AA433988	Hs.98502	CA125 antigen; mucin 16	SS	11.5
424707	BE061914	Hs.10844	Homo sapiens cDNA FLJ14476 fis	SS,SS,TM,Sema	11.5
444359	A0697160	Hs.143594	ESTs, Weakly similar to HS4L_H		11.5
435158	AW663317	Hs.65588	DAZ associated protein 1	rm,SS,rm	11.3
407888	W25317	Hs.37616	Human D9 splice variant B mRNA		11.3
450503	R35917	Hs.301338	hypothetical protein FLJ12587	SS	11.2
427448	BE246449	Hs.2157	Wiskott-Aldrich syndrome (ecze	WH1,PBD,WH2,SS	11.2
406230			Target Exon		11.2
432143	ALD40183	Hs.123484	Homo sapiens, clone IMAGE:4178	SS,TM,cys_rich_FGFR	11.2
433573	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G	SS,TM,7tm_2,EGF,cadherin,	11.1
413728	AJ278465	Hs.75510	annexin A11	annexin,SS,annexin	11.1
431974	AW972689	Hs.200934	ESTs	bZIP	11.0
428167	AA770021	Hs.16332	ESTs	SS,Ig,fn3	11.0
450461	BE408081	Hs.46736	hypothetical protein FLJ23476	SS	10.9
412738	N34731	Hs.74562	slah binding protein 1; FBP in	homeobox	10.9
445434	BE391690	Hs.9265	hypothetical protein FLJ20917	SS,PWWP,Exonuclease,tipoc	10.9
444008	BE544855	Hs.236572	ESTs, Weakly similar to SFR4_H	SS,SS,SAC3_GANP	10.7
444410	BE387360	Hs.33719	ESTs, Moderately similar to S6	SS	10.6
444607	AW405635	Hs.293687	ESTs	SS,PI-PLC-X,PI,PI-PLC-Y,C	10.6
404333			C7001735*gi17768636 dbj BAA95	vwd	10.5
401210			C12000519*gi17710046 ref NP_05		10.5
434743	A1363410		ribosomal protein S18	SS,TM	10.4
434030	AW162336	Hs.3709	low molecular mass ubiquinone-	SS	10.4
450029	AW073380	Hs.267963	hypothetical protein FLJ10535	SS,Pyridox_oxidase,zf-C2H	10.4
439632	AW410714	Hs.334437	hypothetical protein MGC4248	SS,TM,transmembrane4	10.3
438185	Y19188	Hs.320461	ESTs	SS	10.2
432031	AF039196	Hs.272367	hairless protein (putative sin	jmiC	10.2
405371			NM_005569*Homo sapiens LIM do	kinase,UIM,PDZ	10.1
456741	W37608	Hs.184492	ESTs	SS,kinase	10.1
458130	AA115811	Hs.6838	ras homolog gene family, membe	ras,arf	10.0
456977	AK000252	Hs.169758	hypothetical protein FLJ20245		10.0
420029	BE258876	Hs.94446	polyamine-modulated factor 1	aldo_ket_red,SS,TM,gla	10.0
445625	BE246743		hypothetical protein FLJ22635	SS,TM	9.9
423366	Z80345	Hs.127610	acyl-Coenzyme A dehydrogenase,	Acyl-CoA_dh,Acyl-CoA_dh_M	9.8
458216	AW024282	Hs.104938	hypothetical protein MGC15906		9.8
451721	NM_006946	Hs.26915	spectrin, beta, non-erythrocyt	spectrin,PH,CH,SS,Peptida	9.7
421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054	asp,SS,TM,ion_trans,K_tet	9.7

5	431354	BE046956	Hs.251673	DNA (cytosine-5)-methyltransf	SS,PWWP,PHD	9.7
	443780	NM_012068	Hs.9754	activating transcription facto	bZIP,NTP_transf_2,SS,TBC	9.7
	448133	AA723157	Hs.73769	folate receptor 1 (adult)	Folate_rec,SS	9.7
	444202	AL031685	Hs.12785	KIAA0939 protein	SS,TM,Na_H_Exchange,ABC2	9.7
	427640	AF058293	Hs.180015	D-dopachrome tautomerase	MF,Jata_protein_L2,SS,GS	9.6
	419167	AI589535	Hs.94875	ESTs, Weakly similar to A35363	SS	9.6
	424618	L29472	Hs.1802	major histocompatibility compl	TM,Ig,MHC_II_beta,SS,TM,A	9.6
	427497	AW139476	Hs.31240	ESTs		9.6
	420423	AA827718	Hs.88218	ESTs	SS	9.6
10	414756	AW451101	Hs.159489	ESTs, Moderately similar to JC	hexokinase2,hexokinase	9.6
	407893	BE408359	Hs.43621	Homo sapiens, Similar to hypot	SS,SS,arf,ras,fn3,ras	9.5
	408294	BE141732		gb:QVO-HT0101-061099-032-e07 H	Ammonium_transp	9.5
	442232	A1357813	Hs.337460	ESTs, Weakly similar to A47582	SS,TM,TGFb_propeptide,TGF	9.4
	416866	AA297358	Hs.80324	serine/threonine protein phosph	Metallophos,Metallophos	9.4
15	419823	AWZ71708	Hs.118918	ESTs, Weakly similar to M2OM_H	SS,TM	9.4
	422625	AW504698	Hs.155976	cullin 4B	SS,SS,Cullin,Cullin	9.3
	401264			C18000909:gi 5678656 ref NP_0	SS,laminin_Nterm,laminin	9.3
	407507	U73799		gb:Human dynactin mRNA, partia	SS,TM,HCO3_cotransp,CAP_G	9.2
20	400833			C11000890:gi 3746443 gb AAC639	SS,TM,7tm_1	9.2
	422064	AW452589	Hs.335742	ESTs	TM	9.2
	452434	D30934	Hs.29549	C-type lectin-like receptor-1	lectin_c,SS,TM	9.2
	421363	NM_001381	Hs.103854	docking protein 1, 62kD (downs	PH,IRS,TM,PH,IRS,lypsin,	9.1
	427397	A1929685	Hs.177658	calmodulin 1 (phosphorylase ki	efhand,FrnaAD,SS,efhand	9.1
25	414662	AW583672	Hs.256311	granin-like neuroendocrine pep	SS	9.0
	434796	AA812046		ESTs	SS,myb_DNA-binding,myb_DN	9.0
	422639	A1929377	Hs.173724	creatine kinase, brain	ATP-gua_Ptrans,ATP-gua_Pi	9.0
	447867	A1525268	Hs.164303	ESTs	TM	9.0
	442472	AW806859		gb:MRO-ST0020-081199-004-c03 S	SS,TM,Inos-1-P_synth,Ocd	8.9
30	455588	A1129903	Hs.74669	vesicle-associated membrane pr	synaptobrevin,SS,TM	8.9
	454319	AW247736	Hs.101617	ESTs, Weakly similar to T32527	SS	8.9
	429527	AA454184	Hs.289014	ESTs		8.9
	432603	AA554920	Hs.105794	UDP-glucose:glycoprotein gluco	SS,TM	8.9
	410338	W03445	Hs.38205	gb:za05g11.1 Soares melanocyt	kinase	8.9
35	452833	BE559681	Hs.30736	KIAA0124 protein	WD40	8.9
	407363	AF035032	Hs.181125	gb:Homo sapiens clone MCA1L my	SS,Ig,SS,G_glu_transpept	8.8
	414413	BE294877		gb:601174162F1 NIH_MGC_17 Homo	SS	8.8
	431765	AF124249	Hs.268541	novel SH2-containing protein 1	SH2,SS,TM	8.8
	421694	BE387430	Hs.106880	bystin-like		8.8
40	453683	AL079854	Hs.118598	Homo sapiens mRNA for KIAA1878	SS	8.8
	418736	T18979	Hs.87908	Snf2-related CBP activator pro	SS,helicase_CAT_hook,SS,	8.7
	450958	AL137669	Hs.348012	Homo sapiens mRNA; cDNA DKFZp4		8.7
	419725	U66048	Hs.92683	Homo sapiens clone 161455 brea		8.7
	415126	D60945		gb:HUM141D04B Clontech human I	SS,TM	8.7
45	406301			Target Exon	TM	8.6
	418843	AJ251016	Hs.89230	potassium intermediate/small c	TM,CaMBD,SK_channel,TM	8.6
	433396	AJ742071	Hs.133205	ESTs	SS,TM	8.6
	434333	AA186733	Hs.292154	stromal cell protein		8.6
	407065	Y10141		gb:H.sapiens DAT1 gene, partia	SNF,SS,TM	8.6
50	452851	AW173191	Hs.213117	ESTs	SS,Sema	8.6
	422418	AK001383	Hs.116385	hypothetical protein FLJ10521	RhoGEF	8.6
	447859	AK002194	Hs.19851	peroxisomal biogenesis factor		8.6
	420836	AW958453	Hs.204959	hypothetical protein FLJ14886	SS,ras	8.6
	429099	BE439952	Hs.196177	phosphorylase kinase, gamma 2	kinase,SS,SNF2_N,helicas	8.6
55	419639	AK001502	Hs.91753	hypothetical protein		8.6
	429712	AW245825	Hs.211914	ENSP00000233627:NADH-ubiquino	oxidored_q8,SS,TM,rm	8.5
	452554	AW452434	Hs.58006	ESTs, Weakly similar to ALU5_H	SS,PAS,HLH	8.5
	441076	N49809	Hs.11197	Homo sapiens, clone IMAGE:3343		8.5
	428860	U38291	Hs.194301	microtubule-associated protein	M	8.5
60	421901	AB014554	Hs.109299	protein tyrosine phosphatase,	SAM,SS,TM,rm,PDZ	8.4
	441363	AW450211	Hs.126825	ESTs, Weakly similar to A46302	SS,TM,HSP20,7tm_1	8.4
	443801	AW206942	Hs.253594	intron of trichorhinophthalang	GATA	8.4
	432862	AW004958	Hs.236720	amniotless protein	SS,MATH,zf-TRAF,zf-C3HC4	8.4
	431849	AI670823	Hs.85573	hypothetical protein MGC10911	SS,TM	8.4
65	423662	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc	SS	8.3
	404365			Target Exon	SS	8.3
	425694	U51333	Hs.159237	hexokinase 3 (white cell)	hexokinase,hexokinase2,ha	8.3
	423098	AA321980	Hs.204682	ESTs		8.3
	434552	AA639618	Hs.325116	Homo sapiens, clone MGC:2962,	SS	8.2
70	418361	AW505368	Hs.12460	gb:UI-HF-BN0-ahu-d-03-0-UIr1		8.2
	427433	D82070	Hs.177972	chromosome 4 open reading fram	SS,kinase	8.2
	420138	BE268854	Hs.177729	ESTs	SS	8.2
	426391	AW161050	Hs.169611	second mitochondria-derived ac	SS	8.1
	457613	AA598869	Hs.173770	ESTs		8.1
75	427502	AJ811865	Hs.7133	Homo sapiens, clone IMAGE:3161	SS,TM,ABC_tran,Glyco_tran	8.1
	437215	AL117488		Human clone Z3564 mRNA sequenc	SS	8.1
	423384	AL133632	Hs.127808	Homo sapiens mRNA; cDNA DKFZp4		8.1
	447151	AJ022813	Hs.92679	Homo sapiens clone CDABP0014 m	SS,TM,LRR,aminotran_1_2	8.0
	431898	AK000020	Hs.272018	hypothetical protein FLJ20013		8.0
80	454291	AW384847	Hs.213534	ESTs, Weakly similar to MUC2_H	SS,XRCC1_N,BRCT,lactamase	8.0
	430354	AA954810	Hs.239784	human homolog of Drosophila Sc	SS,TM,Ig	8.0
	459302	NM_002314	Hs.36558	LJM domain kinase 1		8.0
	422765	AW409701	Hs.1578	baculoviral IAP repeat-contain	BIR,TK,SS,TM	8.0
	425944	AK000684	Hs.164256	hypothetical protein FLJ20657		7.9
	450873	BE464016	Hs.238956	ESTs	SS,zf-C2H2,rm	7.9

5	454246	AW245185	Hs.6996	ESTs		7.9
	450635	AW403954	Hs.25237	mesenchymal stem cell protein	4HBT	7.9
	422305	A928242	Hs.293438	ESTs, Highly similar to AF1984	SS	7.9
	425760	D17629	Hs.159479	galactosamine (N-acetyl)-6-sul	Sulfatase,SS,TM	7.9
	413534	BE146961		gb:CV4-HT0222-011199-019-b12 H	SS,TM	7.8
	446931	A1348856	Hs.21627	gb:bb05a05.x2 NCL CGAP_Lu26 Ho		7.8
	421726	AK001237	Hs.319088	hypothetical protein FLJ10375	TM	7.8
	427461	AA531527	Hs.332040	hypothetical protein MGC13010	SS,TM,ACAT,LRR	7.8
10	448993	A1471630		KIAA0144 gene product		7.8
	443136	NM_001440	Hs.9018	exostoses (multiple)-like 3	Exostosis,SS,TM	7.8
	427725	U66839	Hs.180533	mitogen-activated protein kina	pkinase	7.8
	400923			Target Exon	SS,TM,DUF289	7.8
	419757	AA773820	Hs.63970	ESTs	SS,TM	7.8
15	458834	A1566883	Hs.196446	ESTs		7.8
	427899	AA829286	Hs.332053	serum amyloid A1	SS,SAA_proteins,SS,SAA_pr	7.7
	452399	BE513301	Hs.28344	hypothetical protein, clone 24	SS,peritipin	7.7
	436543	NM_002212	Hs.5215	Integrin beta 4 binding protei	elf8	7.7
	431811	AB040972	Hs.301696	hypothetical protein FLJ11580	SS,TM,Band_7,AAA,cdc48_N,	7.7
20	414534	BE257293	Hs.76366	BCL2-antagonist of cell death	SS,hormone_rec,zf-C4	7.7
	455885	BE153524		gb:PMO-HT0339-241199-002-C03 H	SS,plinkase	7.7
	427721	A1582843	Hs.180455	RAD23 (S. cerevisiae) homolog	ubiquitin,UBA,Integrin_B,	7.6
	430432	AB037758	Hs.241419	KIAA1337 protein	TM,Patched,TM	7.6
	427273	AW139032	Hs.107376	hypothetical protein DKFZp434N	SS,SS,TM	7.6
25	450334	AF035959	Hs.24879	phosphatidic acid phosphatase	PAP2,SS	7.6
	413564	BE260120		gb:60114699QF1 NIH_MGC_19 Homo		7.6
	410397	AF217517	Hs.63042	DKFZp564J157 protein	SS,homeobox,UPF0160,DUF23	7.6
	439539	BE348395	Hs.121589	ESTs	SS,Fork_head	7.5
	400286			C16000922:gl 7499103 pir T209	TM,ABC_tran,ABC_membrane	7.5
30	416472	AA180756	Hs.340316	ESTs, Moderately similar to AL	zf-C2H2	7.5
	418641	BE243136	Hs.86947	a disintegrin and metalloprote	disintegrin,Reprolysin,Pe	7.5
	419492	AA243547	Hs.19447	PDZ-LIM protein mystique	LIM,SS,SH3,Sorb,Metalloph	7.5
	420970	AA305079	Hs.1342	cytochrome c oxidase subunit V	COX5B	7.5
35	406495			Target Exon	SRCR,TM,Acetyltransf	7.5
	448043	A1458653	Hs.201881	ESTs	PHD	7.4
	401724			C16001374:gl 6755086 ref NP_03	TM,PLAT,SS	7.4
	424263	M77640	Hs.1757	L1 cell adhesion molecule (hyd	fn3,Ig,IRK,SS,TM,fn3,Ig,R	7.4
	428092	AW879141		ESTs	SS,TM	7.3
	453023	AW028733	Hs.31439	serine protease inhibitor, Kun	Kunitz_BPTI,SS,TM,ion_tra	7.3
40	400137			Eos Control		7.3
	436127	W94824	Hs.11565	RIKEN cDNA 2010100012 gene	Corona_7,SS,TM	7.3
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	UPP_synthetase,HMG14_17	7.3
	432747	NM_014404	Hs.278907	calcium channel, voltage-depen	PMP22_Claudin,SS,TM,PMP22	7.3
	448859	BE272448	Hs.265317	hypothetical protein MGC2562	SS,TPR	7.3
45	407619	AL050341	Hs.37165	collagen, type IX, alpha 2	SS,Collagen,SS,Collagen	7.3
	429299	A1620463	Hs.347408	hypothetical protein MGC13102	SS,TM,gla	7.3
	401674			C16001417:gl 7500345 pir T21	FAD-oxidase_C,FAD_binding	7.2
	412289	AW935967	Hs.170162	KIAA1357 protein	SS	7.2
	424198	AB029010	Hs.143026	KIAA1087 protein	SS,TM,Na_Ca_Ex,Cabx-beta,	7.2
50	412173	T71071		gb:yc50b05.r1 Stratagene liver	CPSase_L_chain	7.2
	438113	A1467808	Hs.8882	ESTs	SS,TM,7tm_1	7.2
	428869	A1907018	Hs.15977	Target CAT	rm	7.2
	439963	AW247529	Hs.6793	platelet-activating factor ace	PAF-AH_b,Lipase_GDSL,SS,	7.2
	425041	A1377150	Hs.150914	ESTs	SS	7.2
55	448340	A1492910	Hs.32362	ESTs		7.1
	406779	AA412048	Hs.279574	CGI-39 protein; cell death-reg	SS,SS	7.1
	431005	AA490544	Hs.127269	ESTs, Weakly similar to T02345	WD40	7.1
	421273	AJ245416	Hs.103106	U6 snRNA-associated Sm-like pr	Sm,SS,IRNA-synt_1,GST_C,G	7.1
	409649	AA159216	Hs.55505	hypothetical protein FLJ20442	Y_phosphatase,DSPc,TM	7.0
60	430281	A1878842	Hs.237924	CGI-69 protein	mito_carr,SS,TM	7.0
	444672	Z95636	Hs.11669	laminin, alpha 5	laminin_EGF,Jaminin_G,EGF	7.0
	405928			Target Exon	SS,cystatin,Coprogen_oxid	7.0
	421321	NM_005309	Hs.103502	glutamic-pyruvate transaminase	aminotran_1_2,SS,TM,LRR	6.9
	439905	AW799755	Hs.110953	retinoic acid induced 1	HLH	6.9
65	451937	AF119664	Hs.27299	transcriptional regulator prot	SS,Integrin_B,fn3,Cabx-be	6.9
	426875	AW084791	Hs.133122	hypothetical protein FLJ14524	SS,TM,aminotran_1_2	6.9
	438627	A1087335	Hs.123473	ESTs	TM,Reticulon	6.9
	438951	U51336	Hs.6453	inositol 1,3,4-triphosphate 5/	SS,oxidored_nitro,SS	6.8
	421758	BE397338	Hs.1422	Gardner-Rasheed feline sarcoma	SH2,SH3,plinkase	6.8
70	423228	AL137491	Hs.125511	Homo sapiens mRNA; cDNA DKFZp4	SS,TM,sushi	6.8
	405346			Rag C protein	RCC1	6.8
	432746	AA564512	Hs.24301	polymerase (RNA) II (DNA direc	SS,TM,EF18D	6.8
	452798	A1918771	Hs.257170	ESTs	SS,TM,TNFR_c6	6.7
	426315	AA854219	Hs.348137	Homo sapiens, clone IMAGE:3542	SS,crystall	6.7
75	440317	BE561888		gb:601346093F1 NIH_MGC_8 Homo		6.7
	438857	A1627912	Hs.130783	Forssman synthetase	SS,RA,RasGEF,RasGEFN	6.7
	452072	BE258857	Hs.27744	RAB3A, member RAS oncogene fam	ras,arf,SS,PDEase	6.7
	433938	AF161536	Hs.284292	ubiquinol-cytochrome c reducta	TM	6.7
	423106	N52572	Hs.13702	ESTs, Moderately similar to AL		6.7
80	453101	AW952776	Hs.94943	ESTs	TM	6.7
	420307	AW502869	Hs.66219	ESTs	SS,TM	6.7
	415056	AB004662	Hs.77867	adenosine A1 receptor	7tm_1,SS,TM	6.7
	454262	AW612232	Hs.254835	ESTs	SS,TM,voltage_CLC,CBS	6.7
	409227	AA806165	Hs.130323	Homo sapiens, clone IMAGE:3960		6.6
	413908	BE409966	Hs.323813	Homo sapiens, clone MGC:2867,	SS,zf-C2H2	6.6

5	457274	AW674193	Hs.227152	mannan-binding lectin serine p	SS,TM,SS,TM,Clathrin_lg_c	6.6
	419157	AA234540	Hs.23871	ESTs	pkinae	6.6
	431424	AJ222969		ESTs	SS	6.6
	412464	T78141	Hs.22826	ESTs, Weakly similar to I55214	SS,cadherin,crystall	6.6
	430168	AW968343		DKFZP434I1735 protein	SS,TM,efhand,efhand	6.6
	455035	AW851734		gb:MR2-CT0222-011199-007-e10 C		6.6
	422682	W05238	Hs.94316	ESTs, Weakly similar to T31613	SS,TM,DEAD,helicase_C,Lam	6.6
	453367	AW732847	Hs.70573	PKC1-related HIT protein	SS,TM	6.6
10	450593	AF129085	Hs.25197	STIP1 homology and U-Box conta	TPR,SS,TM,Rhomboid,lactam	6.6
	420319	AW406289	Hs.96593	hypothetical protein	ras,arf	6.6
	431131	N84730	Hs.250616	isocitrate dehydrogenase 3 (NA	isodh,lsodh	6.6
	431297	AA651771	Hs.3076	ESTs		6.6
	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	SS,HECT,phoslip	6.5
	441307	AW071696	Hs.209065	hypothetical protein FLJ14225	SS,TM	6.5
15	454682	AW816029		gb:MR3-ST0220-151299-027-b10 S	filament	6.5
	407299	AA460205	Hs.289770	ESTs, Weakly similar to I38022		6.5
	422637	U25441	Hs.121478	dopamine receptor D3	7tm_1,SS,TM,7tm_1	6.5
	407722	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin	pkf8,SS	6.4
20	417810	D28419	Hs.82609	hydroxymethylbilane synthase	Porphobil_deam	6.4
	445333	BE537641	Hs.44278	hypothetical protein FLJ12538	SS	6.4
	402197			Target Exon	SS,TM,ATP1G1_PLM_MAT8,lg,	6.3
	419390	AJ701162	Hs.90207	hypothetical protein MGC11138	SS,TM,PMP22_Claudin,PMP22	6.3
	447754	AW073310	Hs.163533	intron of HER4		6.3
25	444664	N26362	Hs.11815	map kinase phosphatase-like pr	DSPc,Rhodanese,SS,TM	6.3
	421190	U95031	Hs.102482	mucin 5, subtype B, tracheobro	Cys_knot,vwc	6.3
	432872	AJ908984	Hs.279623	selenoprotein X, 1	DUF25,SS,Ribosomal_L3,PDZ	6.3
	430023	AA158243	Hs.227729	FK506-binding protein 2 (13kD)	SS,FKBP,SS,PDGF,C2,PI-PLC	6.3
	413343	BE392026	Hs.334346	hypothetical protein MGC13045	SS,DnaJ	6.2
30	417852	AJ250562	Hs.82749	transmembrane 4 superfamily me	transmembrane4,SS,TM	6.2
	403128			KIAA1033 protein	SS,TM,tubulin,EGF,F5_F8_1	6.2
	413055	AV655701	Hs.75183	cytochrome P450, subfamily IIE	p450	6.2
	427812	AA770424	Hs.88162	ESTs	SS	6.2
	457761	AW401809	Hs.4779	KIAA1150 protein	SS,LIM,SS	6.2
35	453099	H62087	Hs.31659	thyroid hormone receptor-assoc	SS	6.2
	426048	AJ768853	Hs.134478	ESTs	TM	6.2
	407223	H96850		gb:vw03b12.s1 Soares melanocyt	SS,TM,SS,TM,DOST_48kD	6.2
	445634	AJ624849	Hs.344612	ESTs, Weakly similar to NEL1_H	vwd	6.2
	441197	BE244638	Hs.166	sterol regulatory element bind	HLH	6.1
40	421707	NM_014921	Hs.107054	lectomedin-2	Latrophilin,OLF,7tm_2,Gal	6.1
	435750	AB029012	Hs.4990	KIAA1089 protein	SS,TM	6.1
	432353	NM_016558	Hs.274411	SCAN domain-containing 1	SCAN	6.1
	427326	AJ287878		gb:qv23f06.x1 NCL_CGAP_Lym6 Ho	SS,TM,7tm_1,SS,TM	6.1
	447128	AJ271898		cyclin K		6.1
45	419444	NM_002496	Hs.90443	Target CAT	fer4,SS,TM,V_ATPase_sub_a	6.1
	457978	AA776638		gb:aa78g04.s1 Stratagene schiz	SS,PHIQ,RasGEF,RasGEFN,R	6.1
	410445	AA199830		gb:zq75h01.r1 Stratagene hNT n		6.1
	431857	W19144	Hs.271742	ADP-ribosyltransferase (NAD; p	PARP,PARP_reg,SS,TM,Pepi	6.1
	407143	C14076	Hs.332329	EST	SS,TM	6.0
50	408724	AJ685842	Hs.294143	ESTs, Weakly similar to T22914	SS,pkinae,tubulin	6.0
	436685	W28661	Hs.5288	Homo sapiens mRNA; cDNA DKFZp4	SS,TM,pkinae,Activin_rec	6.0
	441583	AJ791499	Hs.205742	ESTs, Weakly similar to ALUA_H		6.0
	418802	AB028989	Hs.88500	mitogen-activated protein kina	WD40,Pico_P2A,M,SS	6.0
	414927	T83587	Hs.186476	ESTs	SS,Sulfatase	6.0
55	434314	BE392921	Hs.3797	RAB26, member RAS oncogene fam	ras,arf,SS	6.0
	414157	BE297801	Hs.103845	ESTs, Moderately similar to I5	SS	6.0
	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	enolase,SS,Atrophin-1,Atr	6.0
	406487			Target Exon	SS,TM	6.0
	447365	BE383676	Hs.334	Rho guanine nucleotide exchang	SH3,PH,RhoGEF	6.0
60	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20,	WD40,SS,TM,fn3,EGF,fn3,lg	6.0
	442297	NM_006202	Hs.89901	phosphodiesterase 4A, cAMP-spe	PDEase	5.9
	426440	BE382756	Hs.169902	solute carrier family 2 (facil	sugar_tr,SS,TM,sugar_tr	5.9
	418256	AW845318	Hs.12271	f-box and leucine-rich repeat	SS,SS,TM,HSF_DNA-bind	5.9
	431543	AW969619	Hs.259768	adenylate cyclase 1 (brain)	TM	5.9
65	430344	AA476827	Hs.171012	hypothetical protein FLJ22349	HLH	5.9
	428539	AW410063	Hs.184877	solute carrier family 25 (mito	mito_carr,SS,TM,profilin,	5.9
	403938			Target Exon	Ephrin	5.9
	455950	AF111170	Hs.306165	Homo sapiens 14q32 Jagged2 gen	SS,TM,DSL	5.9
	451481	AA300228	Hs.295866	hypothetical protein DKFZp434N		5.9
70	434357	AW732284	Hs.3828	mevalonate (diphospho) decarbo	GHMP_kinases,SS,TM	5.9
	443553	ALD40535	Hs.9573	ATP-binding cassette, sub-famil	ABC_tran,SS	5.9
	433333	AJ016521	Hs.71816	v-akt murine thymoma viral onc	homeobox,pkinae,PH,pkina	5.9
	430600	AW950967	Hs.274348	HLA-B associated transcript-3	ubiquitin,SS,TM,G-patch,a	5.9
	408034	AJ684149	Hs.172035	hypothetical protein similar 1	SS	5.9
75	421542	AA411607	Hs.118964	ESTs, Weakly similar to KIAA11	SS,SS	5.9
	431534	AL137531	Hs.258890	Homo sapiens mRNA; cDNA DKFZp4	SS,TM,ras	5.9
	409608	AF231023	Hs.55173	cadherin, EGF LAG seven-pass G	SS,TM,7tm_2,cadherin,GPS,	5.9
	423464	NM_016240	Hs.128856	CSR1 protein	Collagen,SS	5.9
	422379	AA932860	Hs.133864	ESTs		5.8
80	443887	NM_004729	Hs.5933	Ac-like transposable element	zf-BED	5.8
	450122	BE313765	Hs.343443	ESTs, Weakly similar to I38022	SS,TM,Y_phosphatase,LON,A	5.8
	404807			Target Exon	UPF0027	5.8
	445303	AW362198	Hs.12503	interleukin 15 receptor, alpha	SS,sushi,SS	5.8
	445631	AK001822		Homo sapiens cDNA FLJ10960 fis		5.8
	412091	R05185		gb:ye94d03.r1 Soares fetal liv	SS,TM,IBR,IBR	5.8

445536	W74413	Hs.15251	hypothetical protein	SS	5.8
432866	BE395875	Hs.279609	mitochondrial carrier homolog	mito_carr	5.8
402393			ENSP00000085284*CDNA FLJ20404	RhoGEF,PH,SS,zf-CCCH,vwd	5.8
413041	BE061580	Hs.61622	gb:MR0-BT0249-091299-201-c07 B	SS	5.8
414356	AW505085	Hs.335147	gb:U1-HF-BN0-els-a-10-0-ULr1	SS,TM	5.8
402916			ENSP00000202587*Bicarbonate t	HCO3_cotransp,SS	5.7
459133	U40343	Hs.29656	cyclin-dependent kinase inhibi	ank,SS,Adap_comp_sub	5.7
404757			Target Exon	TM,zf-C2H2	5.7
409879	BE083422	Hs.56851	hypothetical protein MGC2668	SS,TM	5.7
411219	AW832917		gb:CV2-TT0003-161199-013-h06 T		5.7
421871	AK001416	Hs.306122	glycoprotein, synaptic 2	TM,Steroid_dh,SS	5.7
434067	H18913	Hs.124023	Homo sapiens cDNA FLJ14218 fis		5.7
416759	AK000978	Hs.79741	hypothetical protein FLJ10116		5.7
446562	BE272686	Hs.15356	hypothetical protein FLJ20254	hormone,SS,pfkB	5.7
407117	AA146525		gb:zo71c07.s1 Stratagene pancr	SS	5.7
444855	BE409261	Hs.12084	Tu translation elongation fact	GTP_EFTU,GTP_EFTU_D3,GTP_	5.7
421543	AK000519	Hs.105606	hypothetical protein FLJ20512	TM	5.7
407757	BE048414	Hs.165215	hypothetical protein MGC5395	SS,EF1G_domain,GST_C,GST_	5.7
418125	AA642452	Hs.130881	B-cell CLL lymphoma 11A (zinc	SS	5.7
437141	BE304917	Hs.31097	hypothetical protein FLJ21478	SS,TM,Glycos_transf_4	5.7
408905	AV655783	Hs.661	Target CAT		5.7
450787	AB006190	Hs.25475	aquaporin 7	MIP,SS,TM	5.7
432496	D45576	Hs.187959	ESTs		5.7
429367	AB007867	Hs.278311	plaxn B1	Sema,PSI,TIG,SS,TM,TIG,Se	5.7
422708	AB017430	Hs.119324	kinesin-like 4_	kinesin,homeobox,SS,TM,zf	5.7
417442	AA199940	Hs.124039	ESTs		5.7
432751	AF152099	Hs.278911	interleukin 17C	SS	5.7
432004	BE018302	Hs.2894	placental growth factor, vascu	PDGF,SS	5.7
454151	AA047169	Hs.154088	hypothetical protein FLJ22756	SS,TM,Glycos_transf_4	5.7
456145	BE299427	Hs.21446	KIAA1718 protein	SS,DIX,PDZ,DEP,Dishevelle	5.6
417677	NM_016055	Hs.82389	CGI-118 protein		5.6
451558	NM_001089	Hs.26630	ATP-binding cassette, sub-famI	ABC_tran,SRP54,SS,TM,ECH	5.6
408785	AW749126	Hs.170345	hypothetical protein FLJ13710	hormone_rec,zf-C4	5.6
407204	R41833	Hs.140237	ESTs, Weakly similar to ALU1_H	SS,histone,histone	5.6
452849	AF044924	Hs.30792	hook2 protein	bZIP,SS,AhpC-TSA	5.6
439343	AF066161	Hs.114611	hypothetical protein FLJ11808		5.6
459271	AL045934		gb:DKFZp434M116_r1 434 (synony	SS,PI3_P14_kinase,PI3Ka	5.6
401609			C16001614:gil7801278[emb]CAB91		5.6
447827	U73727	Hs.19718	protein tyrosine phosphatase,	Y_phosphatase,ln3,Ig,MAM,	5.6
409125	R17268	Hs.343567	axonal transport of synaptic v	SS,kinesin,PH,FHA,kinesin	5.6
450437	X13956	Hs.24998	hypothetical protein MGC10471	SS	5.6
415514	F11301	Hs.138329	ESTs	SS,TM	5.6
437926	BE383605	Hs.300816	small GTP-binding protein	SS,TM,TPR	5.6
406663	U24683		immunoglobulin heavy constant	SS	5.6
421678	AA419008	Hs.106730	chromosome 22 open reading fra	SS,TM,UBA,Rhomboid,SS,TM	5.6
422472	R59096	Hs.279939	mitochondrial carrier homolog	mito_carr	5.6
414918	AJ219207	Hs.72222	hypothetical protein FLJ13459	SS,TM,efhand	5.6
434906	BE410573	Hs.283636	Homo sapiens, clone IMAGE:4053	SS,TM,Exo_endo_phos,BNRA	5.6
414757	U46922	Hs.77252	fragile histidine triad gene	HIT	5.6
436014	AF281134	Hs.283741	exosome component Rrp46	RNase_PH,RNase_PH_C,SS,TG	5.6
421696	AF035306	Hs.106890	Homo sapiens clone 23771 mRNA		5.6
408015	AW136771	Hs.244349	epidermal differentiation comp		5.6
445871	AJ702901	Hs.145582	ESTs, Weakly similar to FOR4 M	SS,TM,efhand,efhand	5.6
411813	NM_014931	Hs.72172	KIAA1115 protein	SS,TM,Y_phosphatase	5.5
425098	AW295349	Hs.8038	ESTs	SS,TM	5.5
429720	M79091		gb:EST01239 Subtracted Hippoca		5.5
453898	AW003512	Hs.232770	arachidonate lipooxygenase 3	SS,TM,lipoxygenase,PLAT,s	5.5
449225	R39108	Hs.6777	ESTs	SS,TM,Na_sulph_symp	5.5
423233	BE048021	Hs.11067	ESTs, Highly similar to T46395		5.5
432538	BE258332	Hs.278362	male-enhanced antigen	SS,TM,AAA,Ribosomal_L2	5.5
408215	BE614290		syntaxin 10	SS,SS,TM,HLH,TRM,zf-CCCH	5.5
406244			Target Exon		5.5
436041	AJ803516	Hs.272891	hippocalcin-like protein 4	SS,efhand,TGF-beta,TGFb_p	5.5
422013	N92696	Hs.293354	ESTs	SS,TM	5.5
442451	AJ498080	Hs.129616	ESTs	SS	5.5
427859	AA416856	Hs.98170	ESTs	SS,TM,DUF60,bypsin,CUB,u	5.5
436540	BE397032	Hs.14468	hypothetical protein MGC14226	SS,TM	5.5
427747	AW411425	Hs.180655	serine/threonine kinase 12	pkinese,SS,TM,synaplobrev	5.4
441456	AJ458911	Hs.127765	ESTs		5.4
431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD4	integrin_A,FG-GAP,Rhbd_g	5.4
415976	R43144	Hs.21919	ESTs	TM	5.4
447374	AF263462	Hs.18376	KIAA1319 protein	SS,Myosin_tail,M	5.4
431275	T56571	Hs.10041	ESTs	SS,HLH	5.4
404343			C7002191*gil5053028[gb]AAD388	SS,ABC_tran	5.4
431461	BE299671	Hs.256310	likely ortholog of mouse ZFP28		5.4
421779	AJ879159	Hs.108219	wingless-type MMTV integration	SS,wnt,SS	5.4
418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-	SS,TM,zf-C2H2	5.4
457310	W28363	Hs.239752	nuclear receptor subfamily 2,		5.3
417193	AJ922189	Hs.288390	hypothetical protein FLJ22795	SS	5.3
432545	X52486	Hs.3041	uracil-DNA glycosylase 2	cyclin,SS,cyclin	5.3
456573	AJ279811		Homo sapiens, clone IMAGE:3953		5.3
409164	AA706639		gb:ag90e09.r1 Stratagene hNT n	SS,TM,Hin,HLH_signal,tubu	5.3
442296	NM_007275	Hs.8186	lung cancer candidate	SS,TM,Glyco_hydro_56,Glyc	5.3
438670	AJ275803	Hs.123428	ESTs		5.3

	400257		ENSP0000000452:BAD protein (B	SS,hormone_rec,zf-C4	5.3
	449514	AW970440	Hs.23642	SS,PX,arf,lipocalin,PHD,z	5.3
	427336	NM_005658	Hs.2134	MATH,SS,MATH,A2M,N,A2M,NT	5.3
5	414551	AJ815639	Hs.76394	ECH,Peptidase_U7,SS,TM	5.3
	447960	AW954377	Hs.26412	SS,TM,Cbl_N,Cbl_N2,Cbl_N3	5.3
	430605	AJ245433	Hs.247323	SS,TM,G-patch,ubiquitin,a	5.3
	456849	AA622394	Hs.153177	SS,TM	5.2
	430513	AJ012008	Hs.241586	SS,TM,GST_C,abhydrolase	5.2
10	424437	BE244700	Hs.147049	CUT,homeobox,beta-lactama	5.2
	427815	BE072019	Hs.12851	SS,TM,7tm_1	5.2
	417903	NM_002342	Hs.1116	TNFR_c6,SS	5.2
	420476	AW575863	Hs.136232	SS,HLH	5.2
	409960	BE261944		SS,TM	5.2
	436325	AL390088	Hs.7393	SS,Synapsin_C,SS	5.2
15	444439	AJ458883	Hs.143545	SS,TM,PAF-AH_p_II	5.2
	412915	AW087727	Hs.74823		5.2
	418891	NM_002419	Hs.89449	SH3,ptkinase,pyridoxal_deC	5.2
	430323	U04714	Hs.239307	DUF101,SS,IRNA-synL_1b,IR	5.2
20	432396	AW295956	Hs.11900	SS	5.2
	457843	AW138211	Hs.128748		5.2
	429252	NM_004658	Hs.198312	C2,PH,RasGAP,BTK,SS,C2,PH	5.1
	429225	BE250337	Hs.198273	WD40	5.1
	412104	AW205197	Hs.240951	SS,TM	5.1
25	449750	H28586	Hs.32325	SS,ras	5.1
	442725	AJ335786	Hs.131035	SS,SS,TM,PX,PH,PLDc,arres	5.1
	430390	AB023186	Hs.241161	PH,SS,TM	5.1
	421658	X84048	Hs.301760	efhand	5.1
	426928	AF037062	Hs.172914	adh_short,SS,adh_short,TG	5.1
30	428924	AJ016405	Hs.98959	SS,TM,lectin_c	5.1
	458876	AJ650896	Hs.195347		5.1
	402632			Fz,kirgling,Ig	5.1
	413762	AW411479	Hs.848	FKBP,TPR,SS	5.1
	419451	AJ907117	Hs.90535	Sect1,SS,TM	5.1
35	456155	R85182	Hs.7175	SS	5.1
	422396	W21872	Hs.7807		5.1
	413983	BE348384	Hs.279194		5.0
	447598	AJ799968	Hs.199630	SS,TM	5.0
	425858	AA364923		SS,TM,Peptidase_M10,fn2,h	5.0
40	440511	AF132859	Hs.7236	SS,TM,MAGE,Ribosomal_S17,	5.0
	452681	AW449413	Hs.257152		5.0
	412800	AW950852	Hs.74598	homeobox,SS,efhand,hexaki	5.0
	446603	NM_014835	Hs.15519	Oxysterol_BP,SS	5.0
	402684			laminin_Nterm,laminin_Nte	5.0
45	448680	AW245890	Hs.21753	WD40,SS,TM,KOW,HLH	5.0
	431515	NM_012152	Hs.258583	7tm_1	5.0
	427204	AA405404	Hs.215725	SS,SS	5.0
	425169	AW292500	Hs.128514	SS	5.0
	412840	BE295701	Hs.819	homeobox,SS,homeobox,home	5.0
50	440839	AJ142078	Hs.135562	SS	5.0
	443814	BE281240	Hs.9857		5.0
	434243	AA528062	Hs.200358	SS,TM	5.0
	435605	AF151815	Hs.4973	SS,TM,SS,TM,ABC_tran,ABC_	5.0
	417116	Z43916	Hs.7634	SS,TM,filament,IF_tail	5.0
55	403055				5.0
	420856	BE513294	Hs.205736	kazal,SS,TM,Ig,ptkinase	4.9
	405594			E1-E2_ATPase,Hydrolase,SS	4.9
	405334			SS,TM,MIP	4.9
	419493	AF001212	Hs.90744	PCI,SS,CDK5_activator	4.9
60	413764	BE162704		SS	4.9
	409169	F00991	Hs.50889		4.9
	446933	AL137659	Hs.297214	SS,TM,ank,EGF_notch,MATH,	4.9
	409139	AJ681917	Hs.3321	SS,homeobox	4.9
	456672	AJ002016	Hs.114727	SS,PK,PK_C,myosin_head,Rh	4.9
65	420842	AJ083668	Hs.50601	SS	4.9
	421909	NM_013375	Hs.109428		4.9
	418667	AJ077005	Hs.92208	disintegrin,Reprolysin,Pe	4.9
	443496	AJ006973	Hs.9482	VHS,GAT,TM,Heme_oxygenase	4.9
	400933			ICE_p20,ICE_p10,CARD,SS,I	4.9
70	456143	H11097	Hs.61960	SS,ptkinase	4.9
	427527	AJ809057	Hs.153261	SS,TM,Ig	4.9
	414265	BE410411	Hs.75864		4.9
	433933	AJ754389		SS,TM,SS,TM,SH2,Y_phospha	4.9
	452302	AF173867	Hs.28906	SAND,SS	4.9
75	409938	AW974648		SS,Adap_comp_sub,GYF	4.8
	400845			kL_recept_a,fn3,kL_rece	4.8
	425976	C75094	Hs.334514	SS,TM,ptkinase,SH2,SH3,BNR	4.8
	452969	W92792	Hs.77575		4.8
	413163	Y00815	Hs.75216	fn3,Ig_Y_phosphatase,SS,T	4.8
80	434962	AJ001574	Hs.4291		4.8
	418572	AJ751740	Hs.86172	homeobox	4.8
	440869	NM_014297	Hs.7486	lactamase_B,SS,XRCC1_N,BR	4.8
	453446	BE299996			4.8
	412159	AF286598	Hs.9271	bZIP	4.8
	438999	AW276811			4.8

5	420233	AA256714	Hs.194864	hypothetical protein FLJ22578	SS	4.8
	414576	AK000405	Hs.76480	ubiquitin-like 4	ubiquitin,SS,TM,G6PD,G6PD	4.8
	433669	AL047879	Hs.80475	ESTs, Weakly similar to ALU2_H	SS,TM,RNA_pol_L,RasGAP,C2	4.8
	448984	AW751955	Hs.22753	hypothetical protein FLJ22318	SS	4.8
	426912	AL043054	Hs.256657	ESTs, Weakly similar to A46302	SS	4.8
	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	lipoxygenase,PLAT,SS	4.8
	440333	A1378424	Hs.286761	hypothetical protein FLJ21749	SS,TM,IP_trans,pkinase,pk	4.8
	425615	AF023614	Hs.158341	transmembrane activator and CA	TM	4.8
10	458040	BE280562	Hs.287711	hypothetical protein FLJ22692	SS,IRNA-synt_2d	4.8
	458367	AA088470	Hs.83135	Homo sapiens, Similar to RIKEN		4.8
	433294	AA582082	Hs.199410	ESTs		4.8
	437671	AA536047	Hs.9850	hypothetical protein MGC1842		4.8
	425338	H16716	Hs.182648	Homo sapiens cDNA FLJ14444 fis		4.8
15	447946	AI566164	Hs.165827	ESTs	SS,PTN_MK,7tm_1,DAGKc,DAG	4.7
	447205	BE617015	Hs.11006	ESTs, Moderately similar to T1	SS,TM,LRRCT,Sema	4.7
	416880	H99540	Hs.53687	EST		4.7
	440150	AW975738	Hs.7001	Homo sapiens, clone IMAGE:3940	SS,TM,SS,TM,Peptidase_M22	4.7
	426268	AF083420	Hs.168913	serine/threonine kinase 24 (S1	pkinase,pkinase	4.7
20	428253	Y11739	Hs.198313	winged-helix nude	Fork_head,SS,TM,glycolyl	4.7
	450261	AA788727	Hs.34068	ESTs, Weakly similar to A43932	SS	4.7
	439246	AA98072		membrane-associated tyrosine-	SS,SS,TM	4.7
	419120	BE271922		ESTs, Weakly similar to zinc f	SS,TM,DENN,Cytidylyltrans	4.7
	416487	AW190458	Hs.79347	KIAA0211 gene product	SS,zf-C2H2	4.7
25	413837	AW163525		filin-cap (telethonin)	SS,Methyltransf_3	4.7
	419887	AW292562	Hs.187628	ESTs	TM	4.7
	410277	R88621	Hs.26249	ESTs, Weakly similar to T2D3_H	SS,TM,SS	4.7
	415169	W42913	Hs.78089	ATPase, vacuolar, 14 kD	ATP-synt_F,SS,TM,CH,Filam	4.7
	410892	AW809762	Hs.222056	Homo sapiens cDNA FLJ11572 fis		4.7
30	407764	AA527348	Hs.288967	Homo sapiens cDNA FLJ14105 fis	SS,TM,SS,TM,TSPN,isp_3,SE	4.7
	409877	AW502498	Hs.15220	zinc finger protein 106		4.7
	431629	AJ077025	Hs.265827	interferon, alpha-inducible pr	pkinase,SH2,SH3	4.7
	438800	AB037108	Hs.6418	seven transmembrane domain orp	SS,TM	4.7
	420823	R95881	Hs.63609	HpaII tiny fragments locus 9C	TM	4.7
35	418900	BE207357	Hs.3454	KIAA1821 protein	SS	4.7
	402400			Target Exon	SS,TM,RNase_HII,bZIP,DUF2	4.7
	419825	U91616	Hs.91640	nuclear factor of kappa light	ank,SS,TM	4.7
	433319	AA583232		ESTs	SS	4.7
	424959	NM_005781	Hs.153937	activated p21cdc42Hs kinase	pkinase,SH3	4.7
40	432760	NM_014440	Hs.278910	interleukin 1, epsilon	IL1	4.7
	425954	AK000633	Hs.164476	hypothetical protein FLJ20626	SCAN,zf-C2H2,KRAB,SS,KRAB	4.7
	447245	AK001713	Hs.17880	hypothetical protein FLJ10851	E1_dehydrog	4.7
	427101	R87591	Hs.172884	ESTs	SS,TM	4.6
	447544	AA401573	Hs.288284	hypothetical protein FLJ22378	SS,TM	4.6
45	400266			NM_002858: Homo sapiens ATP-bi	ABC_tran	4.6
	412841	AJ751157	Hs.101395	hypothetical protein MGC11352	SS,TM	4.6
	422066	AW249275	Hs.343521	malate dehydrogenase 2, NAD (m	ldh,ldh_C,adh_short,Sema	4.6
	414874	D26351	Hs.77515	Inositol 1,4,5-triphosphate re	TM,RYDR,JTPR,ion_trans,MI	4.6
	418373	AW750770	Hs.84344	CGI-135 protein	SS,TM,PMP22_Claudin,20G-F	4.6
50	424487	T08754	Hs.6259	KIAA1698 protein	SS,SS,TM,Glyco_hydro_31,G	4.6
	426571	AA381642		gb:EST94816 Activated T-cells		4.6
	433941	AA620612		ESTs	SS,TM,TNFR_c6	4.6
	421717	AF230924	Hs.107187	divalent cation tolerant prote		4.6
	450883	NM_001348	Hs.25619	death-associated protein kinase	pkinase,GTP_EFTU,EF3_C,GT	4.6
55	427361	AW732480	Hs.7678	cellular retinoic acid-binding	SS,TM,aminotran_1_2,LRR	4.6
	420421	AF281133	Hs.343589	exosome component Rps41	RNase_PH,RNase_PH_C	4.6
	414513	AW239400	Hs.76297	G protein-coupled receptor kln	pkinase,RGS,pkinase_C,SS,	4.6
	431498	AK001777	Hs.258551	aspartyl aminopeptidase	SS,Peptidase_M18,SS,TM,Y_	4.6
	432593	AW301003	Hs.51483	ESTs, Weakly similar to hypoth	SS,TM,adh_short	4.6
60	404661			C9000306*gi12737280[refXP_D		4.8
	412790	NM_014767	Hs.74583	KIAA0275 gene product	kazal,thyroglobulin_1,zf-	4.6
	456243	AI345001	Hs.82380	menage a trois 1 (CAK assembly	zf-C3HC4	4.6
	426222	BE391706	Hs.168073	DKFZF727M231 protein	GSH_synthase	4.6
	439594	AI245026	Hs.111099	hypothetical protein MGC10974	CLP_protease	4.6
65	409114	AA070021		gb:znm67h03.r1 Stratogene neuro		4.6
	429049	AW452125	Hs.119273	KIAA0296 gene product	SS,TM,trypsin	4.6
	424271	AI991887	Hs.305882	5-oxoprolinase (ATP-hydrolysin		4.6
	418741	H83265	Hs.8881	ESTs, Weakly similar to S41044	SS,TM,pkinase,Activin_rec	4.6
	450493	M93718	Hs.166373	nitric oxide synthase 3 (endot	flavodoxin,FAD_binding,NO	4.6
70	433074	AL045019	Hs.323462	Homo sapiens cDNA FLJ11214 fis	DEAD,helicase_C,dsm,Vira	4.6
	444893	AW249312	Hs.12109	WD40 protein C1a01	WD40	4.6
	420508	AJ270993	Hs.98428	homeo box B6	homeobox,SS,homeobox,home	4.6
	409591	AA532963	Hs.9100	Homo sapiens cDNA FLJ13100 fis	SS,TM,LIM,homeobox	4.6
	456181	L36463	Hs.1030	ras inhibitor	RA,SH2,VP59,SS,TM,Nucleos	4.6
75	439270	BE268278	Hs.28393	hypothetical protein MGC2592	SS,TM,HCO3_cotransp	4.6
	440104	AA132838	Hs.239894	hypothetical protein MGC2803	SS,DS	4.5
	423279	AW959861	Hs.290943	ESTs	SS	4.5
	445087	AW893449	Hs.12303	suppressor of Ty (S.cerevisiae	S1,SH2,Ribosomal_L23,pkin	4.5
	404038			Target Exon	SS,TM,cadherin,cadherin	4.5
80	431832	AW276866	Hs.192715	ESTs	Ets,SAM_PNT	4.5
	433886	AA613596	Hs.28412	ESTs	SS	4.5
	426735	T78716	Hs.120446	ESTs	Oxysterol_BP,PH	4.5
	417825	AW838994	Hs.6363	heparan sulfate 6-O-sulfotrans	SS,TM	4.5
	455600	BE061053		gb:QV0-BT0041-271099-037-d09 B	C4	4.5
	423858	AL137326	Hs.133483	Homo sapiens mRNA; cDNA DKFZp4	SS,TM	4.5

	421680	AL031186	Hs.289106	Human DNA sequence from clone	SS,SS,rm,zf-RanBP,rm,GA	4.5
	408157	AA047685	Hs.62946	ESTs	pkinase	4.5
	434303	AW204058		transforming growth factor bet	SS,TM,SSF,FG-GAP,vwa,inte	4.5
5	440745	AW303627	Hs.143301	ESTs		4.5
	419344	U94905	Hs.277445	diacylglycerol kinase, zeta (1	ank,DAGKa,DAGKc,DAG_FE-bi	4.5
	447208	BE315291	Hs.237971	hypothetical protein MGC5627		4.5
	436163	R84938		gb:Y155104.r1 Soares retina N2		4.5
	456856	AK001528	Hs.347285	Homo sapiens, Similar to DiGeo		4.5
10	410817	AI262789	Hs.93659	protein disulfide isomerase re	SS,thioered	4.5
	434558	AW264102	Hs.39168	ESTs	SS,TM,LRRCT,LRR	4.5
	440548	AL117408	Hs.7274	DKFZP434P1750 protein		4.5
	450200	AW975625	Hs.173088	ESTs	zf-UBP,zf-C3HC4	4.5
	432434	AL161977	Hs.2994	PCTAIRE protein kinase 3	SS,pkinase	4.5
	440042	AI073387	Hs.133898	ESTs	SS	4.5
15	454328	AW372097	Hs.278429	hepatocellular carcinoma-assoc		4.5
	458196	AI802408		ubiquitin A-52 residue ribosom	SS,TM,m3,FKBP,TPR	4.5
	433472	AI541246	Hs.3343	phosphoglycerate dehydrogenase	2-Hacid_DH,2-Hacid_DH_C,M	4.5
	408928	AW295827	Hs.255479	hypothetical protein MGC5566	A_deaminase,A_deaminase	4.5
20	448093	AW977382	Hs.15898	2,4-dienoyl CoA reductase 2, p	adh_short,NDK	4.5
	426272	AW450671	Hs.189284	ESTs		4.5
	453610	AW368882	Hs.33818	RecQ protein-like 5	SS,DEAD,helicase_C,SS,DEA	4.5
	441327	AK001706	Hs.7778	hypothetical protein FLJ10751	SS,TM,7tm_1	4.5
	424681	AA054400	Hs.151706	KIAA0134 gene product	helicase_C,PRK,SS,TM,7tm_	4.5
	443443	AI344042	Hs.9347	regulator of G-protein signal	TM,Na_Pi_cotrans	4.5
25	426677	AW949856	Hs.97165	ESTs	SS	4.5
	412482	AA499930	Hs.334885	mitochondrial GTP binding prot	SS	4.4
	425236	AW067800	Hs.155223	stannocalcin 2	Stannocalcin,SS	4.4
	423229	AC003965	Hs.125532	protease, serine, 26	trypsin,SS	4.4
	412338	AA151527	Hs.69485	hypothetical protein FLJ12436	SS,TM,TIG,Sema,PSI	4.4
30	419395	BE268326	Hs.90280	5-aminomidazole-4-carboxamide	AICARFT_IMPCHas,MGS,AICAR	4.4
	442462	AF031405		gb:AF031405 Soares fetal liver		4.4
	439975	AW328081	Hs.6817	inosine triphosphatase (nucleo	Ham1p_like,SS	4.4
	423876	BE502835	Hs.15463	Homo sapiens, clone IMAGE:2959	SS,ethand	4.4
	423220	BE394920	Hs.125262	aladin	WD40,TM,Activin_recpt,ptin	4.4
35	411574	BE242842	Hs.6780	protein tyrosine kinase 9-like	cofilin_ADF,SS,TM	4.4
	448947	BE615408	Hs.337228	ESTs, Weakly similar to AXHU a	SS,TM,lg,pkinase	4.4
	407755	AI151353	Hs.29742	Homo sapiens serine palmitoyl	SS,TM,aminotran_1_2	4.4
	414849	AW372721	Hs.291623	ESTs, Weakly similar to unname	TM,pkinase	4.4
40	458171	AA20016	Hs.192090	ESTs	SS,TM	4.4
	424443	AI751281	Hs.284161	hypothetical protein from EURO	SS,TM,SS,TM	4.4
	427002	AA524093	Hs.23158	ESTs	SS,zf-C2H2	4.4
	404344			C7002191~gij5053028[gb]AAD388	SS,ABC_tran	4.4
	427458	BE208364	Hs.29283	ESTs, Weakly similar to LKHU p	SS,F5_F8_type_C,EGF,TGT	4.4
45	419764	BE262524	Hs.93183	vasodilator-stimulated phospho	WH1	4.4
	446872	X97058	Hs.16362	pyrimidinergic receptor P2Y, G	7tm_1,SS,TM	4.4
	435615	Y15065	Hs.4975	potassium voltage-gated channe	ion_trans,KCNQ1_channel	4.4
	403945			Target Exon		4.3
	435593	R88872	Hs.4964	DKFZP586J1624 protein	Herpes_HEPA,SS	4.3
50	421899	AJ011895	Hs.109281	Nef-associated factor 1	Virus_HS,bZIP,G-gamma,Myo	4.3
	425245	AI751768	Hs.155314	KIAA0095 gene product	SS,TM	4.3
	423348	AA324687		gb:EST27558 Cerebellum II Homo	SS,TM	4.3
	452105	AA022838	Hs.6570	ESTs, Weakly similar to S10889	SS,TM,TBC,rm	4.3
	431934	AB031481	Hs.272214	STG protein	SS	4.3
55	429499	AA453809	Hs.99350	ESTs		4.3
	453485	BE620712	Hs.33026	hypothetical protein PP2447	SS,TM	4.3
	459393	BE409283	Hs.193264	hypothetical protein MGC3234		4.3
	405364			ENSP00000239138":Guanine nucle		4.3
	428345	AI242431	Hs.118282	PAP-1 binding protein	SS,TM	4.3
60	435327	BE301871	Hs.4867	mannosyl (alpha-1,3)-glycopro	SS,HLH,Myc_N_term,Myc-LZ	4.3
	413053	AW963263	Hs.65377	ESTs, Moderately similar to KJ	TM,SS,TM,EF_TS,UBA,transm	4.3
	409983	D50922	Hs.57729	Kelch-like ECH-associated prot	BTB,Kelch,SS,TM	4.3
	409936	AK001691	Hs.57655	hypothetical protein FLJ10829	SS,TM	4.3
	421592	AF003801	Hs.105941	bagpipe homeobox (Drosophila)	homeobox,SS	4.3
65	424251	AA677466	Hs.143696	coactivator-associated arginin	SS,SNF2_N,helicase_C,brom	4.3
	414788	X78342	Hs.77313	cyclin-dependent kinase (CDC2-	pkinase	4.3
	432805	X94630	Hs.3107	CD97 antigen	SS,TM,7tm_2,GPS,EGF,SS,TM	4.3
	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	SS,TM	4.3
	456863	T16837	Hs.4241	ESTs	fusion_gly,homeobox,TM	4.3
70	417823	R88869	Hs.102447	TSC-22-like	PWWP	4.3
	406821	X57809	Hs.181125	immunoglobulin lambda locus	SS	4.3
	431493	AI791493	Hs.129873	ESTs, novel cytochrome P450	SS,p450,SS	4.3
	412958	BE391579	Hs.75087	Fas-activated serine/threonine	SS,pkinase	4.3
	431658	BE409917	Hs.266935	IRNA selenocysteine associated	rm,SS,RCC1	4.3
75	419579	W49529	Hs.296200	hypothetical protein AF053355_	MSP_domain,SS,TM,CUB,NTR	4.3
	410076	T05387	Hs.7991	ESTs	SS	4.2
	406773	AA812424	Hs.76067	heat shock 27kD protein 1	HSP20,SS	4.2
	424709	AL137589	Hs.152149	hypothetical protein DKFZp434K		4.2
	418419	X55039	Hs.85004	centromere protein B (80kD)	CENP-B,HTH_5	4.2
80	447377	X77343	Hs.334334	transcription factor AP-2 alph	TF_AP-2,TF_AP-2	4.2
	416931	D45371	Hs.80485	adipose most abundant gene tra	C1q,Collagen,SS	4.2
	411674	AW861123		gb:RC3-CT0297-120200-014-a05 C	SS	4.2
	419073	AW372170	Hs.183918	Homo sapiens cDNA FLJ12797 tis	SS,lg,isp_1,ZU5,SS,TM,Nuc	4.2
	406887	AA157857	Hs.182265	keratin 19	filament,bZIP,SS,filament	4.2
	432183	AW151952	Hs.46679	hypothetical protein FLJ20739	SS	4.2

5	418910	Z25821	Hs.89466	Homo sapiens, Similar to dodec	ECH,SS,TM,aminotran_3,ABC	4.2
	437300	AL040504	Hs.25063	PRO0461 protein	SS,TM,pkinase,cyclin,F-bo	4.2
	426815	AA400578	Hs.6473	gbzu70a11.1 Soares_testis_NH		4.2
	421453	AA234652	Hs.104555	neuropeptide FF-amide peptide	SS,bZIP,zf-C2H2,bZIP,zf-C	4.2
	409616	AA076248	Hs.147562	gbzm18c10.1 Stratagene pancr		4.2
	444744	BE394732	Hs.147562	ESTs	SS	4.2
	412575	AA113177	Hs.208713	gbzm29e05.s1 Stratagene pancr	TM,ER_lumen_recept	4.2
	429542	AF038660	Hs.348198	UDP-GalbetaGlcNAc beta 1,4- g	Galactosyl_T_2,Ig,SS,TM,A	4.2
10	435995	BE260415	Hs.326422	hypothetical protein FLJ20262		4.2
	451585	AK001171	Hs.144054	hypothetical protein MGC4549	SS,Metallophos	4.2
	456153	AW972270	Hs.274323	ESTs	SS,TM	4.2
	455340	AW901435	Hs.288626	gb:RC0-NN1012-270300-031-a10 N		4.2
	457268	AW272279	Hs.153768	ESTs, Moderately similar to AL		4.2
	432311	BE083080	Hs.337621	similar to sialyltransferase 7	Glyco_transf_29	4.2
15	409656	NM_005133	Hs.72451	RCE1, prenyl protein protease	Abi,SS,CPSase,I_chain,HMG	4.2
	424919	BE314461	Hs.157240	U3 snRNP-associated 55-kDa pr	WD40,SS,KH-domain	4.2
	416528	H65052	Hs.157239	ESTs		4.2
	415137	AI634834	Hs.823	Homo sapiens PAC clone RPS-108		4.2
20	417334	AA337572	Hs.283670	hypothetical protein MGC4737	SS,TM,Jon_trans	4.2
	451920	AA224483	Hs.20996	DKFZP586K0524 protein	SS,TM,SS,TM	4.2
	413049	NM_002151	Hs.107635	hepsin (transmembrane protease	trypsin,SS,TM,ATP1G1_PLM_	4.2
	458988	AW410431	Hs.339751	CGI-119 protein		4.2
	406964	M21305	Hs.274135	FGENES predicted novel secreta		4.2
25	451595	AW965569	Hs.227789	ESTs	SS,WD40	4.2
	449728	AI820751	Hs.31844	ESTs	SS	4.1
	453245	T99801	Hs.155342	ESTs	TM,ABC_tran	4.1
	432238	AL133057	Hs.24951	Homo sapiens mRNA; cDNA DKFZp4	WD40,LRR	4.1
	430037	BE409649	Hs.183232	mitogen-activated protein kina	pkinase	4.1
30	442196	AI902646	Hs.89040	hypothetical protein FLJ12586	SS,SCAN	4.1
	425251	Z22521	Hs.61273	protein kinase C, delta	pkinase,DAG_PE-bind,pkina	4.1
	415014	AW954064	Hs.16695	ESTs		4.1
	440088	BE559877	Hs.182698	hypothetical protein FLJ22638	SS,zf-C3HC4,SPRY,zf-B_box	4.1
	418837	U48263	Hs.182698	preprondocceptin	Opiods_neuropep,SS	4.1
35	410239	AI568350	Hs.71574	hypothetical protein MGC2650	SS,ART,TM	4.1
	446975	BE246446	Hs.182698	ubiquitin-activating enzyme E1	ThIF,UBACT	4.1
	453968	AA847843	Hs.62711	High mobility group (nonhiston	SS,HMG_box	4.1
	448241	AW811064	Hs.7854	gb:MR2-ST0131-211099-008-c06 S	SS	4.1
	441455	AJ271671	Hs.428	zinc/iron regulated transporte	Zip,SS,TM,Cytidyltransf	4.1
40	450848	AI677994	Hs.198269	fms-related tyrosine kinase 3	flk3,Ig,SS,Ribosomal_L13	4.1
	429218	AA225065	Hs.181780	Target CAT	SS,Nop	4.1
	425437	AK000482	Hs.251216	hypothetical protein FLJ20241		4.1
	405613		Hs.5038	Target Exon	SS,pkinase,LRR,LRRCT,Ribo	4.1
	431239	AL039971	Hs.12185	hypothetical protein DKFZp434A	ank,WH2	4.1
45	436057	AJ004832	Hs.207443	neuropathy target esterase	cNMP_binding,SS,TM,cNMP_b	4.1
	415193	AL048891	Hs.279869	hypothetical protein MGC14333	SS,TM,aminotran_1_2,LRR	4.1
	424619	BE387282	Hs.182698	hypothetical protein MGC10848		4.1
	432968	BE614192	Hs.182698	melanoma-associated antigen re	SS,TM,RGS,DIX	4.1
	428156	BE269388	Hs.71574	mitochondrial ribosomal protei	SS	4.1
50	414084	AW168771	Hs.153961	hypothetical protein FLJ14926	SS,P5CR,EF1B0	4.1
	424964	AW161271	Hs.105739	ARPI (actin-related protein 1,	actin,SS	4.1
	431410	AW299534	Hs.111577	ESTs		4.1
	435968	AW161481	Hs.127762	integral membrane protein 3	TM	4.1
	432351	AI270313	Hs.166887	hypothetical protein MGC12982		4.1
55	426120	AA325243	Hs.85658	copine I	C2,SS,aminotran_5	4.1
	416877	BE386266	Hs.165186	hypothetical protein FLJ23436		4.1
	425970	AK001500	Hs.32148	hypothetical protein FLJ13852	SS,P5CR,Epimerase,zf-C2H2	4.1
	434848	BE256304	Hs.16725	AD-015 protein	SS,TM,SS,TM,LRR,P,Peptida	4.1
	458715	AK000973	Hs.164026	hypothetical protein FLJ10111	IBR,zf-C3HC4,SS,TM,IRF,CK	4.1
60	435851	AA700946	Hs.111556	ESTs		4.1
	425538	BE270918	Hs.172673	Homo sapiens, clone IMAGE:3534	SS,SNF2_N,helicase_C,brom	4.1
	444416	AW268085	Hs.11417	hypothetical protein	zf-C3HC4,SpoA,PHD,TM,syna	4.0
	426831	BE296216	Hs.293937	S-adenosylhomocysteine hydrola	AdoHcyase,SS	4.0
	444596	BE560662	Hs.18490	Rab acceptor 1 (prenylated)	SS,TM,Ilg_chan,ANF_recept	4.0
65	439685	AW956781	Hs.237617	ESTs, Weakly similar to FXD2_H	SS,PWWP,TSC22	4.0
	447402	H54520	Hs.166154	hypothetical protein FLJ20452	SS,TM	4.0
	450184	W31096	Hs.239500	Homo sapiens, clone IMAGE:3447	SS	4.0
	426068	AF029778	Hs.166154	Jagged 2	DSL,EGF,wwc,granulin,SS,T	4.0
	459255	AJ493244	Hs.239500	hypothetical protein MGC13114	SS	4.0
70	403182		Hs.24553	Target Exon	SS	4.0
	432078	BE314877	Hs.61460	hypothetical protein FLJ12541	SS,TM	4.0
	459167	BE504370	Hs.286218	ESTs, Weakly similar to CA13_H	SS	4.0
	452747	BE153855	Hs.347349	Ig superfamily receptor LNIR	SS,TM,Ig,HLH	4.0
	444633	AF111713	Hs.144968	junctional adhesion molecule 1	Ig,SS,TM,HLH	4.0
	434171	BE247688	Hs.115803	KIAA0948 protein		4.0
75	422155	AW249152	Hs.18720	strutin (silent mating type In	SIR2,HLH,Myc_N_term,Myc-L	4.0
	433262	AI571225	Hs.324051	KIAA1535 protein	SS,TM,cNMP_binding,Jon_br	4.0
	442599	AF078037	Hs.54558	RelA-associated inhibitor	SH3,ank,SS,TM,HHH,Ig	4.0
	452500	AW373011	Hs.144968	hypothetical protein FLJ22222		4.0
80	437563	AI217204	Hs.115803	ESTs	SS	4.0
	432234	AA531128	Hs.110477	ESTs		4.0
	433135	AA443873	Hs.18720	dolichyl-phosphate mannosyltra	pyr_redox,SS,Ests	4.0
	447495	AW401864	Hs.258519	programmed cell death 8 (apopt	SS	4.0
	452857	BE072814	Hs.285813	ESTs, Moderately similar to S6	SS,TM	4.0
	427834	AA506101	Hs.285813	hypothetical protein FLJ11807		4.0

453446 967533_1 BE299996 BE297115 BE270415 BE295214 BE296526
 454682 1228976_1 AW816029 AW813292 AW816156 AW813333 AW816159 AW813302 AW813344 AW813172
 455035 1249762_1 AW851734 AW851676 AW851693 AW851713 AW851722 AW851616 AW851731 AW851618 AW851648 AW852215
 455340 1283604_1 AW901435 BE094527
 455557 1325974_1 AW995839 AW995907
 455600 1335877_1 BE061053 BE008959 BE008957 BE091618
 455885 1380385_1 BE153524 BE153576 BE153583
 455928 1383899_1 BE170313 BE158339 BE158290
 456573 201205_1 AI279811 AI301071 AI214696 AI279813 AA588460 AA287256 BE171665
 457268 310453_1 AW272279 AA461542 AA460615
 457978 448900_1 AA776638 BE439540
 458196 503719_1 AI802408 AA907424 AI279233 AI302762 N33153 BE045678 AI863332 AW173558 AI302328 Z20793 D25594 BE326823
 459167 92053_1 BE504370 AI243453 AI809556 AI702878 AI702163 AI300626 AW072219 AI369492 AI349587 AW779061 W78149 AA055693 AA974162 AI394380
 AI830098 AW054857 AI870008 AW207658 AW665508 AW300595 AI192992 AW628019 AI274365 AA906922 N92547 AW054727 AW206667
 AIW136707 AW13761
 459271 969257_1 ALD45934 ALD39532 H55631

TABLE 23C:

Key: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495

Strand: Indicates DNA strand from which exons were predicted

NL_position: Indicates nucleotide positions of predicted exons

Key	Ref	Strand	NL_position
400460	8389428	Plus	35559-36295
400607	9887666	Plus	3112-4159
400833	8705148	Minus	187599-188138
400845	9188605	Plus	34428-34612
400923	7637836	Minus	94518-94659
400933	7651935	Minus	105330-105503
401210	7712287	Plus	166969-167133,169760-169877,171563-171733
401264	9797154	Plus	130810-130927,133367-133504
401278	9799936	Plus	98428-98573
401609	7705041	Minus	9877-11997
401674	7689903	Plus	138786-138927,139157-139298,139440-139599,139960-140159
401724	7656694	Plus	150063-150241
402197	8576113	Plus	199466-199585
402365	9454515	Minus	70928-71185
402393	9929688	Plus	19813-20084,20163-20263
402400	9945145	Minus	80123-80322
402632	9931268	Plus	101166-101419
402884	9926562	Plus	47980-48191
402916	7406502	Minus	361-474,541-687
403055	8748904	Minus	109532-110225
403128	7331426	Plus	122894-123018,123134-123283,123372-123695,123779-123940,124059-124256
403182	9838273	Plus	102163-102345,102545-102725
403938	7711795	Plus	48636-48822
403945	7711869	Minus	32141-32263
404036	8567760	Minus	65247-67529,112537-114863
404333	9802821	Minus	137948-138024,138111-138300
404343	9838093	Plus	122664-122931
404344	9838093	Plus	127865-128384
404365	9964977	Plus	50151-50319,50859-51098
404661	9797073	Plus	33374-33675,33769-34008
404757	7706327	Plus	100933-101083,101580-101782
404807	4165210	Minus	124246-124422
405334	3135285	Plus	139386-139856
405346	2981263	Plus	101982-102171
405364	2281075	Minus	48325-48491,49136-49252
405371	2078469	Minus	47657-47766,48461-48596
405594	6960456	Plus	161628-161734,162823-163014,164439-164652
405928	7717155	Minus	2923-3209
406230	4760409	Plus	71716-72515
406244	7417725	Plus	39422-39595
406301	8575868	Plus	57291-57494
406487	7711306	Plus	82039-82902
406495	7711328	Minus	174661-174978
406613	2957168	Plus	5029-5147

Table 24A lists about 117 genes down-regulated in ovarian cancer compared to non-malignant adult ovaries. These were selected as for Table 23A, except that the numerator was set to the 75th percentile amongst various non-malignant ovary specimens, the denominator was set to the 96th percentile value amongst various ovarian cancers, the numerator was greater than or equal to 75 units, and the ratio was greater than or equal to 2.0 (i.e., 2-fold downregulation in tumor vs. normal ovaries).

TABLE 24A:

Key: Unique Eos probeset identifier number

Ex. Accn: Exemplar Accession number, Genbank accession number

UG ID: UniGene number

Title: UniGene gene title

Protein Dom.: Predicted protein domain

R1: Ratio of normal ovaries to tumor

	Pkey	Ex. Accn	UG ID	Title	Protein Dom.	R1
	428232	BE272452	Hs.183109	monoamine oxidase A	Amino_oxidase,pyr_redox,F	16.9
	433563	AF732637	Hs.277901	ESTs	SS	10.8
5	444931	AV652066		general transcription factor I	SS,Glypican	8.7
	451573	AW130351		ESTs	SS	8.3
	429570	BE242256	Hs.2441	KIAA0022 gene product	lectin_c,SS,TM	7.9
	453510	AI699482	Hs.42151	ESTs	SS	7.5
	410295	AA741357		nidogen (enactin)	SS,EGF,Jdl_receptl_b,thyro	6.9
10	438549	BE386801	Hs.21858	trinucleotide repeat containin	SS,serpin,SS,WD40,FYVE	6.5
	407969	AA046217	Hs.105370	ESTs	SS,Pep_M12B_propep,Reprol	6.2
	414541	BE293116	Hs.76392	aldehyde dehydrogenase 1 fami	aldedh	6.0
	448438	BE613081	Hs.24654	Homo sapiens cDNA FLJ11840 fis		5.7
	441422	RA3777	Hs.21364	ESTs	SS,TM	5.1
15	413391	AI223328	Hs.75335	glycine amidinotransferase (L-	Amidinotransf	3.9
	428022	Z39686	Hs.27865	ESTs	SS	3.6
	423044	AA320829	Hs.97266	protocadherin 18		3.6
	416039	AA376999	Hs.78989	alcohol dehydrogenase 5 (class	adh_zinc,HCV_NS4a,TM,adh_	3.5
	452854	AA437061	Hs.14060	prokineticin 1 precursor	SS	3.4
20	436772	AW975688		metallothionein 1E (functional	SS,TM,7tm_2,HRM	3.2
	415162	AF035718	Hs.78061	transcription factor 21	HLH	3.2
	427794	AA709186	Hs.99070	ESTs	SS	3.1
	433072	AI928037	Hs.158832	ESTs	SS	3.1
	418318	U47732	Hs.84072	transmembrane 4 superfamily me	transmembrane4	2.9
25	410059	NM_007038	Hs.58324	a disintegrin-like and metallo	Reprolysin,isp_1,Pep_M12B	2.9
	431933	AI187057	Hs.132554	ESTs	TM,SS,TM	2.9
	420303	AA256282	Hs.278436	KIAA1474 protein		2.8
	438760	M54938		gb:Homo sapiens retinoic acid-		2.8
	427661	AA410292	Hs.104761	ESTs	SS,wnt	2.8
30	437342	AW903297	Hs.236438	hypothetical protein DKFZp761K	Sec7,PH	2.8
	453828	AW970960	Hs.293821	ESTs	SS,Pep_M12B_propep,Reprol	2.7
	418444	AI902899	Hs.85155	butyrate response factor 1 (EG	zf-CCCH,SS	2.7
	453767	AB011792	Hs.35094	extracellular matrix protein 2	wvc,LRR,SS,LRR	2.7
	413624	BE177019	Hs.75445	SPARC-like 1 (mast9, hev9)	kazal,SS,kazal	2.7
35	413305	NM_000426	Hs.323511	Homo sapiens cDNA: FLJ23176 fi	laminin_B,laminin_EGF,Jam	2.7
	414504	AW069181	Hs.115175	sterile-alpha motif and leucin	SS,kinase,SAM	2.7
	439897	NM_015310	Hs.6763	KIAA0942 protein	Sec7,PH	2.7
	421639	NM_012082	Hs.106309	Friend of GATA2	SS	2.7
	442498	U54617	Hs.8364	Homo sapiens pyruvate dehydrog	HATPase_c,HATPase_c	2.6
40	410494	M36564	Hs.64016	protein S (alpha)	EGF,laminin_G,gla	2.6
	452958	AA883929	Hs.40527	ESTs	SS	2.6
	449648	AW205607	Hs.253499	ESTs	SS	2.5
	435519	AI218950	Hs.125461	hypothetical protein FLJ11539	SS	2.5
	433690	AI373949	Hs.279810	hypothetical protein FLJ10493	SS	2.5
45	424319	AW961026	Hs.96752	ESTs, Weakly similar to ALU8_H	SS	2.5
	420174	AI824144	Hs.199749	ESTs		2.5
	421709	AA159394	Hs.107056	CED-6 protein	PID,Herpes_UL6	2.4
	417622	AW298163	Hs.82318	WAS protein family, member 3	WH2	2.4
	453655	AW960427	Hs.342874	transforming growth factor, be	SS,TM,zona_pellucida	2.4
50	408468	AI909712		phosphatidylinositol transfer	SS,PX,PH,PLDc,PH,PLDc,PX	2.4
	400829			C11000244:gi11056030[ref]NP_0	SS,TM,SS,TFIID_30kD	2.3
	453125	AW779544	Hs.115497	hypothetical protein FLJ22655	ras	2.3
	437862	AW978107	Hs.5884	Homo sapiens mRNA; cDNA DKFZp5	HLH	2.3
	425462	AI491852	Hs.46783	Homo sapiens cDNA: FLJ22382 f		2.3
55	417094	NM_006895	Hs.81182	histamine N-methyltransferase	Acyl-CoA_dh	2.3
	403247			Target Exon		2.3
	441916	AA993571		ESTs		2.3
	422746	NM_004484	Hs.119651	glypican 3	Glypican,SS	2.3
60	416777	AF146760	Hs.79844	DKFZP564M1416 protein	SS,GTP_CDC,SS	2.3
	409403	AA668224	Hs.6634	Homo sapiens cDNA: FLJ22547 fi	SS,TM	2.3
	418956	AA234831		KIAA0788 protein	SS	2.3
	410073	AW408163	Hs.58488	catenin (cadherin-associated p	Vinculin,Stathmin	2.3
	419461	AI452601	Hs.288869	nuclear receptor subfamily 2,	hormone_rec,zf-C4,hormone	2.3
	429319	AL023754	Hs.199068	similar to calcium/calmodulin	SS,kinase	2.2
65	452123	AI267615	Hs.38022	ESTs	SS	2.2
	453305	R39224	Hs.267997	EHM2 gene		2.2
	416157	NM_003243	Hs.342874	transforming growth factor, be	zona_pellucida,SS,TM,zona	2.2
	406637	U14966	Hs.180946	ribosomal protein L5	Ribosomal_L18p	2.2
	414466	AA349211	Hs.76205	cytochrome P450, subfamily XIA	p450	2.2
70	408915	NM_016651	Hs.48950	heptacellular carcinoma novel	SS	2.2
	420929	AI694143	Hs.326248	programmed cell death 4	MA3,LRR	2.2
	456972	AI054347	Hs.2017	ribosomal protein L38	SS,TM	2.2
	409549	AB029015	Hs.54886	phospholipase C, epsilon 2	C2,PH,PI-PLC-Y,PI-PLC-X	2.2
	410209	AI583661	Hs.60548	hypothetical protein PRO1635	SS,TM,Fork_head	2.2
	449500	AW956345	Hs.12926	ESTs	SS,TM	2.2
75	447806	W03616	Hs.10432	ESTs, Weakly similar to I38022		2.1
	441712	AW391927	Hs.7946	KIAA1288 protein		2.1
	445025	AI768895	Hs.295727	ESTs, Weakly similar to ALUB_H	SS,BAG,UPF0001	2.1
	444161	N52543	Hs.142940	ESTs	SS	2.1
80	427156	BE621719	Hs.173802	KIAA0603 gene product	SS,TM,TBC	2.1
	436995	AI160015	Hs.125489	ESTs	SS,TM,RasGEF,acfin,RasGEF	2.1
	408443	N33937	Hs.10336	ESTs	SS	2.1
	448274	AI268097	Hs.67317	Homo sapiens cDNA FLJ11775 fis		2.1
	426354	NM_004010	Hs.169470	dystrophin (muscular dystrophy	ZZ,CH,WW,spectrin,bZIP,SS	2.1
	443906	AA348031	Hs.7913	ESTs		2.1

444815	AA151539	Hs.1227	aminolevulinatase, delta-, dehyd	SS,ALAD	2.1
420728	AA767718	Hs.93581	hypothetical protein FLJ10512	SS,TM,Sema,PSI,lg	2.1
404245			NM_007116*	fibrinogen_C,fn3,SS	2.1
436420	AA443966	Hs.31595	ESTs	SS,TM,PMP22_Claudin,SS,TM	2.1
410066	AL117664	Hs.58419	DKFZP586L2024 protein		2.0
414476	AA301867	Hs.76224	EGF-containing fibulin-like ex	EGF,TIL,SS	2.0
424137	AA335769	Hs.16262	ESTs		2.0
447659	AA017472	Hs.107260	hypothetical protein DKFZp586H	SS	2.0
444862	AI209158	Hs.143929	ESTs	SS,TM	2.0
426086	T94907	Hs.188572	ESTs	PH,CH,spectrin	2.0
435080	AI884710	Hs.201645	ESTs	SS,ATP-synt_L_C	2.0
424651	AI493206		ESTs	SS	2.0
432939	AL038924	Hs.279849	KIAA0438 gene product	zf-C3HC4,myosin_head,DIL	2.0
449088	AI654048	Hs.196558	ESTs	SS,MACPF,sushi,ldl_recept	2.0
428642	NM_014899	Hs.10432	KIAA0878 protein	BTB,ras	2.0
419577	L36531	Hs.91296	integrin, alpha 8	TM,integrin_A,FG-GAP	2.0
450435	AI695975	Hs.201805	ESTs	laminin_B,laminin_EGFJam	2.0
450696	AI654223	Hs.16026	hypothetical protein FLJ23191	SS	2.0
421255	BE326214	Hs.93813	ESTs	TM	2.0
432467	T03667	Hs.239388	Human DNA sequence from clone	SS	2.0
408654	BE018882	Hs.46721	UCC1 protein	SS,Ependymin,SS	2.0
412611	AA732036	Hs.164478	hypothetical protein FLJ21939		2.0
453355	AW295374	Hs.31412	myopodin		2.0
424665	AW368576	Hs.139851	caveolin 2	SS,TM,Caveolin,Caveolin	2.0
458147	AW752597		gblcL3-CT0214-161299-045-B06 C	SS,TM,PMM	2.0
447566	N50432	Hs.102648	ESTs		2.0
414496	W73853		ESTs	SS,TM,phkase,F5_F8_type_	2.0
425618	AW119112	Hs.9052	Homo sapiens cDNA: FLJ22042 fl	SS,TM	2.0
415166	NM_003652	Hs.78068	carboxypeptidase Z	Zn_carbOpept,Fz,Dioxygena	2.0
422157	AW57295	Hs.112318	6.2 kd protein	SS	2.0
450253	AL133047	Hs.24715	Homo sapiens mRNA; cDNA DKFZp4	SH3	2.0
418919	AA232635		ESTs	SS,DUF25	2.0
444846	AI871055	Hs.148477	ESTs	SS,TM	2.0
418781	T41160	Hs.8404	ESTs		2.0

TABLE 24B:

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Accession: Genbank accession numbers			
40	Pkey	CAT Number	Accession
	408468	106033_1	AI909712 AL039752 BE000369 AA376876 N75269 AA345398 AA349053 AW960062 R76169 R70638 AA054770 AI378587 AI338002 AI762398 N47873 AI066549 AI474112 AW450680 AA668668 R76114 AW242828 N58855 AW080313 AI378491 AI807102 AA417043 AI555444 AW263286 AW297099
45	410295	11922_2	AA741357 AI870000 W75997 H50726 AV658709 AI498817 AL037804 W67847 BE018553 AI033256 N76810 N31548 AI032084 N36278 AW075272 AI032081 R35753 W93372 AA700790 AI903697 N52985 R82468 AW580252 AL036760 AI052219 R36621 W07047 AA088621 AI249109 W68776 W69374 AA15
	414496	145392_1	W73853 AA928112 W77887 AW889237 AA148524 AI749182 AI754442 AI338392 AI253102 AI079403 AI370541 AI697341 H97538 AW188021 AI927669 W72716 AI051402 AI188071 AI335900 N21488 AW770478 W92522 AI691028 AI913512 AI144448 W73819 AA604358 N28900 W95221 AI868132 H98
50	418919	180623_1	AA232635 AI373703 AA233330
	418956	180862_1	AA234831 AI700302 AA906216 AA776957 R49415 AI420777 AA666394 AI830619 AA779469 AI972390 N40980 AI094453 AA826397 AA535994 AI868257 AI804295 AA897791 AA232893 AI348680 AI356232 AA235138 F31396 AW079977 H16405
55	424651	241981_1	AI493206 AA732315 AA344619 AA904035 AW952967 AA488889 AA635644 BE245127 AA669979 AA761874 H28767 AA910081 AA837086 AA766495 W76175 AI521825 AA746092 AA743152 AI478562 H88863
	436772	426854_1	AW975688 AA731063 N67084
	438780	46501_1	M64936 AI025512 AI382987 BE061777 AA089966 BE169930 T41176 AW594624 BE502415 AA121893 AI269283 T40311 AI684569 AA257011 AI079277 AI241318 BE327710 AW975215 AW896268 AA884990 BE327514
60	441916	528799_1	AA993571 AA971518 AI937262
	444931	62567_1	AV652066 AA459880 T58512 T58561 AI651255 N49838 H87921 AW264447 AA428067 AA364094 AW955685 D62894 AW341452 AA243652 AI984618 AI816803 AI871252 AI376942 AI740496 AA452836 AI277917 AI149141 AA456147 AI784566 AI003975 AI245674 AI433703 AI200208 AI268985 AI38
	451573	875588_1	AW130351 AW338699 AI803973
65	458147	488021_1	AW752597 AW848781 AW849062 AW848490 AW752699 AW752604 AW752700

TABLE 24C:

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495

Strand: Indicates DNA strand from which exons were predicted

Nt_position: Indicates nucleotide positions of predicted exons

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Pkey	Ref	Strand	Nt_position
400829	8570385	Plus	152176-152616
403247	7656833	Minus	76626-77140
404245	7406725	Plus	36019-36282,37073-37813,38946-39314,40355-40651,42738-43028,43391-43696,45698-46030,51110-51415,52779-53072,54648-54935,55201-55509,55926-56240,56355-56672,57078-57401,59966-60262,62600-62926,63363-63686,66693-67025,68180-68497,68909-69232,71372-71695,720

Table 25A provides UnigenelD, UnigenaTitle, Pkey, and Exemplar Accession for sequences in Table 26. The information in Table 25A is linked by SEQ ID NO: to Table 26.

Table 25A:

Pkey: Unique Eos probeset identifier number

Ex. Accon: Exemplar Accession number, Genbank accession number

UG ID: UniGene number

Title: UniGene title

SEQ ID NO: Sequence identification number for sequences in Table 26

	Pkey	Ex. Accon	UG ID	Title	SEQ ID NO
5	452838	U65011	Hs.30743	preferentially expressed antigen in mela	SEQ ID NO: 1-2
	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	SEQ ID NO: 3-4
10	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular mat	SEQ ID NO: 5-6
	458627	AW088642	Hs.97984	SRY (sex determining region Y)-box 17 (S	SEQ ID NO: 7-8
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	SEQ ID NO: 9-10
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savigny]	SEQ ID NO: 11-12
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	SEQ ID NO: 13-22
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	SEQ ID NO: 23-24
15	451110	AI955040	Hs.265398	PAR-6 beta (partitioning defective 6 h	SEQ ID NO: 25-26
	428187	AI687303	Hs.285529	G protein-coupled receptor 49	SEQ ID NO: 27-28
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	SEQ ID NO: 29-30
	433159	AB035898	Hs.150587	kinesin-like protein 2	SEQ ID NO: 31-32
	426427	M86699	Hs.169840	TTK protein kinase	SEQ ID NO: 33-34
20	425371	D49441	Hs.155981	mesothelin	SEQ ID NO: 35-38
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	SEQ ID NO: 39-40
	456546	AI690321	Hs.203845	KCNK15 potassium channel, subfamily K, m	SEQ ID NO: 41-42
	427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor	SEQ ID NO: 43-44
	445537	AA245671	Hs.12844	EGF-like domain, multiple 6	SEQ ID NO: 45-46
25	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic, stratum com	SEQ ID NO: 47-48
	412078	X69699	Hs.73149	paired box gene 8	SEQ ID NO: 49-52
	409178	BE393948	Hs.50915	kallikrein 6	SEQ ID NO: 53-54
	448243	AW369771		integrin, beta 8	SEQ ID NO: 55-56
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	SEQ ID NO: 57-58
30	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	SEQ ID NO: 59-60
	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	SEQ ID NO: 61-62
	416539	AI733881	Hs.72472	BMP-R1B	SEQ ID NO: 63-64
	423961	D13666	Hs.136348	periostin (OSF-2os)	SEQ ID NO: 65-66
	417433	BE270266	Hs.82128	ST4 oncofetal trophoblast glycoprotein	SEQ ID NO: 67-68
35	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	SEQ ID NO: 69-70
	409542	AA503020	Hs.36563	hypothetical protein FLJ22418	SEQ ID NO: 71-72
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	SEQ ID NO: 73-74
	452747	BE153855	Hs.61460	Ig superfamily receptor LNR	SEQ ID NO: 75-76
	450375	AA009647		a disintegrin and metalloproteinase doma	SEQ ID NO: 77-78
40	426215	AW963419	Hs.155223	stanniocalcin 2	SEQ ID NO: 79-80
	430044	AA464510	Hs.152812	ESTs	SEQ ID NO: 81
	447033	AI357412	Hs.157601	ESTs	SEQ ID NO: 82-87
	410418	D31382	Hs.63325	transmembrane protease, serine 4	SEQ ID NO: 88-89
	411274	NM_002776	Hs.69423	kallikrein 10	SEQ ID NO: 90-91
45	422260	AA315933	Hs.105484	regenerating gene type IV	SEQ ID NO: 92-93
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	SEQ ID NO: 94-95
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	SEQ ID NO: 96-97
	404977			Insulin-like growth factor 2 (somatomedi	SEQ ID NO: 98-99
	427747	AW411425	Hs.180655	serine/threonine kinase 12	SEQ ID NO: 100-101
50	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	SEQ ID NO: 102-103
	431846	BE019924	Hs.271580	uroplakin 1B	SEQ ID NO: 104-105
	425465	L18964	Hs.1904	protein kinase C, iota	SEQ ID NO: 106-107
	432938	T27013	Hs.3132	steroidogenic acute regulatory protein	SEQ ID NO: 108-109
	421451	AA291377	Hs.50831	ESTs	SEQ ID NO: 110-117
55	437478	AL390172	Hs.317432	branched chain aminotransferase 1, cytos	SEQ ID NO: 118-119
	411945	AL033527	Hs.92137	L-myo-2 protein (MYCL2)	SEQ ID NO: 120-121
	424078	AB006625	Hs.139033	paternally expressed 3	SEQ ID NO: 122-123
	406400			kallikrein 8 (neurosin/ovasin) (KLK8)	SEQ ID NO: 124-125
60	428450	NM_014791	Hs.184339	KIAA0175 gene product	SEQ ID NO: 126-127
	438167	R28363	Hs.24266	chemokine binding protein 2 (CCBP2), mRN	SEQ ID NO: 128-129
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	SEQ ID NO: 130-131
	430691	C14187	Hs.157208	aristaless-related homeobox protein ARX	SEQ ID NO: 132-133
	408081	AW451597	Hs.167409	intron of basic-helix-loop-helix-PAS pro	SEQ ID NO: 134
65	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	SEQ ID NO: 135-138
	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	SEQ ID NO: 139-140
	428093	AW594506	Hs.104830	ESTs	SEQ ID NO: 141-144
	431630	NM_002204	Hs.265829	Integrin, alpha 3 (antigen CD49C, alpha	SEQ ID NO: 145-148
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospho	SEQ ID NO: 149-150
70	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	SEQ ID NO: 151-152
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (SEQ ID NO: 153-154
	436972	AA284679	Hs.25640	claudin 3	SEQ ID NO: 155-156
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3) (NGAL)	SEQ ID NO: 157-158
	410001	AB041036	Hs.57771	kallikrein 11	SEQ ID NO: 159-160

TABLE 25B:

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

	Pkey	CAT Number	Accession
80	448243	75629_1	AW369771 AW748174 AA290801 AA419198 AA044331 AA127909 AW995442 AA480343 AA044582 AW956159 AA373451 AA127965 AL134913
	450375	83327_1	AW994956 BE622314 BE006298 BE006312 BE006305 BE006317 BE006303 AA043906 AA234175 AA479726
			AA009547 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663874 H04021 H01532
			AA109993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AJ161014 AA099554 R69067

TABLE 25C:

Key: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495

Strand: Indicates DNA strand from which exons were predicted

NL_position: Indicates nucleotide positions of predicted exons

Pkey	Ref	Strand	NL_position
404977	3738341	Minus	43081-43229
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

Table 26

Seq ID NO: 1 DNA sequence

Nucleic Acid Accession #: NM_006115.1

Coding sequence: 236..1765

1	11	21	31	41	51	
GCTTCAGGGT	ACAGCTCCCC	CGCAGCCAGA	AGCCGGGCTC	GCAGCCCTTC	AGCACCGCTC	60
CGGGACACCC	CACCCGCTTC	CCAGGCGTGA	CCTGTCAACA	GCAACTTCGC	GGTGTGGTGA	120
ACTCTCTGAG	GAATAACCAT	TTTGATTATT	ACTCTCAGAC	GTGGGTGGCA	ACAAGTGACT	180
GAGACCTAGA	AATCCAAGCG	TTGGAGGTCC	TGAGGCCAGC	CTAAGTCGCT	TCAAAATGGA	240
ACGAAGGCGT	TTGTGGGGTT	CCATTCAAGG	CCGATACATC	AGCATGAGTG	TGTGGACAAG	300
CCCAAGGAGA	CTTGTGGAGC	TGGCAGGGCA	GAGCGCTGCT	AAGGATGAGG	CCCTGGCCAT	360
TGCGCGCTGT	GAGTTGCTGC	CCAGGGAGCT	CTTCCCGCCA	CTCTTCATGG	CAGCCTTTGA	420
CGGAGAGACG	AGCCAGACCC	TGAAGGCAAT	GGTGCAGGCC	TGGCCCTTCA	CCTGCTCTCC	480
TCTGGGAGTG	CTGATGAAGG	GACAACATCT	TCACCTGGAG	ACCTTCAAAG	CTGTGCTTGA	540
TGGACTTGAT	GTGCTCCTTG	CCCAGGAGGT	TGCGCCCGAG	AGGTGGAAAC	TTCAAGTGCT	600
GGATTTAAGG	AAGAATCTCT	ATCAGGACTT	CTGACTGTGA	TGGTCTGGAA	ACAGGGCCAG	660
TCTGTACTCA	TTTCCAGAGC	CAGAAGCAGC	TCAGCCCATG	ACAAAGAAGC	GAAGAAGTAGA	720
TGGTTTGAGC	ACAGAGGCGAG	AGCAGCCCTT	CATTCCAGTA	GAGGTGCTCG	TAGACCTGTT	780
OCTCAAGGAA	GGTGCCCTGG	ATGAATTGTT	CTCCTACCTC	ATTGAGAAAG	TGAAGCGAAA	840
GAATAATGTA	CTAGCCCTGT	GCTGTAAAGG	GCTGAAGATT	TTTGCAATGC	CCATGCAGGA	900
TATCAAGATG	ATCCTGAATA	TGGTGACGCT	GGACTCTATT	GAAGATTGCG	AAGTGAATCT	960
TACCTGGAAG	CTACCCACCT	TGGGAAATTT	TTCTCCTTAC	CTGGGCCAGA	TGATTAAATCT	1020
GGGTAGACTC	CTCCTCTCCC	ACATCCATGC	ATCTTCTTAC	ATTTCCCGCG	AGAAGGAAGA	1080
GCAGTATATC	GCCCGAGTTCA	CCTCTCAGTT	CCTCAGTCTG	CAGTGCCTGC	AGGCTCTCTA	1140
TGTGGACTCT	TTATTTTTC	TTAGAGGCGG	CCTGGATCAG	TTGCTCAGGC	ACGTGATGAA	1200
CCCTTGGAA	ACCTCTCAA	TAACTAACTG	CCGCTTTTCG	GAAGGGGATG	TGATGCATCT	1260
GTCCACAGAT	CCGACGGTCA	GTGAGTAAAG	TGTCCTGAGT	CTAAGTGGGG	TCATGCTGAC	1320
CGATGTAAGT	CCCGAGCCCC	TCCAAGCTCT	GCTGGAGAGA	GCCTCTGCCA	CCCTCCAGGA	1380
CCGTGCTTTT	GATGAGTGTG	GGATCAGCGA	TGATCAGCTC	CTTGCCCTCC	TGCTTCCCT	1440
GAGCCACTGC	TCCAGCTTCA	CAACCTTAAG	CTTCTACGGG	AATTCATCT	CCATATCTGC	1500
CTTGACAGAT	CTCCTGCAGC	ACCTCATCGG	GCTGAGCAAT	CTGACCCACG	TGCTGTATCC	1560
TGTCCCTCTG	GAGAGTTATG	AGGACATCCA	TGGTACCTCT	CACCTGGAGA	GGCTTGCCCTA	1620
TCTGCATGCC	AGGCTCAGGG	AGTTGCTGTG	TGAGTTGGGG	CGGCCAGAGA	TGGTCTGGCT	1680
TAGTGGCAAC	CCCTGCTCTC	ACTGTGGGGA	CAGAACTTTC	TATGACCCCG	AGCCCATCCT	1740
GTGCCCCCTG	TTATGCTCTA	ACTAGCTGGG	TGCACATATC	AAATGCTTCA	TTCTGCATAC	1800
TTGGACACTA	AAGCCAGAGT	GTGCATGCAT	CTTGAAGCAA	CAAGCAGGCC	ACAGTTTTCG	1860
ACAAATGTTT	AGTGTGAGTG	AGGAAAACAT	GTTCACTGAG	GAATAAACAT	TCAGACAAAT	1920
GTTCACTGAG	GAATAAACAG	GGAAAGTTGG	GATAGGCAGA	TGTTGACTTG	AGGAGTTAAT	1980
GTGATCTTTG	GGGAGATACA	TCTTATAGAG	TTAGAAATAG	AATCTGAATT	TCTAAAGGGA	2040
GATTCTGGCT	TGGGAAGTAC	ATGTAGGAGT	TAACTCCTGT	GTAGACTGTT	GTAAGAAAC	2100
TGTTGAAAT	AAAGAGAAGC	AATGTGAAGC	AAAAAAGAAA	AAAAAAGAAA		

Seq ID NO: 2 Protein sequence

Protein Accession #: NP_006106.1

1	11	21	31	41	51	
MERRRLWGS	QSRYSMSVM	TSPRRLVELA	QSLKDEAL	AIAALELLPR	ELFPFLEMAA	60
FDGRHSQTLK	AMVQAWPFTC	LPLGVLMKQ	HLHLETFAV	LDGLDVLLAQ	EVRPRRWKLQ	120
VLDLRKNSHQ	DFWTVMWGNR	ASLYSFPPEP	AAQPMTKRR	VDGLSTEAQ	PFIPVEVLVD	180
LFLKEGACDB	LFSYLIEKVK	RKNVLRLLCC	KKLKIIPAMP	QDIKMLKRV	QLDSIEDLEV	240
TCTWKLPTLA	KPSPLYGQMI	NLRRLLSHI	HASSYISPEK	EEQYIAQFTS	QFLSLQCLQA	300
LYVDSLFLPL	GRLDQLLRHV	MNPLETSLIT	NCRLESGDVM	HLSQSPSVSQ	LSVLSLGSVM	360
LTDVSPFLQ	ALLERASATL	QDLVDFECGI	TDDQLLALLP	SLSHCSQLTT	LSFYGNISIS	420
SALQSLQLHL	IGLSNLTHVL	YVPFLESYED	IHGTLHLERL	AYLHARLREL	LCELGRPSMV	480
WLSANPCPHC	GDRTFYDPEP	ILCPCFMPN				

Seq ID NO: 3 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 264..782

1	11	21	31	41	51	
CCCTGCTCCA	GTCACACCCG	GAAGCTGACT	GGTCCACGCA	CAGCTGAAGC	ATGAGGAAAC	60
TCATCGCGGG	ACTAATTTTC	CITAAAATTT	AGACTTGCAC	AGTAAGGACT	TCAACTGACC	120
TTCTCTCAGC	TGAGAACTGT	TTCCAGTATA	TACATCAAGT	CAGTGAAGAT	TCCAGCACCC	180
TGCCGGTGGC	ACTACTGAGA	GACGAGGTGC	CAGGGTGGTT	CCTGAAAGTG	CCTGAGCCCC	240
AACTTATCAG	CAAGGAGCTC	ATCATGCTGA	CAGAACTCAT	GGAGGTCTGG	CATGGCTTAG	300
TGATCGCGGT	GGTGTCCCTC	TTCTGTCAGG	CCTGCTTCTC	CACCGCCATC	AACTACCTGC	360
TCAGCAGGCA	CATGGCCAC	AAGAGTGAAC	AGATACTGAA	AGCGGCGAGT	CTCCAGGTTC	420
CCAGGCCAG	CCCTGGCCAC	CATCATCCAC	CTGCTGTCAA	AGAGATGAAG	GAGACTCAGA	480
CAGAGAGAGA	CATCCCAATG	TCTGATTCCC	TTTACAGGCA	TGACAGGAC	ACACCTCAG	540

ATAGCTTGGG TAGCTCTGCG AGTTCGGCTC CTGCGCTGCC GGCCACAGAG GATGTGGATT 600
 ACACACAAAT CGTCTTTTCT GACCTGGGAG AACTAAAAAA TGACTCCCCG CTGGACTATG 660
 AGAACATAAA GGAATACACA GATTATGTCA ATGTCAATCC AGAAGACAC AAGCCCAATT 720
 TCTGGTATTT TGTCAACCCCT GCTCTGTCTG AGCCAGCGGA ATATGATCAA GTGGCCATGT 780
 GAATTCACAA TATTTTAAAT GGGGTCCAGT TCTCTATGGA TTCTACAT TAATTGTAG 840
 GGAATGCCA TTTTCCCCC TTAACAAGG CATGGGGCTC ACAAGTCTAT GGAGACAGGC 900
 CAAAAGAAT GTGGAGAAGA AAACGTATAA ATACACAGAG GTCCCTCAAG CCCATGGACT 960
 CCTGGTCTGT ACCCAAAAA GCTGTTCTGT CCTCAAAAC AAAACAAGG CTTGGCTGGG 1020
 AAAACAGGCC AATGCCCCGG CAAGAAAGGT TGAGATCAGA TGTAGGAAG AACTTTCAGG 1080
 TAAAGTATGA GAATCATGGA GTCCATCAGC AGAGATAGTA GTGAAGTCTC TCCCAGGGA 1140
 AAATTTTAAA AAGGTGAAT CAGCTGTTGT AGAGTTCTAT TTGGCAATCT CATGGTAAA 1200
 TGACTTCCCT TTGAGTCTTT TAATTATTGG CAATAACAA CTCTTTTAAA AGTTTAAAT 1260
 AAAATAGCAA CCACACCA

Seq ID NO: 4 Protein sequence
 Protein Accession #: Eos sequence
 1 11 21 31 41 51
 MLTEVMEVWH GLVIAVVSFL LQACFLTAI YLLSRHMAHK SEQILKAASL QVPRPSPGHH 60
 HPPAVKEMKE TQTRDIPMS DSLYRHSDT PSDSLDSSCS SPPACQATED VDYTVVPSD 120
 PGEIKNDSP L DYENIKEITD YVNVNPERHK PSFNYFVNPA LSEPAEYDQV AM

Seq ID NO: 5 DNA sequence
 Nucleic Acid Accession #: AB051390.
 Coding sequence: 34..2457
 1 11 21 31 41 51
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 CTGAGCCGGA CTCGGCACT CTGCGCCCTG GCGCTGCCCG TGCGCGCGCG GCTGGCCCTC 120
 TCGAGCAGGA CCCTGACAAA AGTGCCCAAG TCAGAGGGCT ACTGCAGCGG TATCCTGCGC 180
 GCCCAGGGCA GCGCGCGCA GGGCTACACC GAGTTCAGCC TCGCGCTGGA GGGGACCCCG 240
 GACTTCTACA AGCGCGGAAC CAGCTACCGC GTAACACTTT CAGCTGCTCC TCCCTCCTAC 300
 TTCAGAGGAT TCACATTATAT TGCCCTCAGA GAGAACAGAG AGGGTGATAA GGAAGAAGAC 360
 CATCTGGGA CCTCTCAGAT CATAGAGCAA GAAGAAACTC AGTTTATGAG CAATTGCCCC 420
 GTTGCACTCA CTGAAGCAC TCCACGAGG AGGACCCGGA TCCAGGTGTT TTGGATAGCA 480
 CCACAGCGCG GACGAGCTG CGTGATCTG AAGGCCAGCA TCGTACAAAA ACGCATTATT 540
 TATTTTCAAG ATGAGGGCTC TCTGACCAAG AAACCTTTGT AACAGATTG CACATTGTAT 600
 GGGGTGACTG ACACACCCAT CTAGACTGCG TGTGCTTCG GAACTGCCAA GTACAGACTC 660
 ACATTTTATG GGAATTTGTT CGAGAAGACA CACCCAAAGG ATTACCTCG TCGGGCCAAC 720
 CACTGGTCTG CGATCATCGG AGGATCCAC TCCAAAGATT ATGTACTGTG GGAATATGGA 780
 GGATATGCCA GCGAAGCGGT CAAACAAATT GCAGAAATGG GCTCACCCGT GAAATGGAG 840
 GAAGAAATTC GACACACAGG TGATGAGGTC CTCACCGTCA TCAAGCCAA AGCCCAATGG 900
 CCAGCCTGGC AGCCTCTCAA CGTGAGAGCA GCACCTTCAG CTGAATTTTC CGTGGACAGA 960
 ACGCGCCATT TAATGTCTTT CCTGACCATG ATGGGCCCCA GTCCCGACTG GAACGTAGGC 1020
 TTATCTGCGA AAGATCTGTG CACCAAGGAA TGTGGCTGGG TCCAGAGGT GGTGCAAGAC 1080
 CTGATTCCTT GGGACGCTGG CACCGACAGC GGGGTGACCT ATGAGTCACC CAACAAACCC 1140
 ACCATTCCCC AGGAGAAAT CCGGCCCTCG ACCAGCCTGG ACCATCTCA GAGTCTTTTC 1200
 TATGACCCAG AGGGTGGGTC CATCACTCAA GTAGCCAGAG TTGTATCGA GAGATCGCA 1260
 CGGAAGGGTG AACAAATGCA TATTGTACT GACAAATGTC ATGATATTGT AGCTGACCTG 1320
 GCTCCAGAAG AGAAAGATGA AGATGACACC CCTGAAACCT GCATCTACTC CAATCTGTCC 1380
 CCATGTTCCG CAGTCTCTCC CTCCACCTGT GACAAAGGCA AGAGGATGCG ACAGCGCATG 1440
 CTGAAGACAC AGCTGGACCT CAGGTCCCC TGCCCTGACA CCCAGGACTT CCAGCCCTGC 1500
 ATGGGCCCTG GCTGCACTGA CAAAGACGGC TCCACCTGCA CCATGTCCGA GTGGATCACC 1560
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 GTCAACGAGG AGTCTCTCTC CAGCAGCTGC CTGATGACCG AGTGGGGCGA GTGGGACGAG 1740
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 GCAGATGGCT CCAATGTCCA AGCCGAGACA TCACAGGCAG AGAAGTGAT GATGCCAGAG 1860
 TGCCACACCA TCCCATGCTT GCTGTCCCCA TGGTCCGAGT GGAGTGACTG CAGCGTGACC 1920
 TGCGGGAGAG GCATGCGAAC CGACAGCGG ATGCTCAAGT CTCTGGCAGA ACTTGGAGAC 1980
 TGCAATGAGG ATCTGGAGCA GGTGGAGAA TGCAATGCTC CTGAATGCC CATTGACTGT 2040
 GAGCTCACCG AGTGGTCCCA GTGGTGGGAA TGTAACAAGT CATGTGGGAA AGGCCACGTG 2100
 ATTGCAACCC GGATGATCCA AATGAGGCT CAGTTTGGAG GTGCACCTG CCCAGAGACT 2160
 GTGCAGCGAA AAAAGTGCCG CATCGAAAA TGCCCTTGAA ATCCATCCAT CCAAAAGCTA 2220
 CGCTGGAGGG AGGCCCGAGA GAGCGGGCG AGTGAGCAGC TGAAGGAAGA GTCTGAAGGG 2280
 GAGCAGTTCC CAGGTGTAG GATGCGCCCA TGGACGGCCT GGTGAGAAAT CACCAAACTG 2340
 TGCGGAGGTG GAATTCAGGA ACGTTACATG ACTGTAAAGA AGAGATTCAA AAGCTCCAG 2400
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 GGGTACGAGT TCCCGAGGCG TGCACTCTAG ATTCCAGAGT CACCAATGGC TGGATTATTT 2520
 GCTTGTTTAA GACAATTTAA ATTGTGTAAG CTAGTTTCA TTTTTCAGT GTGGTTGCGC 2580
 CAGTAGTCTT GTGGATGCCA GAGACATCCT TTCTGAATAC TTCTTGATGG GTACAGGCTG 2640
 AGTGGGGCGC CCTCACCTCC AGCCAGCCTC TTCTGCGAGA GGAGTAGTGT CAGCCACCTT 2700
 GTACTAAGCT GAAACATGTC CCTCTGGAGC TTCCACCTGG CCAGGGAGGA CGAGACTTT 2760
 GACCTACTCC ACATGAGAG GCAACCATGT CTGGAAGTGA CTATGCTGTA GTCCAGGGT 2820
 GCGGCAGGTA GGAACATTC ACAGATGAAG ACAGCAGATT CCCCACATTC TCATCTTTGG 2880
 CCTGTTCAAT GAAACCATTT TTTGCCATC TCTTCTTAGT GGAACCTTAG GTCTCTTTTC 2940
 AAGTCTCTCT AGTCAATCAAT AGTTCCTGGG GAAAAACAGA GCTGGTAGAC TTGAAGAGGA 3000
 GCATTGATGT TGGGTGGCTT TTGTTCTTTC ACTGAGAAAT TCGGAATACA TTTGTCTCAC 3060
 CCCTGATATT GGTCTCTGAT GCGCCCCCAA CAAAATAAAA TAAATAAATT ATGGCTGCTT 3120
 TATTTAAATA TAAGTAGTGT AGTTTATACA CCTGAGATAA ATAATAAGCT TAGAGTGTAT 3180
 TTTTCCCTTG CTTTGGGGG TTCAGAGGAG TATGTACAAT TCTTCTGGGA AGCCAGCCTT 3240
 CTGAACCTTT TGGTACTAAA TCCATTATGG AACCAAGACA AAGGAAGCAA AATGGTCTC 3300
 TTTAGACACC AATTGGCTTA AATTTTAAAA TCTTCTTACA CACATCTAGA CGTCTAAGTT 3360
 TGCAATCAG TTTTATGCAA GAAACATTT TTGCTATACA AACATTTTGC TAAGTCTGCC 3420
 CAAAGCCCCC CCAATGCATT CCTTCAACAA AATACATCT CTGTACTTTA AAGTTATTTT 3480

AGTCATGAAA TTTTATATGC AGAGAGAAAA AGTTACCGAG ACAGAAAAACA AATCTAAGGG 3540
 AAAGGAATAT TATGGGATTA AGCTGAGCAA GCAATTCCTG TGGAAAGTCA AACCTGTGAG 3600
 TGCTCCACAC CAGGGCTGTG GTCCCTCCAG ACATGCTATG GAATGGCCAC AGGTTTACAC 3660
 TGCTTCCCA GCAATTATAA GCACACCAGA TTCAGGGAGA CTGACCACCA AGGGATAGTG 3720
 TAAAGGACA TTTTCTCAGT TGGGTCCATC AGCAGTTTCT CTCTCTGCAT TTATTGTGTA 3780
 AACTATTGT TTTCTTCTT CTTTATATAG CTTTATTACT GCTTAATCCA AATGTGTACC 3840
 ATTGGTGAGA CACATACAAT GCTCTGAATA CACTACGAAT TTGTATTAAA CACATCAGAA 3900
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 TCAATAAAAA CTCACCTGGT CTTTCATGTC TTTAAGCTAA GTAAGTGTTC AGAAGGTTCT 4020
 TTTTATATT GTCCCTCACC TCCATCATTT TCAATAAAG ATAGGGCTTT TGCTCCCTTG 4080
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 CTTAAATGAA TTGCTTTCTC CCAAAAAAAG CACAATATAA AGAAACACAA GATTTAATTA 4200
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 CTAAGCTATC TATCTAACTC TCAGCCCATG ATAAAGTTCC TTAAGCTGGT GATTCTTAAT 4320
 CAAGGACAAG CCACCTTAGT GTCTCATGTT TGTATTGGT CCCAGTTGGG TACATTTTAA 4380
 AATCCTGATT TTGGAGACTT AAAACCCAGT TAATGGCTAA GAATGGGTAA CATGACTCTT 4440
 GTTGGATTGT TATTTTGTG TTGCAATGGG GAATTTATAA GAAGCATCAA GTCTCTTCTT 4500
 TACCAAGATC TTGTAGGAGT GTTTATAGTT CTTTGGCTAA ACAAATCATT TTGGAATAA 4560
 AGATTTTTTA CTACAAAAAT G

Seq ID NO: 6 Protein sequence

Protein Accession #: BAB18461

1 11 21 31 41 51
 MRLSPAPLKL SRTALLALA LPLAALAFS DETLDKVPKS EGYCSRILRA QGTRREGYTE 60
 PSRLVEGDDP FYKPGTSYRV TLSAAPPSTYF RGTLLIALRE NREGDKEDDH AGTFQIIDE 120
 ETQPMNSCPV AVTESTPRRR TRIQVFWIAP PAGTGCVILK ASIVQKRIIY PQDEGSLTKK 180
 LCBQDSTFDG VTDKPIIDCC AGCTAKYRLT FYGNWSEKTH PKDYPRRANH WSAITGGSHS 240
 KNYVLWYEGG YASEGVKQVA ELGSPVKMEB EIRQSDSEVL TVIKAKAQWP AMQPLNVR 300
 PSAEFSVDRT RHLMSFLTMM GPSPDWNVGL SAEDLCTKEC GWVQKVVDL IPWDAGTDSG 360
 VTYESPKNPT IQEKIRPLT SLDHQPSPFY DPEGGSITOV ARVVIERLAR KGEQCNIVPD 420
 NVDDIVADLA PEEKDEDDTP ETCIYSNWSF WSACSSSTCD KGRMRQRML KAQLDLSVPC 480
 PDTQDPQPCN GPGCSDEEDGS TCTMSEMITW SPCISCSGNG MRSRERYVKQ FPDGGSVCTL 540
 PTEETKCTV NEECSPSSCL MTEWGEWDEC SATCGMGKK RHRMIKNPA DGSMDCAETS 600
 QAEKMMPEC HTIPCLSPW SEWSDCSVTC GKGMRTRQRM LKSLAEGLDC NEDLEQVEKC 660
 MLPECPIDCE LTWESQWSEC NKSCGKGHVI RTRMIQMEPQ FGGAPCPETV QRKCRIRKC 720
 LRNPSTQKLR WREARESRRS EQLKEESEGE QFPGCRMWPH TAWSECTKLC GGGIQERYMT 780
 VKRPFSSQF TSCKDKKIR ACNVHPC

Seq ID NO: 7 DNA sequence

Nucleic Acid Accession #: NM_022454

Coding sequence: 205..1449

1 11 21 31 41 51
 GCAGTGTAC TAGGCGGCT GGGGGCCCTG GGTACGCTGT AGACCAGACC GGCACAGGCC 60
 AGAACACGGG CGGCGGCTTC GGGCGGGGAG ACCCGGCGAG CCTCGGGGCT ATCTCAGTGC 120
 CTCATTCCCC ACCCCCTCCC CCGGGTCGGG GGAGGCGCGG CGTCCGGCGG AGGGTTGAGG 180
 GGAGCGGGGC AGGCGCTGGG CGCCATGAGC AGCCCGGATG CGGGATACGC CAGTGACGAC 240
 CAGAGCCAGA CCCAGAGCGC GCTGCCCGCG GTGATGGCGG GGCTGGGCCC CTGCCCCCTG 300
 GCGAGTGC GAGAGCCCAT CGGGGACATG AAGGTGAAGG GCGAGGCGCC GCGCAACAGC 360
 GGAGCACCGG CGGCGGCGCG GGGCGGAGCT AAGGGCGAGT CCGGTATCCG GCGGCGGATG 420
 AACGCTTTCA TGGTGTGGG TAAGGACGAG CGCAAGCGGC TGGCGCAGCA GAATCCAGAC 480
 CTGCACAACG CCGAGTTGAG CAAGATGCTG GGCAAGTCTT GGAAGGCGCT GACGCTGGCG 540
 GAGAGCGCGC GCTTCGTGGA GGAGGCGAG CGGTGCGCGG TGCAGCATAT GCAGGACACC 600
 CCCAACTACA AGTACCGGCC CGGCGGCGCG AAGCAGGTGA AGCGGTGGA GCGGGTGGAG 660
 GCGGCTTCTC TGACGCGGCT GGCTGAGCGG CAGGCGGCGG CGCTGGGCCC CGAGGGCGGC 720
 CGGTGGGCA TGGAGCGGCT GGGCTCCAG TTCCCGGAGC AGGGCTTCCC CGCGGCGCGG 780
 CCGCTGCTGC CTCGCGCAT GGGCGGCCAC TACCGGACT GCCAGAGTCT GGGCGGCGCT 840
 CGGTGAGCG GCTACCGGTT GCCACGCCC GACAGTCCC CGCTGGACGG CGTGAGACCC 900
 GACCGGCTT TCTTCGCGC CCGATGCCC GGGAGTCCC CGGCGGCGG CACCTACAGC 960
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Seq ID NO: 8 Protein sequence

Protein Accession #: NP_071899

1 11 21 31 41 51
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 LQFPEQGFFA GPPLLPFHMG GHYRDCQSLG APPLDGYPLP TPDTSPLDGV DFDPAFFAAP 240
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GSPGAGGGRG PQMQPQHQHQ HQHQHHPGP GQSPFPPEAL PCRDGTDPSQ PAELLGEVDR 360
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Seq ID NO: 9 DNA sequence
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Seq ID NO: 10 Protein sequence
Protein Accession #: Q9H8V3

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 10 VTLLFPNDCL EIARKRHKVI GTFRSPHQGT RPPASLKHII LMPLSQIKKV LDIRETEDCH 720
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Seq ID NO: 11 DNA sequence
 Nucleic Acid Accession #: XM_044166
 Coding sequence: 1..1576

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Seq ID NO: 12 Protein sequence
 Protein Accession #: XP_044166

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 85 ALYKEAELRL KGSSNTTECV PVPTSEHVAE IVGRQGGKIK ALRAKNTNTYI KTPVRGEEPV 180
 FMVTGRREDV ATARRBIISA AEHPSMIRAS RNKSGAAGFV APALPGQVTI RVRVPYRVVG 240

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 KARAGPPGAH RSPATSAGPE LAGLPRRPPG EPLQSPSKLG GGGLRSPGGG RDCMVCFESE 480
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Seq ID NO: 13 DNA sequence
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Seq ID NO: 14 Protein sequence
 Protein Accession #: Bos sequence

1 11 21 31 41 51
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 MMALTFTIYI GCGLSIFLS VTLVTYIAFE KIRRDYPSKI LIQLCAALL LNLVFLDLSW 660
 IALYKMGGLC ISVAVFLHYF LLVSPTMGL EAFHMYLALV KVPNTYIRKY ILKFCIVGNG 720
 VPVVVITIL TISFDNYGLG SYGKFPNGSP DDFCWINNNA VFYITVGVY CVIFLLNVSM 780
 FIVVLQLCR IKKKQLGAG RKTSLQDLRS IAGLTFLGI TWGPAFFANG FVNVTFMYLE 840
 AIFNTLQGFY IFIFYCVAIG NVRKQWRRYL CCGKRLAEN SDWSKTATNG LKQTVNQGV 900
 SSSNSLQSS SNSTNSTILL VNNDCSVHAS GNGNASTERN GVSPSVQNGD VCLHDFTRGQ 960
 RMFNEKEDSC NGKGRMALRR TSKRGLHPI EQM

Seq ID NO: 15 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..2904

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	TTC	AAGATAT	TCCTTGTCT	CATTGTGCTT	CATGTGCTTC	TGGTAACATC	CCTGGAAGAA 120
	GAT	ACTGATA	ATTCAGTTT	GTCAACACCA	CCTGAGTTTA	CTTTAAGCTT	ACTCCCTTCA 180
	AAC	GAAACAG	AAAAAATCA	AATCACTATA	GTAATAACCT	TCATGCTTC	AGGCTGCAAA 240
	CCC	CAGAGAA	ATATCTGCAA	TTTGTCTCT	ATTGCAATG	ACTCAGCATT	TTTTAGAGGT 300
10	GAG	ATCATGT	TTCAATATGA	TAAAGAAAGC	ACTGTTCCCT	AGAATCAACA	TATAACGAAT 360
	GGC	ACCTTAA	CTGGAGTCT	GTCTCTAAGT	GAATTAACA	CATTAAATTG	TACATTCACA 420
	ATA	AAACTGA	ATAATACAAT	GAATGCATGT	GCTGTAATAG	CTGCTTTGGA	AAGAGTAAAG 480
	ATT	CGACCAA	TGGAACACTG	CTGCTGTTCT	GTCAAGATAC	CCTGCCCTTC	CTCCCAAGAA 540
	GAG	TGGAAA	AGCTTCAGTG	TGACCTGCAG	GATCCCATTG	TCTGTCTTGC	TGACCATCCA 600
15	CGT	GGCCAC	CATTTCCTC	CAGCCAATCC	ATCCCACTGG	TGCTCGGGC	CAGTGTGCTT 660
	TCC	CAGGTCC	CCAAAGCTAC	CTCTTTGCT	GAGCCTCCAG	ATTATTCACC	TGTGACCCAC 720
	AAT	GTTCCCT	CTCCCAATAG	GGAGATTCAA	CCCCCTTCAC	CCCAGCCTTC	AGCTCCCATTA 780
	GCT	CCAGCC	CTGCCATTGC	CATGCCCCCA	CAGTCTGAAA	GGATCTCTTC	CCCTATGCCC 840
	CAA	ACCATG	TCTCGGCAC	CCCACCTCT	GTGAAAGCCT	CATTTTCTCT	TCCCACCGTG 900
20	TCT	GCCCTG	CGAATGTCAA	CACTACCAGC	GCACCTCCTG	TCCAGACAGA	CATCGTCAAC 960
	ACC	CAGTA	TTCCTGATCT	TGAGAACCAG	GTGTTGCAGA	TGGAGAAGGC	TCTGTCTTGT 1020
	GGC	AGCCTG	AGCCTAACCT	CGCAGGAGAA	ATGATCAACC	AAGTCAGCAG	ACTCCTTCAT 1080
	TCC	CGCCTG	ACATGCTAG	CCCTCTGGCT	CAAAGATTGC	TGAAAGTAGT	GGATGACATT 1140
	GGC	CTACAG	TGAACCTTTC	AAACACGACT	ATAAGTCTAA	CCTCCCTTTC	TTTGGCTCTG 1200
25	GCT	GTGATCA	GAGTGAATGC	CAGTAGTTTC	AACACAATA	CCTTGTGTCG	CCAAGACCTT 1260
	GCA	AATCTTC	AGGTTTCTCT	GGAAACCCAA	GCTCCTGAGA	ACAGTATTGG	CACAATTACT 1320
	CTT	CCTTCAT	CGCTGATGAA	TAATTTACCA	GCTCATGACA	TGGAGCTAGC	TTCCAGGGTT 1380
	CAG	TTCAATT	TTTTGAAAC	ACCTGCTTTG	TTTCAGGATC	CTTCCCTGGA	GAACCTCTCT 1440
30	CTG	ATCAGCT	ACGTCAATTC	ATCGAGTGT	GCAAACTGAA	CGTCAAGGAA	CTTGACNAGA 1500
	AAC	GTGACAG	TCACATTAAA	GCACATCAAC	CCGAGCCAGG	ATGAGTTAAC	AGTGAGATGT 1560
	GT	ATTGTTGG	ACTTGGGAC	AAATGGTGGC	AGAGGAGGCT	GCTCAGACAA	TGGCTGCTCT 1620
	GT	CAAGACA	GGAGATTGAA	TGAAACCATC	TGTACCTGTA	GCCATCTAAC	AAGCTTCGGC 1680
	GTT	CTGCTG	ACCTATCTAG	GACATCTGTG	CTGCTGCTC	AAATGATGGC	CTGACGTTTC 1740
	ATT	ACATATA	TGGTGTGGG	GCITTCATCA	ATTTTCTGT	CAGTGACTCT	TGTAACCTAC 1800
35	AT	AGCTTTTG	AAAAGATCCG	GAGGGATTAC	CCTTCCAAAA	TCTCATCCA	GCTGTGTGCT 1860
	GCT	CTGCTTC	TGCTGAACCT	GGTCTTCCTC	CTGGACTCGT	GGATTGCTCT	GTATAAGATG 1920
	CA	AGGCTCT	GCATCTCAGT	GGCTGTATT	CTTCATTATT	TCTCTTGGT	CTCAATTCACA 1980
	TG	GATGGGCC	TAGAAGCAAT	CCATATGTAC	CTGGCCCTTG	TCAAAGTATT	TAATACTTCT 2040
	AT	CGGAAAT	ACATCTCTAA	ATTCTGCATT	GTCGGTTGGG	GGGTACCAGC	TGTGGTTGTG 2100
40	ACC	ATCATCC	TGACTATATC	CCCAGATAAC	TATGGGCTTG	GATCCTATGG	GAATTCCTCC 2160
	AAT	GGTTAC	CGGATGACTT	CTGCTGGATC	AACAACAATG	CAGTATTCTA	CATTACGGTG 2220
	GT	GAGATATT	TCTGTGTGAT	ATTTTGTCTG	AACGTCAGCA	TGTTCAATGT	GGTCCCTGGT 2280
	CAG	CTCTGT	GAATTAAGAA	GAAGAAGCAA	CTGGGAGCCC	AGCGAAAAAC	CAGTATTCAA 2340
	GAC	CTCAGGA	GTATCGCTGG	CCITACATTT	TACTTGGGAA	TAACTTGGGG	CTTTGCCCTC 2400
45	TT	TGCTGGG	GACCAGTTAA	CGTGACCTTC	ATGTATCTGT	TGCCATCTT	TAATACCTTA 2460
	CA	AGGATTTT	TCATATTACT	CTTTTACTGT	GTGGCCAAAG	AAAATGTCAG	GAAGCAATGG 2520
	AG	GCGGTATC	TTTGTGTGG	AAAGTTACGG	CTGGCTGAAA	ATTCTGACTG	GAGTAAAACT 2580
	G	CTACTAATG	GTTTAAAGAA	GCAGACTGTA	AACCAAGGAG	TGTCCAGCTC	TTCAAATTC 2640
	TT	CAGTCAA	CGAGTAATCG	CACATACTCC	ACCACACTGC	TAGTGAATAA	TGATTGCTCA 2700
50	GT	ACACGCAA	GCGGGAATGG	AAATGCTTCT	ACAGAGAGGA	ATGGGCTCTC	TTTTAGTGTT 2760
	C	AGATGGAG	ATGTGTGCTC	TCACGATTTT	ACTGGAATAA	AGCACATGTT	TAACGAGAAG 2820
	GA	AGATTCTCT	GCAATGGGAA	AGGCCGTATG	GCTCTCAGAA	GGACTTCAAA	GCGGGGAAGC 2880
	TT	CACTTTA	TTGAGCAAA	GTGA			

Seq ID NO: 16 Protein sequence

Protein Accession #: Eos sequence

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55	MV	FSVRQCGH	VGRTEEVLLT	FKIFLVIICL	HVVLVTSLEE	DTDNSSLSP	PDVTLSSLPS 60
60	NET	EKTKITI	VKTENASGVK	PQRNICNLSS	ICNDSAFFRG	EIMFQYDKES	TVPQNQHITN 120
	GT	LTVGLSL	ELWTLNCTFT	IKLNTMNAAC	AVIAALERVK	IRPMEHCCCS	VRIPCPSPE 180
	ELE	KLQCDLQ	DPIVCLADHP	RGPPFSSSQS	IPVVPRAITV	SQVPKATSPA	EPPDYSPVTH 240
	NVP	SPIGEIQ	PLSPQPSAPI	ASSPAIDMPP	QSETISSPMP	QTHVSGTTPP	VKASFSSPTV 300
65	SAP	ANVNTTS	APPVQTDIVN	TSSISDLENQ	VLQMEKALS	GSLEPNLAGE	MINQVSRLLH 360
	SPP	DMLAPLA	QRLKVVDDI	GLQLNFSNTT	ISLTSPLSAL	AVIRVNASSF	NTTTFVAQDP 420
	AN	LQVSLQ	APENSIGTIT	LPSSIMMNL	AHDMELASRV	QNFFFETPAL	QDPSLENLS 480
	LIS	VYISSV	ANLTVRNLTR	NVTVLKHIN	PSQDELTVRC	VFMDLGRNGG	RGWSNDNGCS 540
	V	KDRRLNETI	CTCSHLTSFG	VLLDLSRTSV	LPAQMMLT	ITYIGCOLSS	IFLSVTLVTY 600
70	I	APKIRRDY	PSKILQLCLA	ALLLLNLVFL	LDSWIALYKM	QGLCISVAVF	LHYFLLVSP 660
	WM	GLEAFHMY	LALVKVNTY	IRKYILKPCI	VGWGVPAVVV	TIILTIISPDN	YGLSGYKQFP 720
	NG	SPDDPCMI	NNNAVFIYIV	VGYPFVIFLL	NVSMFIVLV	QLCRIKKKKQ	LGAQRKTSIQ 780
	DL	RSIAGLTF	LLGITWGFAP	PAMGPVNVTF	MYLPAIFNTL	QGFFIFIFYC	VAKENVKQW 840
	RR	YLCCGKLR	LAENSWSKT	ATNGLKKQTV	NQGVSSSSNS	LQSSSNSTNS	TTLVNNDCS 900
75	V	HASGNGNAS	TERNGVSFSV	QNGDVCLHDF	TGKQHMFPNEK	EDSCNGKGRM	ALRRTSKRGS 960
	L	HFIQ					

Seq ID NO: 17 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..2811

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	GAT	ACTGATA	ATTCAGTTT	GTCAACACCA	CCTGAGGTG	AAACAACAAG	CCTCAATGAT 180
85	GTT	ACTTTAA	GCTTACTCCC	TTCAAACGAA	ACAGCGCTCA	AACCCACAG	AAATATCTGC 240

5	AATTGTGTCAT	CTATTTGCAA	TGACTCAGCA	TTTTTTAGAG	GTGAGATCAT	GTTTCAATAT	300
	GATAAAGAAA	GCACGTGTCC	CCAGAATCAA	CATATAACGA	ATGGCACCTT	AACTGGAGTC	360
	CTGTCTCTAA	GTGAATTAAG	ACGCTCAGAG	CTCAACAAAA	CCCTGCAAAAC	CCTAAGTGAG	420
	ACTTACTTTA	TAAATGTGTC	TACAGCAGAG	GCCCAAGCA	CAITTAATTTG	TACATTACCA	480
	ATAAACTGTA	ATAATACAA	GAATGCATGT	GCTGTAATAG	CTGCTTTGGA	AAGAGTAAAG	540
	ATTGACCAA	TGGAACACTG	CTGCTGTTCT	GTGAGGATAC	CCTGCCCTTC	CTCCCCAGAA	600
	GAGTTGGAAA	AGCTTCAGTG	TGACCTGCAG	GATCCCATTG	TCTGTCTTGC	TGACCATCCA	660
	CGTGGCCAC	CATTTCTCTC	CAGCCAATCC	ATCCCACTGG	TGCCCTCGGC	CAGTGTGCTT	720
10	TCCCAGGTCC	CCAAAGCTAC	CTCTTTTGCT	GAGCCTCCAG	ATTATTCAAC	TGTGACCCAC	780
	AATGTTCCCT	CTCCAATAGG	GGAGATTCAA	CCCCCTTCAC	CCCAGCCTTC	AGCTCCCAT	840
	GCTTCCAGCC	CTGCCATTGA	CATGCCCCCA	CAGTCTGAAA	CGATCTCTTC	CCCTATGCC	900
	CAAAACCATG	TCTCCGGCAC	CCCACCTCCT	GTGAAAGCCT	CATTTCTCTC	TCCCACCGTG	960
	TCTGCCCTTG	CGAATGTCAA	CACTACCAGC	GCACCTCTGT	TCCAGACAGA	CATCGTCAAC	1020
15	ACCAGCAGTA	TTTCTGATCT	TGAGAACCAA	GTGTTGCAGA	TGGAGAAGGC	TCTGTCTCTG	1080
	GGCAGCCTGG	AGCCTAACCT	CGCAGGAGAA	ATGATCAACC	AAGTCAGCAG	ACTCCTTCAT	1140
	TCCCAGCTCG	ACATGCTGGC	CCCTCTGGCT	CAAAGATTGC	TGAAAGTAGT	GGATGACATT	1200
	GGCCTACAGC	TGAACCTTTC	AAACACGACT	ATAAGTCTAA	CCTCCCTTTC	TTTGGCTCTG	1260
	GCTGTGATCA	GAGTGAATGC	CAGTAGTTTC	AACACAACCT	CCTTTGTGGC	CCAAGACCTC	1320
20	GCAAACTCTC	AGGTTTCTCT	GGAAACCCAA	GCTCCTGAGA	ACAGTATTGG	CACAATTACT	1380
	CTTCTCTCAT	CGCTGATGAA	TAAATTTACCA	GCTCATGACA	TGGAGCTAGC	TTCCAGGGTT	1440
	CAGTTCAATT	TTTTTGAAGC	ACCTGCTTTG	TTTCAGGATC	CTTCCCTGGA	GAACCTCTCT	1500
	CTGATCAGCT	ACGTCAATATC	ATCGAGTGT	GCAAACTGGA	CCGTGAGGAA	CTTGACAAGA	1560
	AACGTGACAG	TCACATTAAA	GCACATCAAC	CCGAGCCAGG	ATGAGTTAAC	AGTGAGATGT	1620
25	GTATTTTGGG	ACTTGGGCGC	AAATGGTGGC	AGAGGAGGCT	GGTCAGACAA	TGGCTGCTCT	1680
	GTCAAGACGA	GGAGATTGAA	TGAACCATC	TGTACCTGTA	GCCATCTAAC	AAGCTTCGGC	1740
	GTTCTGCTGG	ACCTATCTAG	GACATCTGTG	CTGCCCTGCT	AAATGATGGC	TGTGAGTTTC	1800
	ATTACATATA	TGTGTTGGG	GCTTTCATCA	ATTTTCTGT	CAGTGACTCT	TGTAACCTAC	1860
	ATAGCTTTTG	AAAAGATCCG	GAGGGATTAC	CCTTCCAAAA	TCCTCATCCA	GCTGTGTGCT	1920
30	GCTCTGCTTC	GCTGAACTCT	GGTCTTCTCT	CTGAGCTGCT	GGATTGCTCT	GTATAAGATG	1980
	CAAGGCTCTC	GCATCTCACT	GGCTGTATTT	CTTCAATATT	TTCTCTTGGT	CTCAATCACA	2040
	TGAGTGGGCG	TAGAGCAATT	CCATATGTAC	CTGGCCCTTG	TCAAAGTATT	TAATACCTAC	2100
	ATCCGAAAT	ACATCTCTAA	ATTCTGCATT	GTCCGTTGGG	GGGTACACAG	TGTGGTTGTG	2160
	ACCATCATCC	TGACTATATC	CCCAGATAAC	TATGGGCTTG	GATCCTATGG	GAAATCCCTC	2220
35	AATGTTTAC	CGGATGACTT	CTGCTGATC	AACAACAATG	CAGTATTCTA	CATTACGGTG	2280
	GTGGGATATT	TCTGTGTGAT	ATTTTGTGCT	AACGTCAGCA	TGTTCAATTG	GGTCTGCTGT	2340
	CAGCTCTGTC	GAAATTAAGA	GAAGAAGCAA	CTGGGAGCCG	AGCGAAATAC	CAGTATTCAA	2400
	GACCTCAGGA	GTATGCTGG	CCTTACATTT	TACTGCGGAA	TAACTTGGGG	CTTTCCTCTC	2460
	TTTGCCTGGG	GACCACTTAA	CGTGACCTTC	ATGTATCTGT	TTGCCATCTT	TAATACCTTA	2520
40	CAAGGATTTT	TCATATTCTG	CTTTTACTGT	GTGGCCAAAG	AAAATGTGAG	GAAGCAATGG	2580
	AGGCGGTATC	TTTGTGTGG	AAAGTTACGG	CTGGCTGAAA	ATTCGGAAGA	TGCTTCTACA	2640
	GAGAGGAATG	GGGCTCTCTT	TAGTGTTCAG	AATGGAGATG	TGTGCTTCA	CGATTTCATC	2700
	GGAAACAGC	ACATGTTTAA	CGAGAAGGAA	GATTCTCTGA	ATGGGAAAGG	CCGTATGGCT	2760
	CTCAGAAGGA	CTTCAAAGCG	GGGAAGCTTA	CACCTTTATTG	AGCAATATGT	A	

45	Seq ID NO: 18 Protein sequence						
	Protein Accession #: Bos sequence						
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50	MVFSVRQCGH	VGRTEEVLLT	FKIFLVIICL	HVVLVTSLEB	DTDNSSLSP	PEVETTSLND	60
	VTLSLLPSNE	TGVRPQRNIC	NLSSICND	PFREIMFQY	DKESTVPQNG	HITNGTLTGV	120
	LSLSLKRSE	LAKTLQTLSE	TYFIMCATAS	AQSTLNCTFT	IKLNNTWNA	AVIAALERVK	180
	IRPMHCCCS	VRIPCPSPSE	ELEKLQDLQ	DEIVCLADHP	RGPFPSSSQS	IPVVPRTVL	240
	SOVPKATSEA	EPFDYSPVTH	NVPSPIGEIQ	PLSQPSAPI	ASSPAIDMPP	QSETISSPMP	300
55	QTHVSGTPPP	VKASFSSPTV	SAPANVNTTS	APPVQTDIVN	TSSISDLENQ	VLQMEKALSL	360
	GSLEPNLAGE	MINQVRLLE	SPPDMLAPLA	QRLKVVDDI	GLQLNFSNTT	ISLTSPLSL	420
	AVIRVNASSP	NTTTFVAQDT	ANLQVLSLET	APENSIGTIT	LPSSLMNPL	AHDMELASRV	480
	QNFNFPETPAL	FQDPSLENLS	LISYVSSSV	ANLTVRLNTR	NVTVLKHIN	PSQDELTVRC	540
	VFNDLGRNGG	RGWSNDNGCS	VKDRRLNETI	CTCSHLTSPG	VLLDLRTSV	LPAQMMALTF	600
60	ITYIGGLSS	IFLSVTLVNTY	IAPFKIRRDY	PSKILILQCA	ALLLNILVFL	LDSNIALYKM	660
	QGLCISAVAF	LHYFLVLSFT	WMGLEAFHMY	LALVKVFNTY	IRKYLKFCI	VGMGVPAVVV	720
	TIILTISPND	YGLGSYKFP	NGSPDDFCMI	NNNAVFIYTV	VGYPCVIFLL	NVSMFIVVLV	780
	QLCRIKKKKQ	LGAQRKTSIQ	DLRSIAGLTF	LLGITWGFAP	FAWGPVNVTF	MYLFAIFNTL	840
	QGFPIPIFYC	VAKENVKRW	RRYLCCGKLR	LAENSGWAST	ERNGVSPSVQ	NGDVCLHDFP	900
65	GRQHPFNEKE	DSCNGKGRMA	LRRTSKRGSL	HPIEQM			

70	Seq ID NO: 19 DNA sequence						
	Nucleic Acid Accession #: Bos sequence						
	Coding sequence: 1..3045						
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	GATACCTGATA	ATTCCAGTTT	GTACCAACCA	CCTGCTAAAT	TATCTGTTGT	CAGTTTGGC	180
	CCCTCTCCCA	ATGAGGTTGA	AACAACAAGC	CTCAATGATG	TACTTTAAG	CTTACTCCCT	240
80	TCAAACGAAA	CAGAAAAAAC	TAAATCACT	ATAGTAAAAA	CCTTCAATGC	TTGAGGCGTC	300
	AAACCCGAGA	GAAATATCTG	CAATTGTGCA	TCTATTGCA	ATGACTCAGC	ATTTTGTAGA	360
	GGTGAGATCA	TGTTTCAATA	TGATAAAGAA	AGCACTGTTC	CCCAGATCA	ACATATAACG	420
	AATGGCACTT	TAACTGGAGT	CCTGTCTCTA	AGTGAATTAA	AACGCTCAGA	GCTCAACAAA	480
	ACCCTGCAAA	CCCTAAGTGA	GACTTACTTT	ATAATGTCTG	CTACAGCAGA	GGCCCAAGC	540
	ACATTAAAT	GTACATTCAC	AATAAACTG	AATAATACAA	TGAATGCATG	TGCTGCAATA	600
	CGCGCTTTGG	AAAGAGTAAA	GATTGACCA	ATGGAACACT	GCTGCTGTTT	TGTGAGGATA	660
	CCCTGCCCTT	CCTCCGACGA	AGAGTTGGGA	AAGCTTCAGT	GTGACCTGCA	GGATCCCAT	720
	GTCTGTCTTG	CTGACCATCC	ACGTGGCCCA	CCATTCTCTT	CCAGCCAAAT	CATCCCATG	780
85	GTGCTCGGG	CCACTGTGCT	TTCCAGGTC	CCCAAAGCTA	CCTCTTTTGC	TGAGCTTCCA	840
	GATTATTAC	CTGTGACCCA	CAATGTTCCC	TCTCCAATAG	GGGAGATTCA	ACCCCTTCTA	900

5	CCCCAGCCTT	CAGCTCCCAT	AGCTTCCAGC	CCTGCCATTG	ACATGCCCCC	ACAGTCTGAA	960
	ACGATCTCTT	CCCCTATGCC	CCAAACCCAT	GTCTCCGGCA	CCCCACCTCC	TGTGAAGACC	1020
	TCATTTTCCT	CTCCCACCGT	GTCTGCCCTT	GCGAATGTCA	ACACTACCAG	CGCACTCTCT	1080
	GTCCAGACAG	ACATCGTCAA	CACCAGCAGT	ATTTCTGATC	TTGAGAACCA	AGTGTTCGAG	1140
	ATGGAGAAAG	CTCTGTCTCT	GGGCAGCCTG	GAGCCTAACC	TCGCAGGAGA	AATGATCAAC	1200
	CAAGTCAGCA	GACTCTCTCA	TTCCCGCCTT	GACATGCTGG	CCCTCTGGC	TCAAAGATTG	1260
	CTGAAAGTAG	TGGATGACAT	TGGCCTACAG	CTGAACCTTT	CAAAACAGAC	TATAAGTCTA	1320
	ACCTCCCTCT	CTTTGGCTCT	GGCTGTGATC	AGAGTGAATG	CCAGTAGTTT	CAACACAAC	1380
10	ACCTTTGTGG	CCCAGAGCCC	TGCAAACTCT	CAGGTTTCTC	TGGAACCCCA	AGCTCCTGAG	1440
	AACAGTATTG	GCACAATTAC	TCTTCTCTCA	TCGCTGATGA	ATAATTIACC	AGCTCATGAC	1500
	ATGGAGCTAG	CTTCCAGGGT	TCAGTTCAAT	TTTTTGGAAA	CACCTGCTTT	GTTCAGGAT	1560
	CCTTCCCTGG	AGAACCTCTC	TCTGATCAGC	TACGTCATAT	CATOGAGTGT	TGCAAACTGT	1620
	ACCGTCAGGA	ACTTGACAA	AAACGTGACA	GTCACTTAA	AGCACATCAA	CCCGAGCCAG	1680
15	GATGAGTTAA	CAGTGAGATG	TGTATTTTGG	GACTTGGGCA	GAAATGCTGG	CAGAGGAGGC	1740
	TGGTCAGACA	ATGGCTGCTC	TGTCAAAGAC	AGGAGATTGA	ATGAAACCAT	CTGTACTCTG	1800
	AGCCATCTAA	GACGCTTCGG	CGTCTGCTG	GACCTATCTA	GGACATCTGT	GCTGCGCTGT	1860
	CAAATGATGG	CTCTGACGTT	CATTACATAT	ATTGGTTGTG	GGCTTTCATC	AATTTTCTGT	1920
	TCAGTGACTC	TGTAAACCTA	CATAGCTTTT	GAAAAGATCC	GGAGGGATTA	CCCTCCCAA	1980
20	ATCCTCATCC	AGCTGTGTGC	TGCTCTGCTT	CTGCTGAACC	TGGTCTTCTT	CCTGGACTCG	2040
	TGGATTGCTC	TGTATAAGAT	GCAAGGCTCT	TGCATCTCAG	TGGCTGTATT	TCTTCTATTAT	2100
	TTTCTCTTGG	TCTCATTAC	ATGGATGGGC	CTAGAAGCAT	TCCATATGTA	CCTGGCCCTT	2160
	GTCAAAATAT	TTAATACCTA	CATCCGAAAA	TACATCTCTA	AATTCGTGAT	TGTCGGTTGG	2220
	GGGGTACAG	CTGTGGTTGT	GACCATCATC	CTGACTATAT	CCCCAGATAA	CTATGGGCTT	2280
25	GGATCCTATG	GAAAATTCCT	CAATGGTTCA	CCGGATGACT	TCTGCTGGAT	CAACAACAAT	2340
	GCAGTATTCT	ACATTACGGT	GGTGGGATAT	TCTGTGTGA	TATTTTGTCT	GAACGTCAGC	2400
	ATGTTCTATT	TGGTCTCTGT	TCAGCTCTGT	CGAATTAAAA	AGAAGAAGCA	ACTGGGAGCC	2460
	CAGGAAAAAA	CCAGTATCTA	AGACCTCAGG	AGTATCGCTG	GCCTTACATT	TTTACTGGGA	2520
	ATAACTTGGG	CGTTTGCTCT	CTTTGCTGGG	GAGCCAGTTA	ACGTGACCTT	CATGTATCTG	2580
30	TTTGCCATCT	TTAATACCTT	ACAAGGATTT	TTCATATTCA	TCTTTTACTG	TGTGGCCAAA	2640
	GAAAAATGTC	GGAAGCAATG	GAGGCGGTAT	CTTTGTGTGT	GAAAGTTACG	GCTGGCTGAA	2700
	AATTCTGACT	GGATATAAAT	TGCTACTAAT	GGTTTAAAGA	AGCAGACTGT	AAACCAAGGA	2760
	GTGTCCAGCT	CTTCAAAATC	CTTACAGTCA	AGCAGTAAC	CCACTAACTC	CACCACACTG	2820
	CTAGTGAATA	ATGATTGCTC	AGTACACGCA	AGCGGGAATG	GAAATGCTTC	TACAGAGAGG	2880
35	AATGGGCTCT	CTTTTAGTGT	TCAGAATGGA	GATGTGTGCC	TTCAGATT	CACCTGGA	2940
	CAGCACATGT	TTAACGAGAA	GGAAGATTCC	TGCAATGGGA	AAGGCCGTAT	GGCTCTCAGA	3000
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Seq ID NO: 20 Protein sequence:

Protein Accession #: Eos sequence

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	PSSNEVETTS	LNDVTLSSLF	SNETEKTKIT	IVKTFNASGV	KPQRNICNL	SIQNDSAFFR	120
	GEIMFQYDKE	STVPONQHIT	NGTLTGVL	SELKRSELNK	TLQTLSETYF	IMCATAEQS	180
45	TLNCTPTIKL	NMTMCAAI	AALERVKIRP	MEHCCSVRI	PCPSSPEELG	KLQCDLQDPI	240
	VCLADHPRGP	PFSSSQIPV	VPRATVLSQV	PKATSPAEFP	DYSPVTHNVP	SPIGEIQPLS	300
	PQPSAPIASS	PAIDMPPQSE	TISSPMPQTH	VSGTTPPVKA	SFSSPTVSAP	ANVNTTSAPP	360
	VQTDIVNTSS	ISDLENQVLQ	MEKALSLSGL	EPNLAGEMIN	QVSRLLHSPP	DMLAPLAQRL	420
50	LKVVDDIGLQ	LNFENTTISL	TSPSLALAVI	RVNASSFNTT	TFVAQDPANL	QVSLQTAPE	480
	NSIGITILPS	SIMNMLPAHD	MELASRVQFN	FFETPALFQD	PSLENLSLIS	VISSSVANL	540
	TVRNLTNRVT	VLKHIINPQ	DELTVRVCFW	DLGRNGGRGG	WSDNGCSVRD	RRLNETICTC	600
	SELTSFVGLL	DLKRTSVLPA	QMMALTPTIT	IGCGLSSIFL	SVTLVITYIAF	EKIRREDYPSK	660
	ILIQLCALAL	LNLVFLDLS	WIALYKMQGL	CISVAVFLHY	FLLVSPFTWMS	LEAFHMYLAL	720
55	VKVFENTYIRK	YLKFCIVGM	GVPVAVVTII	LTISPNDYGL	GSYKGFPMGS	PDDFCWINNN	780
	AVFYITVVG	VCVIFLLNVS	MEIVVLVQLC	RIKKKKQLGA	QRKTSIQDLR	SIAGLTFLLG	840
	ITWGFAPFAW	GPVNVTPMYL	PAIFNTLQGE	FIFIFYCVAK	ENVRKQWRRY	LCCGKLRLAE	900
	NSDWSKATATN	GLKQKTVNQG	VSSSSNSLQS	SSNSTNSTTL	LVNNDCSVHA	SGNGMASTER	960
	NGVSFSVQNG	DLKCHDPTGK	QHMFNEKEDS	CNGKGRMALR	RTSKRGSLEH	IEQM	

Seq ID NO: 21 DNA sequence

Nucleic Acid Accession #: NM_005756.1

Coding sequence: 37..3117

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	AGCCAGCCCG	AGGACGCGAG	CGGCAGGTGT	GCACAGAGGT	TCTCCACTTT	TTTTTCTGAA	60
	CTCGCGGTCA	GGATGGTTTT	CTCTGTCAGG	CAGTGTGGCC	ATGTTGGCAG	AACGGAAGAA	120
	GTTTTACTGA	CGTTCAAGAT	ATTCTTGTCT	ATCATTTGTC	TTCATGTCTG	TCTGGTAACA	180
	TCCCTGGAAG	AAGATACTGA	TAATTCCAGT	TTGTCAACCAC	CACCTGCTAA	ATTATCTGTT	240
70	GTCACTTTTG	CCCCCTCCTC	CAATGAGGTT	GAACAACAA	GCCTCAATGA	TGTTACTTTA	300
	AGCTTACTCC	CTTCAACGCA	AACAGAAAA	ACTAAATCA	CTATAGTAAA	AACCTTCAAT	360
	GCTTCAGGCG	TCAAAACCCA	GAGAAATATC	TGCAATTTGT	CATCTATTTG	CAATGACTCA	420
	GCAATTTTTA	GAGGTGAGAT	CATGTTTCAA	TATGATAAAG	AAAGCACTGT	TCCCAGAAAT	480
	CAACATATAA	CGAATGGCAC	CTTAACTGGA	GTCCTGTCTC	TAAGTGAATT	AAAAAGCTCA	540
	GAGCTCAACA	AAACCTTGCA	AAACCTAAGT	GAGACTTACT	TTAATAATGT	TGCTACAGCA	600
75	GAGGCCCAAA	GACATTAA	TTGTACATTC	ACATAAATAC	TGAATAATAC	AATGAATGCA	660
	TGTGCTGCAA	TAGCCGCTTT	GGAAAGAGTA	AAGATTGAC	CAATGGAACA	CTGCTGCTGT	720
	TCTGTGAGAA	TACCTCTGCC	TTCTCCCA	GAAGAGTTGG	GAAAGCTTCA	GTGTGACCTG	780
	CAGGATCCCA	TGCTCTGTCT	TGCTGAACAT	CCACGTGGCC	CACCAATTTT	TTCCAGCCAA	840
80	TCCATCCGAG	TGGTGCCTCG	GGCCACTGTG	CTTTCOCAGG	TCCCCAAGC	TACCTCTTTT	900
	GCTGAGCCTC	CAGATTATTC	ACCTGTGACC	CACAATGTTT	CCTCTCCAAT	AGGGGAGATT	960
	CAACCCCTTT	CACCCAGGCC	TTCAGCTCCC	ATAGCTTCCA	GCCCTGCCAT	TGACATGCCC	1020
	CCACAGTCTG	AAACGATCTC	TTCCCTATG	CCCCAAACCC	ATGCTCTCCG	CACCCACCTT	1080
	CCTGTGAAAG	CCTCATTTTC	CTCTCCCAAC	GTGCTGCCCC	CTGCGAATGT	CAACACTACC	1140
85	AGCGCACCTC	CTGTCCAGAC	AGACATGCTC	AACACCAGCA	GTATTTCTGA	TCTTGAGAAC	1200
	CAAGTGTGTC	AGATGGAGAA	GGCTCTGTCC	TTGGGCAGCC	TGGAGCCTAA	CCTGCGAGGA	1260

5 GAAATGATCA ACCAAGTCAG CAGACTCCTT CATTCGCCGC CTGACATGCT GGCCCTCTCG 1320
 GCTCAAGATG TGCTGAAAGT AGTGGATGAC ATTGGCCTAC AGCTGAACCTT TTCAAACACG 1380
 ACTATAAGTC TAACCTCCCC TTCTTTGGCT CTGGCTGTGA TCAGAGTGAA TGCCAGTAGT 1440
 TTCAACACAA CTACCTTTGT GGCCCAAGAC CCTGCAAAATC TTCAGGTTTC TCTGGAACCC 1500
 CAAGCTCCTG AGAAGAGTAT TGGCACAATT ACTCTTCCTT CATCGCTGAT GAATAATTTA 1560
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 TTGTTTCAGG ATCCTCCCTT GGAGAACCTC TCTCTGATCA GCTACGTCAT ATCATCGAGT 1680
 GTTGCAAAAC TGACCGTCAG GAACTTGACA AGAAACGTGA CAGTCACATT AAAGCACATC 1740
 10 AACCCGAGCC AGGATGAGTT AACAGTGAGA TGTGTATTTT GGGACTTGGG CAGAAATGGT 1800
 GGCAGAGGAG GCTGGTCAGA CAATGGCTGC TCTGTCAAAG ACAGGAGATT GAATGAAACC 1860
 ATCTGTACCT GTAGCCATCT AACCAAGCTC GGCGTTCTGC TGGACCTATC TAGGACATCT 1920
 GTGCTGCCGT CTCAATGAT GGCTCTGAGC TTCATTACAT ATATTGGTTG TGGGCTTTCA 1980
 TCAATTTTTC TGTCACTGAC TCTTGTAACC TACATAGCTT TTGAAAGAT CCGGAGGAGT 2040
 15 TACCCCTTCCA AAATCCTCAT CCAGCTGTGT GCTGCTCTGC TTCTGCTGAA CCTGCTCTTC 2100
 CTCTCGGACT CGTGGATGCT TCTGTATAAG ATGCAAGGCC TCTGCTCTC AGTGGCTGTA 2160
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 25 TTCATGTATC TGTTTGCCAT CTTTAATACC TTACAAGGAT TTTTCATATT CATCTTTTAC 2700
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 CACAATGTGA GATGATGAAA AATCAACTCA TTTTATTCTC GGCAACATCT GGAGAAGCAT 3240
 35 AAGCTAATTA AGGCGATGA TTATTATTAC AAGAAGAAAC CAAGACATTA CACCATGGTT 3300
 TTTAGACATT TCTGATTGGG TTTCTTATCT TTCATTTTAT AAGAAGGTTG GTTTTAAACA 3360
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 40 GTCAAAAATC TTAATCTTAC ATTTTGTGTG ATTTATTTTC TACTGTGTAA ATGTATTCTT 3600
 TTGTAGAATC ATGTTGTGTT TGTCTCACTG GATAATTCAG AAAATCCTTG CTCGTTCCGC 3660
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 TCAAGAAAAA ATGATCCCGA CCAGACTGAG AAAATGTAAG CAGACAGTGC CACAGTTAGC 3780
 TCATACAGTG CATTGAGGAA AGTTAGGAAA AGATGCCCCC ACTGGGCAGA CACAGCCCTA 3840
 45 TGGGTGATGG TTTGACAAAC AGAGTGAGAG ACCATATTTT AGCCCCACTC ACCCTCTTGG 3900
 GTGCACGACC TGTACAGCCA AACACAGCAT CCAATATGAA TACCATCCCC CTGACCGCAT 3960
 CCCAGTAGT CAGATTATCT AATCTGCACC AAGATGTTTA GCTTTATACC TTGGCCACAG 4020
 AGAGGGATGA ACTGTCATCC AGACCATGTG TCAGGAAAAA TGTGAACGTA GATGAGGTAC 4080
 ATACACTGGC CATTCTCAAA TCCCAGAGC CTTTAGGAAC AGGAGAGTAG ACTAGGATTG 4140
 50 CTCTCTCTAA AAGGTACAT ATATATGGAA AAAAATCATA TTGCCGTTCT TTAAGAGGCA 4200
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 TTGTTTTTAA AATGTTGCTT GAAGAATGCA CAGTGACAAG GGGAGTAGCT ATTGGGAACA 4320
 GGGAACTGTC CTACACTGCT ATGTTGCTA CATGTATCGA GCCTTGATTG CTCTAGTTA 4380
 TATACAGGGT CTATCTGCTC TCCTACCTAC ATCTGCTTGA GCAGTGCCTC AAGTACATCC 4440
 55 TTATTAGGAA CATTTCAAAC CCCTTTGTG TAAGTCTTTC ACTAAGGTTT TCTGTGATAT 4500
 ATTTCAAGTG AATGTTGAT CTCAGACTAA CCATAGTAAT AATACACATT TCTGTGAGTG 4560
 CTGACTGTCT TTGCAATAT TTCTTTCTG ATTTATTTAA TTTTCTTGTA TTTATATGTT 4620
 AAAATCAAAA ATGTTAAAT CAATGAAATA AATTGTCAGT TAAGA

Seq ID NO: 22 Protein sequence

Protein Accession #: NP_005747.1

1 11 21 31 41 51
 MVFSVRQGH VGRTEEVLLT FKIPFLVILC HVVLVTSLEB DTNSSLSPF PAKLSVVSFA 60
 PSSNEVETTS LNDVTLSELL SNETGVKPKR NICNLSSICN DSAFFRGEIM FOYDKBSTVP 120
 65 QNQHITNGTL TGVLSLSELK RSELRKTLQT LSETYFIMCA TBAQSTLINC TPTIKLNMIM 180
 NACAVIAALE RVKIRPMERC CCSVRIPCPS SPEELEKIQC DLQDPIVCLA DHPRGPPFSS 240
 SQSIPVVPRA TVLSQVPKAT SFARPPDYSP VTHNVPSPIG EIQLPSQPS APIASSPAID 300
 MPPQSETISS PMPQTHVSGT PFPVKASFSS PTVSAPANVN TTSAPPVQTD IVNTSSISDL 360
 70 ENQVLQMEKA LSLGSLFENL AGEMINQVSR LLHSPPDMLA PLAQRLLKVV DDIGLQLNFS 420
 NTTISLTSPS LALAVIRVNA SSFNTTTFVA QDPANLQVSL ETQAPENSIG TITLPSLIMN 480
 NLPAMDMLA SRVQNFPEET PALFQDPSLE NLSLISYVIS SSVANLTVRN LTRNVTVTLK 540
 HINPSQDEL T VRCVFDLGR NGRGGHSDN GCSVKDRRLN ETICTCSHLT SPGVLLDLR 600
 TSVLPQAMMA LTFITYIGCG LSSIFLSVTL VTYIAFEKIR RDYPSKILIQ LCAALLLLNL 660
 75 VFLDSDWIAL YMQGLCISV AVFLEYPLLV SFTWMLGELF HMYLALVKVF NTYIRKYILK 720
 PCIVGNGVPA VVVITLITIS PDNYGLGSYG KFPNGSPDDF CWLNNAVPI ITVVGYPCVI 780
 FLLNVSMPIV VLVLQCRICK KQQLGAQRKT SIQDLRSIAG LTFLLGITWG PAFPAWGPVN 840
 VTFMYLPAIF NTLQGFIFI FYCVARENVR KQWRRYLCCG KRLAENSOW SKTATNGLKK 900
 QTVNQGVSSS SNSLQSSSS TNSTLLVNN DCSVHASGNG NASTERNGVS PSVQNGDVCL 960
 80 HDFTGKQHMF NEKEDSCNGK GRMALRRTSK RGLRHFIEQM

Seq ID NO: 23 DNA sequence

Nucleic Acid Accession #: NM_001565.1

Coding sequence: 67..363

1 11 21 31 41 51
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AGCACCATGA ATCAAACTGC GATTCTGATT TGCTGCCTTA TCCTTCTGAC TCTAAGTGGC 120
ATTCAGGGAG TACCTCTCTC TAGAACCGTA CGCTGTACCT GCATCAGCAT TAGTAATCAA 180
CCTGTTAATC CAAGGTCTTT AGAAAACTT GAAATTATTC CTGCAAGCCA ATTTTGTCCA 240
CGTGTTGAGA TCATTGCTAC AATGAAAAAG AAGGGTGAGA AGAGATGTCT GAATCCAGAA 300
TCGAAGGCCA GGTGAATTT ACTGAAAGCA GTTAGCAAGG AATGTCTAA AAGATCTCCT 360
TAAACCCAGA GGGGAGCAA ATCGATGACG TGCTTCCAAG GATGGACCAC ACAGAGGCTG 420
CCTCTCCCAT CACTTCCCTA CATGGAGTAT ATGTCAAGCC ATAATTGTTT TTAGTTTGCA 480
GTTACACTAA AAGGTGACCA ATGATGGTCA CCAATCAGC TGCTACTACT CCTGTAGGAA 540
GGTAAATGTT CATCATCTTA AGCTATTGAG TAATAACTCT ACCCTGGCAC TATAATGTAA 600
GCTCTACTGA GGTGCTATGT TCTTAGTGGA TGTCTGACC CTGCTTCAAA TATTTCCCTC 660
ACCTTTCCCA TCTTCCAAGG GTACTAAGCA ATCTTTCTGC TTGGGGTTT ATCAGAAATC 720
TCAGAAATCT AATAAATCAA AAGGTATGCA ATCAATCTG CTTTTTAAAG AATGCTCTTT 780
ACTTCATGGA CTTCCTACTG CATCTCTCCA AGGGGCCCAA ATTCTTTCAG TGGCTACCTA 840
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CTTAATTAAAT GAAAGACTGT ACAAAGTATA AGTCTTAGAT GTATATATTT CCTATATTGT 960
TTTCAGTGTA CATGGAATAA CATGTAATA AGTACTATGT ATCAATGAGT AACAGGAAAA 1020
TTTTAAAAAT ACAGATAGAT ATATGCTCTG CATGTTACAT AAGATAAATG TGCTGAATGG 1080
TTTTCAATA AAAATGAGGT ACTCTCCTGG AAATATTAAG
  
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Seq ID NO: 24 Protein sequence
Protein Accession #: NP_001556.1

25

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1 11 21 31 41 51
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MNQTALICC LIPLTLGGIQ GVPLSRTVRC TCISISNQPV NPRSLERLEI IPASQFCPRV 60
EIIATMKKKG EKRLNPESK AIKMLLKAVS KEMSKRSP
  
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Seq ID NO: 25 DNA sequence
Nucleic Acid Accession #: XM_030559
Coding sequence: 1..1119

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1 11 21 31 41 51
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AGCAAGTTTG GAGCTGAATT TCGTCGGTTT TCGCTGGAAA GATCAAAACC TGGAAAATTT 120
GAGGAGTTTT ATGGATTACT ACAACATGTT CATAAGATCC CCAATGTTGA CGTTTGGTGA 180
GGCTATGCGAG ACATCCATGG AGACTTACTA CCTATAAATA ATGATGATAA TTATCAGAAA 240
GCTGTTTCAA CGGCCAATCC ACTGCTTAGG ATATTATATC AAAAGAAGGA AGAAGCAGAC 300
TACAGTGCCT TTGGTACAGA CACGCTAATA AAGAAGAAGA ATGTTTAAAC CAACGTATTG 360
CGTCCTGACA ACCATAGAAA AAAGCCACAT ATAGTCATTA GTATGCCCCA AGACTTTAGA 420
CCTGTGTCTT CTATTATAGA CGTGGATATT CTCCAGAAA GGCATCGTAG GGTACGCTTT 480
TACAAATAGG GCACGGAGAA ACCCCTAGGA TTCTACATCC GGGATGGCTC CAGTGTCAAG 540
GTAAACCCAC ATGGCTTAGA AAAGGTTCCA GGGATCTTTA TATCCAGGCT TGTCCAGGGA 600
GGTCTGGCTC AAGATACAGG ACTATTAGCT GTTAATGATG AAGTTTATGA AGTTAATGGC 660
ATAGAAAGTT CAGGGAAGAG CCTTGATCAA GTAAACAGCA TGATGATTGC AATAGCCGT 720
AACCTCATCA TAACAGTGAG ACCCGCAAAC CAGAGGAATA ATGTTGTGAG GAACAGTCGG 780
ACTTCTGGCA GTTCCGGTGA GTCTACTGAT AACAGCCTTC TTGGCTACCC ACAGCAGATT 840
GAACCAAGCT TTGAGCCAGA GGATGAAGAG AGCGAAGAAG ATGACATTAT CATTAAGAC 900
AATGGAGTGC CACAGCAGAT TCCAAAAGCT GTTCTTAATA CTGAGAGCCT GGAGTCATTA 960
ACACAGATAG AGCTAAGCTT TGAGTCTGGA CAGAATGGCT TTATCCCTCT TAATGAAGTG 1020
AGCTTAGCAG CCATAGCAAG CAGCTCAAAC ACGGAATTTG AAACACATGC TCCAGATCAA 1080
AAACTCTTAG AAGAAGATGG AACAATCATA ACATTATGA
  
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Seq ID NO: 26 Protein sequence
Protein Accession #: XP_030559

55
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1 11 21 31 41 51
| | | | |
MNRSHRHGAG SGCLGTMEVK SRFGAEFRFP SLERSKPKGF EEFYGLLQHV HKIPNVLDLV 60
GYADIHGDLL PINDDNYHK AVSTANPLLR IFIQKKEAD YSAFGDTLLI KKNVLTNVL 120
RPNHHRKKPH IVISMPQDFR PVSSIIDVDI LPETHRRVRL YKYGTEKPLG FYIRDGSSVR 180
VTFHGLEKVP GIFISRLVPO GLAQSTGLLA VNDEVLEVNG IEVSOKSLDQ VIDMMLANSR 240
NLIIITVRPAN QRNVVVRNSR TSGSSGQSTD NSLLGYPQOI EPSFEPEDED SEEDDIIIED 300
NGVPPQIPKA VENTBSLESL TQIELSPESG QNGFIPSENV SLAAIASSEN TEFETHAPDQ 360
KLEEDGTII TL
  
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Seq ID NO: 27 DNA sequence
Nucleic Acid Accession #: NM_003667.1
Coding sequence: 1..2651

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1 11 21 31 41 51
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GAGCCCGAGG GCAGGATGTT GCTCAGGGTG GACTGCTCCG ACCTGGGGCT CTCGGAGCTG 180
CCTTCCAACC TCACGCTCTT CACCTCTTAC CTAGACCTCA GTATGAACAA CATCAGTCAG 240
CTGCTCCCGA ATCCCTGCCC CAGTCTCCGC TTCTGGAGG AGTTACGCTC TGGGGGAAAC 300
GCTCTGACAT ACATTCCCAA GGGAGCATT ACTGGCTTTT ACAGTCTTAA AGTTCTTATG 360
CTGCAGAATA ATCAGCTAAG ACACGTACCC ACAGAAGCTC TGCAGAAATT GCGAAGCCTT 420
CAATCCCTGC GTCTGGATGC TAACCACATC AGCTATGTGC CCCCAGCTG TTTCACTGGC 480
CTGCAATCCC TGAGGCACTT GTGGCTGGAT GACAATGCGT TAACAGAAAT CCCGTCOCAG 540
GCTTTTAGAA GTTTATCGGC ATTGCAAGCC ATGACCTTGG CCCTGAACAA AATACACCAC 600
ATACCAAGCT ATGCTTTTGG AAACCTCTCC AGCTTGTGAG TTCTACATCT CCATAACNAT 660
AGAATCCACT CCTCGGGAAA GAAATGCTTT GATGGGCTCC ACAGCCTAGA GACTTTAGAT 720
TTAAATTACA ATAACTTTGA TGAATTCCCC ACTGCAATTA GGACACTCTC CAACCTTAAA 780
GAACCTACAT TCTATGACAA TOCCATCCAA TTTGTTGGGA GATCTGCTTT TCAACATTTA 840
CCTGAACATA GAACACTGAC TCTGAATGGT GCCTCACAAA TAACGTGAAT TCCTGATTTA 900
ACTGGAACCT CAAACCTGGA GAGTCTGACT TTAACCTGGAG CACAGATCTC ATCTCTCTCT 960
  
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CAAACCGTCT GCAATCAGTT ACCTAATCTC CAAGTGCTAG ATCTGTCTTA CAACCTATTA 1020
 GAAGATTAC CCAGTTTTC AGTCTGCCAA AAGCTTCAGA AAATTGACCT AAGACATAAT 1080
 GAAATCTACG AAAATAAAGT TGACACTTTC CAGCAGTTGC TTAGCTTCCG ATCGCTGAAT 1140
 5 TTGGCTTGGG ACACAAATTCG TATTATTAC CCCAATGCAT TTCCACTTT GCCATCCCTA 1200
 ATAAAGCTGG ACCTATCGTC CAACCTCCTG TCGTCTTTTC CTATAACTGG GTTACATGGT 1260
 TAACTCACT TAAATTAAC AGGAAATCAT GCCTTACAGA CTTGATATC ATCTGAAAAC 1320
 TTCCAGAAC TCAAGGTAT AGAAATGCCT TATGCTTACC AGTGCTGTGC ATTTGGAGTG 1380
 TGTGAGAAAT CCTATAAGAT TTCTAATCAA TGAATAAAG GTGACACAG CAGTATGGAC 1440
 10 GACCTTCATA AGAAGATGC TGAATGTTT CAGGCTCAAG ATGAACGTGA CCTTGAGAT 1500
 TTCCTGCTTG ACTTTGAGGA AGACCTGAAA GCCCTTCATT CAGTGCAGTG TTCACCTTCC 1560
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 TGGACCATAG CAGTCTGGC ACTTACTGT AATGCTTTGG TGACTTCAAC AGTTTTCAGA 1680
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 CTCACGGAG CTTCCAGTGC CGTGTGGCT GGTGTGGATG CGTTCACCTT TGGCAGCTTT 1800
 15 GCACGACATG GTGCTCGTGC GGAGAATGGG GTTGGTTGCC ATGTCACTTG TTTTGTGTCC 1860
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 30 CCATGTCTTA A

Seq ID NO: 28 Protein sequence

Protein Accession #: NP_003658.1

1 11 21 31 41 51
 35 | | | | |
 MDTSLRGLVLL SLPLVLLQAT GGSSPRSGVL LRGCPTHCHC EPDGRMLLRV DCSDLGLSEL 60
 PSNLSVFTSY LRLSMNNISQ LLPNPLPSLR FLEELRLAGN ALTYIPKAP TGLYSLKVLN 120
 LQNNQLRHVP TBAQNLRLSL QSLRLDANHI SYVPPSCFSG LHSRLHLWLD DNALTEIPVQ 180
 AFRSLALQA MTLALNKH IIPDYAFGNLS SLVVLHLHNN RIHSLGKKCF DGLHSLLETD 240
 40 LMYNNLDEFP TAIRTLNLK ELHFDNPIQ FVGRSAFQHL PELRTLTLNG ASQITEPPDL 300
 TGTANLESLT LTGAQISSLP QTVCNQLPNL QVLDLSYNLL EDLPSPFVQC KLQKIDLRHN 360
 EYIEIKVDTP QLLSLSLSLP LAMNKIAI IH PNAFSTLPSL IKLDLSSNLL SFFPITGLHG 420
 LTHLKLGTNH ALQSLISSEN FPELKVIE MP YAYQCCAFGV CENAYKISNQ WNKGDNSMMD 480
 DLHKKDA GMP QAQDERDLEK FLDFEEDLK ALHSVQCSPS PGFPKPCHEH LDGWLIRIGV 540
 45 WTIAVLALTC NALVTSTVFR SPLYISPIKL LIGVIAAVNM LTGVSSAVLA GVDATFPGSF 600
 ARHGAWENG VGCHVIGFLS IPASSSVFL LTLAALERGF SVKYSKAFET KAPFSSLKVI 660
 ILLCALLALT MAAVPLLGGG KYGASPLCLP LPFGEPTMGM YMVALLILNS LCFLMNTIAY 720
 TLKLYCNLDKG DLENWDCSM VKHIALLLFT NCILNCPVAF LSPFSLINLT FISPEVIKFI 780
 LLVVVPLPAC MLLPLYILFN PHFKEDLVSL RKQTYVWTRS KHPSLMSINS DDVEKQSCDS 840
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Seq ID NO: 29 DNA sequence

Nucleic Acid Accession #: NM_002497.1

Coding sequence: 135..1472

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 GGCACTGGCC GGCCATGCTC TCCCGGGCTG AGGACTATGA AGTGTGTGAC ACCATTGGCA 180
 60 CAGGCTCCTA CGGCGCTGCG CAGAAGATCC GGAGGAAGAG TGATGGCAG ATATTAGTTT 240
 GGAAGAAGCT TGACTATGCC TCCATGACAG AAGCTGAGAA ACAGATGCTT GTTCTGAAG 300
 TGAATTTGCT TCGTGAACCTG AAACATCCAA ACATCGTTGG TTACTATGAT CGGATTATTG 360
 ACCGACCAAA TACAACACTG TACATTGTAA TGAATATTG TGAAGGAGGG GATCTGGCTA 420
 GTGTAATTAC AAAGGGAACC AAGGAAAGGC AATACTAGA TGAAGAGTTT GTTCTTCGAG 480
 65 TGATGACTCA GTTGACTCTG GCCCTGAAGG AATGCCACAG ACGAAGTGAT GGTGTCATA 540
 CGGTATTGCA TCGGGATCTT AAACAGCCCA ATGTTTTCTT CGATGCCAG CAAAACGTCA 600
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 TTGTGGGCAC ACCTTATTAC ATGTCTCTCT AACAATGAA TCGCATGTCC TACAATGAGA 720
 AATCAGATAT CTGGTCATTG GGCTGCTTGC TGTATGAGTT ATGTGCATTA ATGCCTCCAT 780
 70 TTACAGCTTT TAGCCAGAAA GAACTCGCTG GGAATAACAG AGAAGGCAAA TTCAGGCGAA 840
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 75 CGCAGGATT CAGCCCTGTA TTGAGTGAGC TGAACCTGAA GGAAATTCAG TTACAGGAGC 1080
 GAGAGCGAGC TCTCAAAGCA AGAGAAGAAA GATTGGAGCA GAAAGAACAG GAGCTTGTG 1140
 TTCGTGAGAG ACTAGCAGAG GACAACTGCG CTAGAGCAGA AAATCTGTTG AAGAATACA 1200
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 GGAGTGAGAA TCTTGAGAGT CAGCTCACAT CTAAGTCCAA GTGCAAGGAC CTGAAGAAAA 1380
 80 GGCTTCAGC TGCCAGCTG CGGGCTCAAG CCTGTCTAGA TATTGAGAAA AATTACCAAC 1440
 TGAAGAAGCAG ACAGATCCTG GGCATGCGCT AGCCAGGTAG AGAGACACAG AGCTGTGTAC 1500
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 85 TTCTTCAGCA CCAATGTGAC AAAATGTTCA CATTTAATTT TTTCTTCTTC TTTTAAAGAC 1680
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 GAACATGAGA TGTGACATTC TAAATCTTGG GAGAAAAAAT AATATTAGGA AAAAAATATT 1800

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 CCAGTTAGAT GCAATTTGGT CATTAAATACC ATGACATCTT GCTTATAAAT ATTCCATTGC 1980
 TCTGTAGTTC AAATCTGTGA GCTTTGTGAA AATTCATCAC TGTGATGTTT GTATTCTTTT 2040
 TTTTTCCTG TTTAACAGAA TATGAGCTGT CTGTCAATTA CCTACTTCTT TCCCACTAAA 2100
 TAAAGAATT CTTCAAGTTA

Seq ID NO: 30 Protein sequence
 Protein Accession #: NP_002488.1

1 11 21 31 41 51
 MPBRAEDYEV LYTIGTGSYG RQKIRKRSK GKILVWKELD YGSMTEAEKQ MLVSEVNLLR 60
 ELKHFNIVRY YDRIDRTNT TLYIVMEYCE GGDLASVITK GTKSRQYLDE EFLVRVMTQL 120
 TLALKECHRR SDGGHTVLHR DLKPAHVFLD GKQNVKLQDF GLARILNHDY SFATKFTVGT 180
 YYMSPEQMNR MSYNEKSDIW SLGCLLYELC ALMPPTTAPS QKELAGKIRE GKFRIRIPRY 240
 SDELNEIITR MLNLKDYHRP SVEEILENPL IADLVADQER RNLEERRGRL GEPEKSQDSS 300
 FVLSELKLKE IQLQERERL KAREERLEQK EQELCVREER AEDKLARAEN LLKNVSLIKE 360
 RKFLSLASNP ELLNLPSSEI KKVHPSGES KENIMRSENS ESQLTSSKSC KDLKKRLHAA 420
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Seq ID NO: 31 DNA sequence
 Nucleic Acid Accession #: NM_020242
 Coding sequence: 72..4240

1 11 21 31 41 51
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 TGCAGAAAGA TCTGGGTGCA CTGATGGAGA GCAGAACTTA TGCTTATCTG TGCTTCTCTC 240
 CACGAGTCTC CGGCTGCATC CCAACCCCTGA GCCCAAGACC TTCACGTTTG ATCATGTTGC 300
 AGATGTGGAT ACCACTCAGG AATCTGTATT TGCAACTGTG GCTAAAAGCA TTGTGGAGTC 360
 TTGCATGAGC GGTATATAAT GTACCATCTT TGCAATGGA CAGACTGGCT CAGGGAAGAC 420
 ATTTACTATG ATGGGACCAT CTGAATCTGA TAATTTTCTT CATAACTCTG GAGGAGTAAT 480
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 10 TGCTGAGGAA AATGGAAGT TGGTAGGTCA CCAAAATTTG CATCAGAAGA TTCAGTACGT 4140
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 TTATGCCATA ATCTCCTTTG ATCTTATGG AAGTCTAAC AATATATGGT GGTTCACACA 4620
 CCTGCAAGTA GTTAAATGAG TGAATAGTA GCAGGTACAA GAAGCAAACT TGTTAATATA 4680
 20 GATTATTTTT GTATCTTAC TTTAGGTATT TTACTTGAGC ATTTTCCATG ACTGTAAATA 4740
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Seq ID NO: 32 Protein sequence
Protein Accession #: NP_064627

25 1 11 21 31 41 51
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 LHSNPEPKTF TFDHVADVD TQESVFATVA KSIVESCMSG YNGTIFAYGQ TGSCKTPTMM 120
 GPSSSDNFSH NLRGVIPRS EYLPFLIDRE KEKAGAGKSP LCKCSPIETI NEQIYDLDS 180
 30 ASAGLYLEEH IKKGVFVGA VEQVVTSAAB AYQVLSGSMR NRRVASTSMN RESSRSHAVP 240
 TITIESMEKS NEIVNIRTS LNLVDLAGSE RQKDTAEGM RLKEAGNINR SLSCIGQVIT 300
 ALVDVNGNGK RHVCYRDSKL TFLRLDLSGG NAKTAIIANV HPGSRCPBGT LSTLNFAQRA 360
 KLILKNAVVN EDTQNVSQL QAEVKRLKEQ LAELASGQTP PESFLTRDKK KTNVMEYFQE 420
 AMLFFKSKSE EKSLIEKVT QLEDLTKEE KFIQSNKIV KFREDQIIRL EKLHKESRGG 480
 35 FLPEBQRLLL SELRNEIQT LREQIEHPRV AKYAMENHSL REENRRLRL EPVKRAQEMD 540
 AQTIAKLEKA PSEISGMEKS DRNQQGFSPK AQKEPCLFAN TEKLAQLLQ IQTELNNKQ 600
 EYEEFKELTR KRQLESESL QSLQKANLNL ENLLEATKAC KRQEVSLNK IHAETLKIT 660
 TPTKAYQLHS RVPKLSPEM GSPGSLYTQN SSILDNDILN EPVPPMNEQ APEAISEELR 720
 TVQEQMSALQ VLKDEEHKN LKLGQHVDEL EHHSTQMOEL FSSERIDWTK QOEELLSQLN 780
 40 VLEKQLQETQ TKNDLFSEV HDLRVVLHSA DKELSSVKLE YSSFKTNQEK EFNKLSERHM 840
 HVQLQLDNL LENEKLESK ACLQDSYDNL QEIMKFEIDQ LSRNLQNFKK ENETLKSDLN 900
 NIMELLEAEK ERNKLQLQF EDKENSKE ILKVLAVRQ EKQKETAKCE QQMAKVQKLE 960
 ESLIATEKVI SLEKSRDSD KCVVADLMNQ IQELRTVECE KTETIDTLKQ ELKDINCKYN 1020
 SALVDREESR VLIKKQVDI LDLEKTLRL ILSEDIERDM LCEDLAHATE QLNMLTEASK 1080
 45 KHSGLLQSAQ EELTKKALI QELQKLNQK KEEVEQKKNE YNFKMRQLEH VMDAAEDPO 1140
 SPKTPPHFQT HLAKLLETQE QEIEDGRASK TSLEELVTKL NEDREVNAE ILRMKEQLRE 1200
 MENLLESQ LLEKNWLLQ LQDDIKRQKE NSDQNHDPNQ QLRNEQEEBI KERLAKSKIV 1260
 EEMLMKADL EESQSAALYNK EMECLRMDE VERTQTLSEK AFQKEQQLRS KLEEMYEERE 1320
 RTSQEMEMLR KQVECLAEN GKLVGHNLEH QKIQYVVRK KENVRLAEST EKLRAENVFL 1380
 KEKKRSES

Seq ID NO: 33 DNA sequence
Nucleic Acid Accession #: BC000633.1
Coding sequence: 1..2574

55 1 11 21 31 41 51
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 60 AACCCAGAGG ACTGGTGGAG TTGTTGCTC AAACAGTGT TCCGCTAAGT 240
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 65 AAAAGTAAAC AACTTCTTCA AAAAGCTGTA GAACGTGGAG CAGTACCAGT AGAAATGCTG 540
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 70 CAACTAACA AACTAAACA GTCATGCCA TTTGGAAGAG TCCAGTTAA CCTTCTAAAT 840
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 ACCTCTAGAT CAGAAATGCC AGATTGTTT GTGCTTGGAT CTAAACCAAG TGGAAATGAT 960
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 80 GATTACATGA GCTGTTTAG AACTCCAGTT GTAAAGAAATG ACTTTCACC TGCTTGTGCA 1440
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GTAAATGGAGT GTGGAATAT TGATCTTAAT AGTTGGCTTA AAAAGAAAAA ATCCATTGAT 1860
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AAGCTAATTG ATTTTGGGAT TGCAAAACCA ATGCAACCAAG ATACAACAAG TGTGTGTTAA 2040
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GGATGATTTT TGTACTATAT GACTTACGGG AAAACACCAT TTCAGCAGAT AATTAATCAG 2220
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Seq ID NO: 34 Protein sequence:

Protein Accession #: AAH00633.1

1 11 21 31 41 51
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AIQEPDDARD YPQMARANCK KPAPVHISFA QFELSQGNVK KSKQLLKAV ERGAVPLEML 180
EIALRNINLQ KQQLLSEEEK KNLSASTVLT AQESFSGSLG HLQNRNNSCD SRGQTTKARF 240
LYGENMPQD AEIGYRNSLR QTNKTKQSCF FGRVPVNNLL SPDCDVKTDD SVVPCFMRQ 300
TSRSECRDLV VPSGKPSGND SCBLRNLSKV QNSHFKEPLV SDEKSSSELI TDSITLKNKT 360
ESSLLAKLEE TKETQEPEVE ESNKQWQSK RKSECTINQNE AASNHWQIV ELARKVNTAQ 420
KHITTFEPVF SVSQSPPIIS TSKWDFPKSI CHTPSSNTLD DYMSCFRTPV VKNDFPPACQ 480
LSTPYGQAPC PQQQHQILA TPLQNLQVLA SSSANECISV KGRYISILKQ IGSQSSSKVP 540
QVLNEKKQIY AIKVNLEEA DNQTLDSYRN EIAYLNKLOQ HSDKIIRLYD YEITDQYIYM 600
VMECGNIDLN SWLKKKSID PWERKSYWKN MLEAVHTIQ HGIVHSDLPK ANPLIVDGNL 660
KLIDFGLTANQ MQPDTTSVVK DSQVGTNYM PPEAIKDMSS SRENGSKSK ISPSSDVWSL 720
GCILYYMTYG KTFPQQLINQ ISKLHAIIDP NHEIEFPDIP EKDLQDVLCR CLKRDPKQRI 780
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Seq ID NO: 35 DNA sequence

Nucleic Acid Accession #: NM_005823.2

Coding sequence: 85..1953

1 11 21 31 41 51
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CCCTCAGAGG CCCTGGCTGG AGAGACAGGG CAGGAGGCTG CACCCCTGGA CGAGATCTCG 240
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GAGGTGTCTG GCCTGAGCAC GGAGCGTGTG CGGAGCTGG CTGTGGCCTT GGCACAGAAG 360
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GGGCCCCAGG CCTGCACCGG TTTCTTCTCC GCATCACGA AGGCCAATGT GGACCTGCTC 540
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CCTGCTGGG ATCCCGCCTT GGCCAGGAGC AGGCAGGGGT GATCCCCGT CCACCCCAAG 2040
AGAACTCGG CTCAGTAAAC GGAACATGC CCCCTGCAGA CAGCT

Seq ID NO: 36 Protein sequence

Protein Accession #: NP_005814.1

1 11 21 31 41 51
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DVRALGGLAC DLGPRFVAES AEVLLPRLVS CPGPLDQDQO EAARAALQGG GPYPGPPSTW 240
SVSTMALRG LLPLVGLPPII RSIPOGIVAA WRQSRSDPS WRQPERTILR PRFRREVERT 300
ACPSGKKARE IDESLIFYKK WELEACVDAA LLATQMDRVN AIPPTYEQLD VLKHKLDELY 360

PQGYPESVIQ HLGYLFLKMS PEDIRKWNVT SLETLKALLE VNKGHEMSQ VATLIDRFVK 420
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 RLAFQNMNGS EYFVKIQSFL GGAPTEDLKA LSQNVSMDL ATPMKLRIDA VLPLTVAEVQ 540
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 PCLLGPVPVL TVLALLLAST LA

Seq ID NO: 37 DNA sequence
 Nucleic Acid Accession #: NM_013404.1
 Coding sequence: 89..1975

1 11 21 31 41 51
 | | | | |
 TGGCCGGCCA CTCCCGTCTG CTGTGACGGC CGGACAGAGA GCTACCGGTG GACCCACGGT 60
 GCCTCCCTCC CTGGGATCTA CACAGACCAT GGCCTTGCAA CGGCTCGACC CCTGTGGTTC 120
 CTGTGGGGAC CGCCCTGGCA GCTCCTGTCT CTTGCTCTTC AGCCTCGGAT GGGTGCATCC 180
 CGCGAGGACC CTGGCTGGAG AGACAGGGAC GGAGTCTGCC CCGCTGGGGG GAGTCTTGAC 240
 AACCCCGCAT AACATTTCAC GCTCTCCCC TCGCCAACTC CTGGCTTCC CGTGTGCGGA 300
 GGTGTCCGGC CTGAGCAGCG AGCGTGTCCG GGAGCTGGCT GTGGCTTGG CACAGAAGAA 360
 TGTCAAGCTC TCAACAGAGC AGCTGGGCTG TCTGGCTCAC CGGCTCTCTG AGCCCCCGGA 420
 GGACCTGGAC GCGCTCCCAT TGGACCTGCT GCTATTCTCT AACCCAGATG CGTGTCTGGG 480
 GCGCCAGGCC TGCACCGGTT TCTTCTCCCG CATCACGAAG GCCAATGTGG ACCTGCTCCC 540
 GAGGGGGGCT CCGCAGGAGC AGCGGCTGCT GCTGCGGCT CTGGCTGCT GGGTGTGGG 600
 GGGGTCTCTG CTGAGCAGGG CTGATGTGGG GGTCTGGGA GGGCTGGCTT GCGACCTGCC 660
 TGGGCGCTTT TGGGCGAGT CGGCCGAAGT GCTGCTACCC CGGCTGGTGA GCTGCCCCGG 720
 ACCCTTGGAC CAGGACCAAG AGGAGGAGCG CAGGGCGGCT CTGCAGGGG GGGGACCCCC 780
 CTACGCGCCC CCGTCCGACAT GGTCTGTCTC CACGATGGAC GCTCTGGGGG GCTGCTGCC 840
 CGTGTGGGCT CAGCCATCCA TCCGAGCAT CCGCAGGGC ATCGTGGGCG CGTGGCGGCA 900
 AGCTCTCTCT CCGGACCCAT CCGTGGGGCA GCTGGAACGG ACCATCTCC GGCCTGGGTT 960
 CCGGCGGGAA GTGGAGAACA CAGCTGTGCC TTCAGGCAAG AAGGCCCGCG AGATAGACGA 1020
 GAGCCTCATC TTCTACAAGA AGTGGGAGCT GGAAGCTTGC GTGGATGGCG CCCTGCTGGC 1080
 CACCCAGATG GACCGCGTGA ACGCCATCCC CTTCACCTAC GAGCAGCTGG ACCTCTTAAA 1140
 GCATAAAGCT CTGAGCTCTT ACCCAAGAG TTACCCCGAG TCTGTGATCC AGCACTTGGG 1200
 CTACCTCTTC CTCAAGATGA GCGCTGAGGA CATTCGCAAG TGAATGTGA CGTCCCTGGA 1260
 GACCTTGAAG GCTTTGCTTG AAGTCGACAA AGGGCACGAA ATGAGTCTCT AGGCTCTCTG 1320
 GCGGCCCTCC CCACAGGTGG CCACCTGAT CGACCGCTTT GTGAAGGGAA GGGGCCAGCT 1380
 AGACAAGAC ACCCTAGACA CCGTACCGCC CTCTACCTCT GGGTACCTGT GCTCCCTCAG 1440
 CCGCGAGGAG CCGCTGAAGG TGCCCCCAG CAGCATCTGG GCGGTCAAGC CCGAGGACCT 1500
 GGACAGGTGT GACCCAGGCG AGCTGGAAGT CCTCTATCCC AAGGCCCGCC TTGCTTTCCA 1560
 GAACATGAAC GGGTCCGAAT ACTTCGTGAA GATCCAGTCC TTCCTGGTG GGGCCCCCAC 1620
 GGAGGATTGG AAGCGGCTCA CTCAGCAGAA TGTGAGCATG GACTTGCCCA CGTTCATGAA 1680
 GCTGCGGAGC GATGCGGTGC TGCGGTGAC TGTGGCTGAG GTGCAGAAAC TTCTGGGACC 1740
 CCAAGTGGAG GAGCTGAAGC CGGAGGAGCG GCACCGCCCG GTGCGGGAAT GGATCCTACG 1800
 GCAGCGGAGC GACGACCTGG ACACGCTGGG GCTGGGGCTA CAGGGCGGCA TCCCAACGG 1860
 CTACCTGGTC CTAGACCTCA GGTGCAAGA GACCTCTCTG GGGACGCCCT GCTCTCTAGG 1920
 ACCTGGACCT GTTCTCACCG TCCTGGCACT GCTCCTAGCC TCACCCCTGG CCTGAGGGCC 1980
 CCACTCCCTT GCTGGCCCCA GCGCTGCTGG GGATCCCGCG CTGGCCAGGA GCAGGCAAGG 2040
 GTGATCCCGG TTCCACCCCA AGAGAAGTCC CGCTCAGTAA ACGGGAACAT GCCCCCTGCA 2100
 GACACGT

Seq ID NO: 38 Protein sequence
 Protein Accession #: NP_037536.1

1 11 21 31 41 51
 | | | | |
 MALQRLDPCW SCGDRPGSLL FLLFSLGWVH PARTLAGETG TESAPLGGVL TTPHNISLS 60
 PRQLLGFPFA EVGGLSTERV RELAVLAQK NVKLSTEQLR CLAHLSEPP EDLDALPLDL 120
 LLFLNPDAFS GPQACTRFFS RITKANVDLL PRGAPERQRL LPAALACWGV RGSLLSEADV 180
 RALGGACDL PGRFVAESAE VLLPRLVSCP GPLDQDQQA ARAALQGGP PYGPPSTWSV 240
 STMDALRGLL PVLGQPIIRS IPQGIWAAR QRSRDPSPWR QPERTILRPR FRREVEKTAC 300
 PSGKAREID ESLIFYKWE LEACVDAALL ATQMDRVNAI PFTYEQLDVL KHLDELVPQ 360
 GYPESVIQHL GYLFLKMSPE DIRKWNVTSL ETLKALLEVD KGHEMSQAP RRPLPQVATL 420
 IDRFVKGGRQ LDKDTLDTLT AFYPGYLCSL SPEELSVPV SSINAVRPQD LDTCDPRQLD 480
 VLYPKARLAF QNMNGSEYFV KIQSPLGGAP TEDLKALSQQ NVSMDLATFM KLRTDAVLPL 540
 TVAEVQKLLG PHVEGLKAE EHRPVRDWIL RQRQDDLDTL GLGLQGGIFN GYLVLDSLQV 600
 ETLSGTFCLL GPGPVLTVLA LLLASTLA

Seq ID NO: 39 DNA sequence
 Nucleic Acid Accession #: NM_001508.1
 Coding sequence: 1..1362

1 11 21 31 41 51
 | | | | |
 ATGGCTTCAC CCAGCTCTCC GGGCAGTGAC TGCTCCCAA TCATTGATCA CAGTCATGTC 60
 CCCGAGTTTG AGGTGGCCAC CTGGATCAAA ATCACCTTA TTCTGGTGA CCTGATCATC 120
 TTCTGATGG GCTTCTGGG GAACAGCGTC ACCATTCCGG TCACCCAGGT GCTGCAGAAG 180
 AAAGGATACT TGCAGAAGGA GGTGACAGAC CACATGGTGA GTTTGGCTTG CTGGACATC 240
 TTGGTGTTC TCATCGGCAT GCGCATGGAG TTCTACAGCA TCATCTGGAA TCCCTGACC 300
 ACGTCCAGCT ACACCTGTCT CTGCAAGCTG CACACTTCTC TCTTCGAGGC CTGCAGTAC 360
 GCTACGCTGC TGCACTGTCT GACGCTCAGC TTTGAGCGCT ACATCGCCAT CTGTACCCC 420
 TTCAGGTACA AGCTGTGTGC GGGACCTTGC CAGGTGAAGC TGCTGATTGG CTTCGTCTGG 480
 GTCACTCTCG CCGTGTGGC ACTGCCCTTG CTGTTTGCCA TGGTACTGAC GTACCCCTG 540
 GTGAAGGTGC CCAGCCACCG GGGTCTCACT TGCAACCGCT CCAGCACCGG CCACCAAGAG 600
 CAGCCCGAGA CCTCCAATAT GTCCATCTGT ACCAACCTCT CCAGCCGCTG GACCGTGTTC 660
 CAGTCCAGCA TCTTCGGGCG CTGCTGGTCT TACCTCTGGT TCCTGCTCTC CGTAGCCTTC 720
 ATGTGCTGGA ACATGATGCA GGTGCTCATG AAAAGCCAGA AGGGCTCGCT GCGCGGGGGC 780
 ACGCGGCTTC GCGACTGAG AAGTCCGAG AGCGAAGAGA GCAGGACCGC CAGGAGGCG 840
 ACCATCATCT TCCTGAGGCT GATTGTTGTG ACATTGGCGG TATGCTGSAT GCCCAACCA 900
 ATTCGAGGGA TCATGGCTCG GCGCAACCC AAGCAAGACT GAGCAGGATC CTACTTCCGG 960

GCGTACATGA TCCTCTCCCTC CTCTCGGAG ACGTTTCTCT ACCTCAGCTC GGTCAATCAAC 1020
 CCGCTCCTGT ACACGGTGTCT CTCGACGAGC TTTCCGGCGG TGTTCGTGCA GGTGCTGTGC 1080
 TGCCGCTCTG CGCTGCAGCA CGCCAAACCAC GAGAAGCGCC TGCGCGTACA TGCGCACTCC 1140
 ACCACCGACA GCGCCCGCTT TGTGACGCGC CCGTTGCTCT TCGCGTCCCG GCGCCAGTCC 1200
 TCTGCAAGGA GAATCAGAAA GATTTCTTA AGCACTTTTC AGAGCGAGGC CGAGCCCCAG 1260
 TCTAAGTCCC AGTCATTGAG TCTCGAGTCA CTAGAGCCCA ACTCAGGCGC GAAACCAGCC 1320
 AATTCTGCTG CAGAGAATGG TTTTCAGGAG CATGAAGTTT GA

Seq ID NO: 40 Protein sequence
 Protein Accession #: NP_001499.1

1 11 21 31 41 51
 MASPSLEPGSD CSQIIDHSHV PEFEVATWIK ITLILVYLII FVMGLLGNSV TIRVTQVLQK 60
 KGYLQKEVTD HMVSLACSDI LVPLIGMPME FYSIIWNPLT TSSYTLSCKL HTFLFRACSY 120
 ATLLHVLTLT FERYIALCHP FRYKAVSGPC QVKLLIGFVW VTSALVALPL LFAMGTEYPL 180
 VNVPSHRGLT CNRSSTRHHE QPETSNSMIC TNLSSRWTFV QSSIFGAPVV YLVVLLSVAF 240
 MCNMNQVLM KSKQKSLAGG TRPPQLRKEB SEESRTARRQ TIIFLRILIV TLAVCWMPNQ 300
 IRRIMAAAKP KHDWTRSYFR AYMLLPFSE TFFYLSVIN PLLYTVSSQQ FRRVFVQVLC 360
 CRLSLQHANH SKRLRVHAHS TTDSARFVQR PLLFASRRQS SARRTKIKPL STPQSRBPQ 420
 SKSQSLSELS LEPSNGAKPA NSAAENGFBQ HEV

Seq ID NO: 41 DNA sequence
 Nucleic Acid Accession #: NM_022358
 Coding sequence: 65..1057

1 11 21 31 41 51
 GGAGCGCGCG GTCCGGGCAC ACGGAGCAGG TTGGGACCGC GCGGGTACC GGGGCGGGG 60
 CGCCATCGCG AGGCGGAGCG TCGCGCGGCG CGGGCTGGTC CTGTGCACCC TGTGTTACCT 120
 GCTGGTGGCG GCTGCTGTCT TCGACGCGCT CGAGTCCGAG GCGGAAAGCG GCGCCAGCG 180
 ACTGCTGGTC CAGAGCGGCG GCGCTCTCCG GAGGAAGTTC GCGTCTCGG CGAGGACTA 240
 CGCGAGCTG GAGCGCTGGG GCTCCAGGC TGAGCCCCAC GCGCGCGCGC GCCAGTGAA 300
 GTTCCCGCGC TCCTTCTACT TCGCCATCAC CGTCATCACT ACCATCGGGT ACGGCCACGC 360
 CGCGCCCGGT ACGGACTCCG GCAAGGCTCT CTGCATGTTT TACGCGCTCC TGGGCATCCC 420
 GCTGACGCTG GTCACTTTCC AGAGCCTGGG CGAACGGCTG AACGCGTGG TGGGCGCCT 480
 CCTGTGGCG GCCAAGTGCT GCCTGGGCGT CGCGTGGACG TCGGTGCCA CGGAGAACT 540
 GGTGGTGGCG GGGCTGCTGG GGTGTGCGCG CACCTGGGCC CTCGGGGCGG TCGCCTTCTC 600
 GCACCTCGAG GCGTGACCTT TCTTCCACGC CTACTACTAC TGCCTCATCA CCCTCACCAC 660
 CATCGGCTTC GCGGACTTCG TGSCACTGCA GAGCGGCGAG GCGCTGCAGA GGAAGCTCCC 720
 CTCAGTGGCC TTAGCTTCC TCTACATCTT CCTGGGCTC ACGGTCTATT GCGCCTTCTC 780
 CAACCTGGTG GTCTGCGCTT TCCTCGTTGC CAGCGCGCAG TGGCCCGAGC GCGCTGCCCC 840
 CCCCCCAGC CGCGCGCCCT CGGGGGCGCC CGAGAGCCGT GGCCTCTGGC TGCCCCCGCG 900
 CCGGCGCGC TCGGTGGGCT CCGCTCTGT CTTCTGCCAC GTGCACAAGC TGGAGAGGTG 960
 CGCGCGCGC AACCTGGGCT TTTGCGCCCC CTCGAGCCCG GGGTCTGTG GTGCGGGCA 1020
 GGTCTCCAGG GGTGGGCGCC GGTGGAAGTC CATCTGACAA CCCCACCCAG GCCAGGGTGC 1080
 AATCTGGAAT GGGAGGCTCT GGCTTCAGCT ATCAGGCGAC CCTCCCGAGG GATTGGAAC 1140
 GGATGACGGG CCTCTAGGCG GTCTTCTGCC ACGAGCAGTT TCTCAATTAT GTCTGTGGCT 1200
 AAGTCCCTCT CCTCTTTCC AAAAATATAT TACAGTCACA CCATAAAAAA AAAAAA 1260
 AAAAAA AAAAAA AAAAA

Seq ID NO: 42 Protein sequence
 Protein Accession #: NP_071753

1 11 21 31 41 51
 MRRPSVRAAG LVLCTLCYLL VGAAPVDALE SEABSGRQRL LVQKRGALRR KGFSAEDYR 60
 ELERLALQAE PHRAGRQWKP PGSPFYFAITV ITTIGYGHAA PGTDGKVPK MFYALLGIPL 120
 TLVTFQSLGE RLNAVVRLL LAACKCLGLR WTCVSTENLV VAGLLACATL LALGAVAFSH 180
 FEGWTFPHAY YYCFITLTTI GFQDFVALQS GEALQRLPY VAFSFLYILL GLTVIGAFIN 240
 LVVLRFLVAS ADWPERAARP PSPRPFGAPE SRGLMLPRRP ARSVGSASVF CHVKLERCA 300
 RDNLQPSPPS SPGVVRGQQA PRPGARWESI

Seq ID NO: 43 DNA sequence
 Nucleic Acid Accession #: NM_000869.1
 Coding sequence: 220..1656

1 11 21 31 41 51
 GGAAACATGA TCCAGCTGAA GGAAGTATTG CAGGAAAACT TGGCAGCTCC CCAACCTTGG 60
 TGGCCAGGGG AGTGTGAGGC TGCAGCCTCA GAAGGTGTGA GCAGTGGCCA CGAGAGGCCA 120
 GCTGGCTGGG ACATGAGGTT GGCAGAGGGC AGGCAAGCTG GCGCTTGGTG GCGCTCGCCC 180
 TGAGCACTCG GAGGCACTCC TATGCTTGA AAGCTCCTA TGCTGCTGTG GGTCCAGCAG 240
 GCGTGTCTCG CCTGTCTCT CCCCACATC CTGGCACAGG GAGAAGCCAG GAGGAGCCGA 300
 AACACCAACA GCGCGCTCT GCTGAGGCTG TCGGATTACC TTTGACCAA CTACAGGAAG 360
 GGTGTGCGCC CCGTGAAGGA CTGAGGGAAG CCAACCAACG TATCCATTGA CGTCATTGTC 420
 TATGCCATCC TCAACGTGGA TGAGAAGAAT CAGGTGCTGA CCACCTACAT CTGGTACCGG 480
 CAGTACTGGA CTGATGAGTT TCTCCAGTGG AACCTGAGG ACTTTGACAA CATCACCAAG 540
 TTGTCCATCC CCAACGACAG CATCTGGGTC CCGGACATTC TCATCAATGA GTTCGTGGAT 600
 GTGGGGAAGT CTCAAATAT CCGTACGCTG TATATTGGGC ATCAAGGCGA AGTTGAGAAC 660
 TACAAGCCCC TTCAAGTGGT GACTGCTGT AGCCTCGACA TCTACAACTT CCGCTTCGAT 720
 GTCCAGAACT GCTCGCTGAC CTTCAACAGT TGGCTGCACA CCATCCAGGA CATCAACATC 780
 TCTTTGTGGC GCTTCCAGA AAAGGTGAAA TCCGACAGGA GTGTCTTCAT GAACAGGGA 840
 GAGTGGGAGT TGCTGGGGT GCTGCCCTAC TTTCCGGAGT TCAGCATGGA AAGCAGTAAC 900
 TACTATGCAG AATGAAGTT CTATGTGCTC ATCCGCGGCG GCGCCTCTT CTATGTGCTC 960
 AGCTGCTAC TGCCAGCAT CTCTCTCATG GTCATGAGCA TCGTGGGCTT CTACCTGCC 1020
 CCAACAGTG GCGAGAGGCT CTCTTCAAG ATTACACTCC TCTGGGCTA CTGGTCTTC 1080
 CTGATCATCG TTTCTGACAC GCTGCCCGCC ACTGCCATCG GCACTCCTCT CATGTGTGTC 1140
 TACTTTGTGG TGTGATGGC TCTGCTGGTG ATAAGTTTGG CCGAGACCAT CTTCATTGTG 1200

CGGCTGGTGC ACAAGCAAGA CCTGCAGCAG CCGGTGCCTG CTGGCTGCG TCACCTGGTT 1260
 CTGGAGAGAA TCGCTGGCTG ACTTTGCTG AGGGAGCAGT CAACCTCCCA GAGGCCCCCA 1320
 GCCACCTCCC AAGCCACCAA GACTGATGAC TGCTCAGCCA TGGGAAACCA CTGCAGCCAC 1380
 ATGGGAGGAC CCCAGGACTT CGAGAAGAGC CCGAGGGACA GATGTAGCCC TCCCCACCA 1440
 CCTCGGGAGG CCTCGCTGCG GGTGTGTGGG CTGCTGCAGG AGCTGTCTTC CATCCGGCAA 1500
 TTCTCGGAAA AGCGGGATGA GATCCGAGAG GTGGCCGAG ACTGGCTGCG CGTGGGCTCC 1560
 GTGCTGGACA AGCTGCTATT CCACATTAC CTGCTAGCGG TGCTGGCTTA CAGCATCACC 1620
 CTGGTTATGC TCTGCTCCAT CTGGCAGTAC GCTTGTAGTG GTACAGCCCA GTGGAGGAGG 1680
 GGGTACAGTC CTGGTTAGGT GGGGACAGAG GATTTCTGCT TAGGCCCTTC AGGACCCAGG 1740
 GAATGCCAGG GACATTTTCA AGACACAGAG AAAGTCCCGT GCCCTGTTTC CAATGCCAAT 1800
 TCATCTCAGC AATCACAAGC CAAGGTCTGA ACCCTTCCAC CAAAACTGG GTGTTCAAGG 1860
 CCCTTACACC CTGTCCCAC CCCAGCAGC TCACCATGGC TTTAAACAT GCTCTCTTAG 1920
 ATCAGAGAAA ACTCGGCAC TCCCTAAGTC CACTCTAGTT GTGAGCTTTT CCCCATTGAC 1980
 CCTCACTGA ATAAGGGACT TTGGAATTCT GCTTCTCTTT CACAACCTTG CTTTTAGGTT 2040
 GAAGGCAAAA CCAACTCTCT ACTACACAGG CCTGATAACT CTGTACGAGG CTCTCTTAAC 2100
 CCCTAGTGTG TTTTCTTCT TCACTCACT TGTGGCAGCT TCCCTGAACA CTCATCCCCC 2160
 ATCAGATGAT GGGAGTGGGA AGAATAAAAT GCAGTGAAC CC

Seq ID NO: 44 Protein sequence

Protein Accession #: NP_000860.1

1 11 21 31 41 51
 MLLWVQALL ALLLFTLLAQ GEARRSRNVT RPALLRLSDY LLNTRYKGVF FVRDWRKPTT 60
 VSDIVIVYAI LNVDEKNQVL TTYIYRQYM TDEFLQWNP DFDNITKLSI PTDSIWNVDI 120
 LINEFVDVVK SPNIPVYVYR HQGEVQNYKQ LQVVTACSLD IYNFPDVGNC CSLTFTSWLH 180
 TIQINISLW RLPEKVKSYR SVFMNQGEWE LLGVLPHYRE FMESSNYFA EMKFYVVIIR 240
 RPLFYVSVLL LPSIFLWMDL IVGFYLPFNS GERVSFKITL LLGYSVFLII VSDTLPTAI 300
 GTPILGVYVF VCMALLVSL AETIFIVRLV HKQDIQQVPF AMLRHLVLER IAWLLCLREL 360
 STSQRPFPAT QATKTDDCSA MGNHCSHMGG PQDFEKSFRD RCPSPPPPRE ASLAVCGLLQ 420
 ELSSIRQFLE KRDEIREVAR DMLRVGSVLD KLLPHIYLLA VLAYSITLVM LNSIWQYA

Seq ID NO: 45 DNA sequence

Nucleic Acid Accession #: NM_015507

Coding sequence: 241..1902

1 11 21 31 41 51
 CCGCAGAGGA GCCTCGGCCA GGCTAGCCAG GGCGCCCCCA GCCCCTCCCC AGGCCGCGAG 60
 CGCCCTGCGC GCGGTGCGCT GCGTCCCTCC CCAGACTGCA GGGACAGCAC CGGTAACCTG 120
 CGAGTGGAGC GAGGAGCCCG AGCGGCTGAG GAGAGAGGAG GCGGCGGCTT AGCTGCTACG 180
 GGGTCCGGCC GCGGCCCTCC CGAGGGGGGG TCAGGAGGAG GAAGGAGGAC CCGTGCAGAG 240
 ATGCTCTGCG CCGGAGGCTC TGCGCTCCCG CTGCTGCTCT CCGTGGTGGC AGGTGGTTTC 300
 GGGAAACCGG CCACTGCAAG GCATCACGGG TTGTTAGCAT CGGCACGTCA GCCTGGGGTC 360
 TGTCACTATG GAACATAACT GGCTGCTGCG TACGGCTGGA GAAGAAACAG CAAGGGAGTC 420
 TGTGAAGCTA CATGCGAACC TGGATGTAAG TTTGGTCACT GCGTGGGACC AAACAAATGC 480
 AGATGCTTTC CAGGATACAC CGGGAACACC TGCAGTCAAG ATGTGAATGA GTGTGGAATG 540
 AAACCCCGCG CATGCCAACA CAGATGTGTG AATACACAGC GAAGCTACAA GTGCTTTTGC 600
 CTCAGTGGCC ACATGCTCAT GCCAGATGCT ACCTGTGTGA ACTCTAGGAC ATGTGCCATG 660
 ATAACTGTGC AGTACATAGT TGAAGACACA GAAGAAGGGC CACAGTGCCT GTGTCCATCC 720
 TCAGGACTCC GCCTGGCCCC AAATGGAAGA GACTGTCTAG ATATTGATGA ATGTGCTCTT 780
 GGTAAAGTCA TCTGTCCCTA CAATCGAAGA TGTGTGAACA CATTTGGAAG CTACTACTGC 840
 AAATGTACCA TTGTTTTCGA ACTGCAATAT ATCAGTGGAG GATATGACTG TATAGATATA 900
 AATGAATGTA CTATGGAATG CCATACGTGC AGCCACCATG CCAATTGCTT CAATACCCAA 960
 GGGTCTTCA AGTGTAAATG CAAGCAGGGA TATAAAGGCA ATGGACTTCG GTGTCTGTCT 1020
 ATCCCTGAAA ATTCTGTGAA GGAAGTCCCT AGAGCACCTG GTACCATCAA AGACAGAATC 1080
 AAGAAGTTGC TTGCTCACAA AAACAGCATG AAAAAGAAGG CAAAAATTAA AAATGTTACC 1140
 CCAGAACCCA CAGGAGCTCC TACCCCTAAG GTGAACCTGC AGCCCTTCAA CTATGAAGAG 1200
 ATAGTTTCCA GAGCGGGGAA CTCTCATGGA GGTAAAAAAG GGAATGAAGA GAAATGAAA 1260
 GAGGGGCTTG AGTATGAGAA AAGAGAAGAG AAAGCCCTGA AGAATGACAT AGAGGAGOGA 1320
 AGCCTGCGAG GAGATGTGTT TTTCCCTAAG GTGAATGAAG CAGGTGAATT CGGCTGATT 1380
 CTGGTCCAAA GAAAGCGCT AACTTCCAAA CTGGAACATA AAGATTAAA TATCTGGTT 1440
 GACTGCAGCT TCAATCATGG GATCTGTGAC TGGAAACAGG ATAGAGAAGA TGATTTTGAC 1500
 TGGAACTCTG CTGATCGAGA TAATGCTATT GGCTTCTATA TGGCAGTTCG GGCCTTGGCA 1560
 GGTCAACAAG AAGACATTGG CCGATTGAAA CTTCTCTTAC CTGACCTGCA ACCCCAAAGC 1620
 AACTTCTGTT TGCTCTTTGA TTACGGCTG GCGGAGAGCA AAGTCGGGAA ACTTCGAGTG 1680
 TTTGTGAAAA ACAGTAACAA TGCCCTGGCA TGGGAGAAGA CCAAGAGTGA GGATGAAAAG 1740
 TGGAGACAGG GGAATAATCA GTTGTATCAA GGAACGTATG CTACCAAAAG CATCATTITT 1800
 GAAGCAGAAC GTGGCAAGGG CAAACCCGCG GAAATCGCAG TGGATGGCGT CTGCTTGTGT 1860
 TCAGGCTTAT GTCCAGATAG CCTTTTATCT GTGGATGACT GAATGTTACT ATCTTTATAT 1920
 TTGACTTTGT ATGTGAGTTC CCGTGTTTT TTGATATTGC ATCATAGGAC CTCTGGCATT 1980
 TTAGAATTAC TAGCTGAAAA ATTGTAATGT ACCAACAGAA ATATTATTGT AAGATGCCCT 2040
 TCTGTATATA GATATGCCAA TATTGTCTTT AAATATCATA TCACTGTATC TTCTCAGTCA 2100
 TTTCTGAATC TTTCACATT ATATTATAAA ATATGGAAT GTCACTTTAT CTCCCTCTCT 2160
 CAGTATATCT GATTGTGATA AGTAAGTTGA TGAGCTTCTC TCTACACAT TTCTAGAAAA 2220
 TAGAAAAAAA AGCAGACAGA AATGTTTAACT TGTTTGACTC TTATGATACT TCTTGGAAAC 2280
 TATGACATCA AAGATAGACT TTTGCCTAAG TGGCTTAGCT GGGCTTTTCA TAGCCAAACT 2340
 TGTATATTAA AATTCTTTGT AATAATAATA TCCAAATCAT CAAAAAATA AAAAAAAA

Seq ID NO: 46 Protein sequence

Protein Accession #: NP_056322

1 11 21 31 41 51
 MPLPWSLALP LLLSVWAGGF GNAASARHNG LLASARQPGV CHYGTKLACC YGWRNRSKGV 60
 CEATCEPGCK FGECVGNPKC RCFPGYTGKT CSQDVNECGM KPRPCQHRVC NTHGSYKCP 120
 LSGHMLMPDA TCVNSRTCAM INCQYSCBDT EBGPOCLCPS SGLRLAPNGR DCLDIDECAS 180
 GKVICPYNRR CVNTFGSYCC KCHIGPELQY ISGRYDCIDI NECTMDSEHC SEHANCENTQ 240

GSPKCKCKQG YKGNGLRCSA IPENSVKEVL RAPGTIKDRI KLLAHKNSM KKKAKIKNVT 300
 PEPTRTPTPK VNLQPFNVEE IVSRGNSHG GKKGNEEKMK EGLEDEKREE KALKNDIEER 360
 SLRGDVFFPK VNEAGEFLGI LVQRKALTSK LEHKDLNISV DCSFNHIGCD WKQDREDDFD 420
 WNFADRDNAI GFYMAVPALA GHKQDIGRLK LLLPDLQPOS NFCLLFYRL AGDKVGLRV 480
 FVKNSNNALA WKTTSSEDEK WKTGKIQLYQ GTDATKSIIF EAERGKGTG EIAVDGVLLV 540
 SGLCPDLSLLS VDD

Seq ID NO: 47 DNA sequence
 Nucleic Acid Accession #: NM_005046
 Coding sequence: 16..777

1 11 21 31 41 51
 | | | | |
 GGATTTCGG GCTCCATGGC AAGATCCCTT CTCTGCCCC TGCAGATCCT ACTGCTATCC 60
 TTAGCCTTGG AAATGCGAGG AGAAGAAGCC CAGGGTGACA AGATTATTGA TGGCGCCCCA 120
 TGTGCAAGAG GCTCCACCCC ATGGCAGGTG GCGCTGTCCA GTGGCAATCA GCTCCACTGC 180
 GGAGGCGTCC TGGTCAATGA GCGCTGGGTG CTCCTGCGG CCCACTGCAA GATGAATGAG 240
 TACACGGTGC ACTTGGGCGG TGATAAGCTG GCGACAGGA GAGCTCAGAG GATCAAGGCC 300
 TCGAAGTCAT TCGGCCACCC CGGCTACTCC ACACAGACCC ATGTTAATGA CCTCATGTCTC 360
 GTGAAGCTCA ATAGCCAGGC CAGGCTGTCA TCCATGGTGA AGAAAGTCAG GCTGCCCTCC 420
 CGCTGGGAAC CCGCTGGAAC CACCTGTACT GTCTCGGCT GGGGCACTAC CACGAGCCCA 480
 GATGTGACCT TTCCCTCTGA CCTCATGTGC GTGGATGTCA AGCTCATCTC CCCCAGGAC 540
 TGACGGAAGG TTACAAGGA CTTACTGGAA AATTCCATGC TGTGGCTGG CATCCCCGAC 600
 TCCAGAAAAA ACGCTGCAA TGGTGACTCA GGGGACCGT TGGTGTGAG AGGTACCTCG 660
 CAAGGTCTGG TGTCTGGGG AACTTTCCCT TGGGCGCAAC CCAATGACCC AGGAGTCTAC 720
 ACTCAAGTGT GCAAGTTCAC CAAGTGGATA AATGACACCA TGAAGAACCA TCGCTAACGC 780
 CACACTGAGT TAATTAACTG TGTGCTTCCA AAGAAAAATG CACAGGAGTG AGGAGCGCGA 840
 TGACCTATGA AGTCAAAATT GACTTTACCT TTCTCAAAG ATATATTTAA ACCTCATGCC 900
 CTGTTGATAA ACCAATCAAA TTGGTAAAGA CCTAAACCA AAACAAATAA AGAAACACAA 960
 AACCTCAA

Seq ID NO: 48 Protein sequence
 Protein Accession #: NP_005037

1 11 21 31 41 51
 | | | | |
 MARSLLLPLQ ILLLSLALET AGEAAQDKI IDGAPCARGS HPWQVALLSG NQLHCGGVLV 60
 NERNVLTAAH CKNEYTVHL GSDTLGDRRA QRIKASKSFR HPGYSTQTHV NDMLVLKLS 120
 QARLSSMVKK VRLPSCRCEP GTTCTVSGWG TTTSPDVTFP SDLMCVDVKL ISPQDCTKVY 180
 KDLLENSMLC AGIPDSKRNA CNGDSGGPLV CRGTLQGLVS WGTFFCGQPN DPGVYTVCK 240
 PTKWINDTKM KHR

Seq ID NO: 49 DNA sequence
 Nucleic Acid Accession #: NM_003466.1
 Coding sequence: 11..1363

1 11 21 31 41 51
 | | | | |
 GAATTGCGG ATGCTCACA ACTCCATCAG ATCTGGCCAT GGAGGGCTGA ACCAGCTGGG 60
 AGGGGCTTT GTGAATGGCA GACCTCTGCC GGAAGTGGTC CGCCAGCGCA TCGTAGACCT 120
 GGGCCACAG GGTGAAGGC CCTGCGACAT CTCTCGCCAG CTCCGGTCA GCCATGGTTG 180
 CGTCAGCAAG ATCTTGGCA GGTACTACGA GACTGGCAGC ATCCGGCTGT GAGTGATAGG 240
 GGGTCTCAAG CCAAGGTGG CCAACCCCAA GGTGGTGGAG AAGATTGGGG ACTACAAACG 300
 CCAGAACCTT ACCATGTTT CCGGGAGAT CCGAGACCGG CTCTGGCTGT AGGGGCTCTG 360
 TGACAATGAC ACTGTGCCA GTGTGAGTCT CATTAATAGA ATCATCCGGA CCAAGTGCA 420
 GCAACCATTC AACCTCCCTA TGGACAGCTG CGTGGCCACC AAGTCCCTGA GTCCCGGACA 480
 CACGCTGATC CCGAGCTCAG CTGTAACCTC CCGGAGTCA CCGAGTCCG ATTCCCTGGG 540
 CTCCACCTAC TCAATCAATG GGCTCCTGGG CATCGCTCAG CCTGGCAGCG ACAAGAGGAA 600
 AATGGATGAC AGTATCAGG ATAGCTGCG ACTAAGCATT GACTCACAGA GCAGCAGCAG 660
 CGGACCCGGA AAGCACCTTC GCACGGATGC CTTACGCCAG CACCACCTCG AGCGCTCGA 720
 GTGCCCATTT GAGCGGCAGC ACTACCCAGA GGCTATGCC TCCCGGACCC ACACCAAGG 780
 CGAGCAGGGC CTCTACCCCG TGCCCTTGCT CAACAGCACC CTGAGCAGCG GGAAGGCCAC 840
 CCTGACCCCT TCCACACGCG CACTGGGGCG CAACCTCTCG ACTACCCAGA CTACCCCGT 900
 GGTGGCAGAT CCTCACTCAC CCTTGGCCAT AAAGCAGGAA ACCCCGAGG TGTCCAGTTC 960
 TAGCTCCACC CCTCTCTCT TATCTAGCTC CGCCTTTTG GATCTGAGC AAGTGGCTC 1020
 CGGGGTCGCG CCGTTCAATG CCTTTCCCA TGCTGCCTCC GTGTAAGGCG AGTTCACGGG 1080
 CCAGGCCCTC CTCTCAGGGC GAGAGATGGT GGGGCCACG CTGCCCGGAT ACCACCCCA 1140
 CATCCCAACC AGGGGACAGG GCAGCTATGC CTCTCTGCC ATCGCAGGCA TGGTGGCAGG 1200
 AAGTGAATAC TCTGGCAATG CCTATGGCCA CACCCCTAC TCCTCTTACA GCGAGGCTCG 1260
 GCGCTCCCC AACTCCAGCT TGCTGAGTTC CCCATATTAT TACAGTTCCA CATCAAGGCC 1320
 GAGTGCACCG CCCACCACTG CCACGGCCTT TGACCATCTG TAGTTGAAGC TT

Seq ID NO: 50 Protein sequence
 Protein Accession #: NP_003457

1 11 21 31 41 51
 | | | | |
 MPHSIRSGL GGLNQLGGAF VNGRPLPEVV RQRIVDLAQ GVRPCDISRQ LRVSHGCVSK 60
 ILGRYYTGS IRPGVIGGSK PKVATPKVVE KIGDYKRQNP TMFAWEIRD LLAEGVCDND 120
 TVPSVSSINR IIRTKVQPP NLPMDSCVAT KSLSPGHTLI PSSAVTPPES PQSDSLGSTY 180
 SINGLLGIAQ PGSDKRKMD SDQDSCLRSI DSQSSSSGPR KHLRTDAFSQ HHLEPLECPF 240
 ERQHYPEAYA SPSTTKGEQG LYPLLLNST LDGKATLTP SNTPLGRNLS THQYTPVVD 300
 PHSPFAIKQE TPEVSSSSST PSSLSAFL DLQQVSGVPP PFNAFFHAAS VYQFTGQAL 360
 LSGREVMGPT LPGYPPHPT SQGSGYASSA IAGMVAGSEY SGNAYGHTPY SSSYSEAWRFP 420
 NSSLLSPYY YSSSRPSAP PTTATAFDHL

Seq ID NO: 51 DNA sequence
 Nucleic Acid Accession #: NM_013952
 Coding sequence: 161..1357

1 11 21 31 41 51
 5 TTCAGAAGGA GGAGAGACAC CGGGCCCGAG GCACCCCTCG GGGCGGGCGG ACCCAAGCAG 60
 TGAGGGGCTG CAGCCGGCCG GCCAGGGCAG CGGCAGGCGC GGCCCGGACC TACGGGAGGA 120
 AGCCCCGAGC CCTCGGCGGG CTGCGAGCGA CTCCCGCGGG ATGCCTCACA ACTCCATCAG 180
 ATCTGGCCAT GGAGGGCTGA ACCAGCTGGG AGGGGGCTTT GTGAATGGCA GACCTCTGCC 240
 GGAAGTGGTC GGCAGCGCA TGTAGACCT GGCCACCAG GGTGAAGGC CCTGCCACAT 300
 CTCTGCCAG CTCCCGCTCA GCCATGGCTG CGTCAGCAAG ATCCTTGGCA GGTACTACGA 360
 10 GACTGGCAGC ATCCGCGCTG GAGTGATAGG GGGCTCCAAG OCCAAGGTGG CCACCCCAA 420
 GGTGGTGAAG AAGATTGGGG ACTACAAACG CCAGAACCCCT ACCATGTTTG CCTGGAGAT 480
 CCGAGACCGG CTCTGGCTG AGGGCGTCTG TGACAATGAC ACTGTGCCCA GTGTCACTC 540
 CATTAAATGA ATCATCCGGA CCAAAGTGCA GCAACCATTC AACCTCCCTA TGGACAGCTG 600
 CGTGGCCACC AAGTCCCTGA GTCCCGGACA CACGCTGATC CCAGCTCAG CTGTAACTCC 660
 15 CCGGAGTCA CCCCAGTGG ATTCCCTGGG CTCCACTAC TCCATCAATG GGCTCCTGGG 720
 CATCGCTCAG CCTGGCAGG ACAAGAGGAA AATGGATGAC AGTGATCAGG ATAGCTGCCG 780
 ACTAAGCATT GACTACAGA GCAGCAGCAG CGGACCCCGA AAGCACCTTC GCACGGATGC 840
 CTTCAAGCAG CACCACTCG AGCCGCTCGA GTGCCCATTT GAGCGGCGC ACTACCCAGA 900
 GGCTATGGC TCCCGCAGC ACACCAAGAG CGAGCAGGGC CTCTACCCGC TGCCCTTGCT 960
 20 CAACAGCACC CTGCGGAGC GGAAGGCCAC CCTGACCCCT TCCAACACGC CACTGGGGGG 1020
 CAACCTCTCG ACTACACAGA CCTACCCGCT GGTGGCAGCT CCGCCCTTTT GGATCTGCAG 1080
 CAAGTGGCT CCGGGGTCCC GGCCTTCAAT GCCTTTCCCC ATGCTGCCCT CGTGTACGGG 1140
 CAGTTCACGG GCCAGGCCCT CCTCTCAGGG CGAGAGATGG TGGGGCCGAC GCTGCCCGGA 1200
 TACCCACCCC ACATCCCGAC CAGCGGACAG GGCAGCTATG CCTCTCTGCG CATCGCAGGC 1260
 25 ATGTGGCAG GAATGGAATA CTCTGGCAAT GCCTATGGCC ACACCCCTA CTCCTCTAC 1320
 AGCGAGGCTG GGGGCTTCCC CAACTCCAGC TTGCTGAGTT CCCCATAITA TTACAGTTCC 1380
 ACATCAAGGC CGAGTGACAC GCCCACACT GGCACGGCCT TTGACCATCT GTAGTTGCCA 1440
 TGGGGACAGT G

30 Seq ID NO: 52 Protein sequence
 Protein Accession #: NP_039246
 1 11 21 31 41 51
 35 MPNHSIRSGH GGLNQLGGAF VNGRPLPEVV RQRIVDLAHQ GVRPCDISRQ LRVSHGCVSK 60
 ILGRYYETGS IRPGVIGGSK PKVATPKVVE KIGDYKRNQ TMFAHEIRDR LLAEGVCDND 120
 TVPSVSSINR IIRTRVQPPF NLFMDSCVAT KSLSPGHTLI PSSAVTPPES PQSDSLGSTY 180
 SINGLLGIAQ PGSDKRKMD SDQDSCLRSI DSQSSSSGPR KHLRTDAFSQ HLEPLECPF 240
 ERQHYPEAYA SPSTKGEQG LYPLPLINST LDDGKATLTP SNTPLGRNLS THQTYPVVAA 300
 PPFWICKSA PGSRPSMPP MLPPCTGSSR ARPSSQGERN WGPRCPDTHP TSPPADRAAM 360
 PPLPSQANWQ EVNTLAMFMA TPPTPTARP GASPTPAC

40 Seq ID NO: 53 DNA sequence
 Nucleic Acid Accession #: NM_012427
 Coding sequence: 43..924
 1 11 21 31 41 51
 45 CTGTGGTTC CTCTCTACTT GGGGAAATCA GGTGCAGCGG CCATGGCTAC AGCAAGACCC 60
 CCTCGGATGT GGGTGTCTCT TGCTCTGATC ACAGCCTTGC TTCTGGGGGT CACAGAGCAT 120
 GTTCTCGCCA ACAATGATGT TTCTGTGAC CACCCCTCTA ACACCGTGCC CTCTGGGAGC 180
 50 AACCAAGACC TGGAGCTGG GGCAGGGGAA GAGCCCGGT CGGATGACAG CAGCAGCCGC 240
 ATCATCAATG GATCCGACTG CGATATGCAC ACCAGCCGCT GGCAGGCCGC GCTGTTGCTA 300
 AGGCCCAACC AGCTCTACTG CCGGGCGGTG TTGGTGATC CACAGTGGCT GCTCACGGCC 360
 GCCCACTGCA GGAAGAAAGT TTTCAGAGTC GTCTCGGCC ACTACTCCCT GTCCACAGTT 420
 TATGAATCTG GGCAGCAGAT GTTCCAGGGG GTCAAAATCCA TCCCCACCC TGGCTACTCC 480
 55 CACCCCTGGC ACTCTAAGCA CCTCATGCTC ATCAAACTGA ACAGAAAGAT TCGTCCCACT 540
 AAAGATGTCA GACCCATCAA CGTCTCCTCT CATTGTCCCT CTGCTGGGAC AAAGTGCTTG 600
 GTGTCTGGCT GGGGACACAC CAAGAGCCCC CAAGTGCACT TCCCTAAGGT CCTCCAGTGC 660
 TTGAATATCA GGTGCTAAG TCAGAAAAGG TGGAGGATG CTTACCCGAG ACAGATAGAT 720
 GACACCATGT TCTGCGCGCG TGACAAAGCA GGTAGAGACT CCTGCCAGGG TGATTCTGGG 780
 60 GGGCCTGTGG TTGCAATGG CTCCCTGCAG GGAATCGTGT CCGGGGAGA TTACCTTTGT 840
 GCCCGGCCCA ACAGACCGGG TGTCTACAG AACCTCTGCA AGTTACCAA GTGGATCCAG 900
 GAAACCATCC AGGCCAATC CTGAGTCATC CCAGGACTCA GCACACGGC ATCCCCACCT 960
 GCTGCAGGGA CAGCCCTGAC ACTCTTTTCA GACCTCATT CCTTCCAGA GATGTTGAGA 1020
 65 ATGTTCACTT CTCAGCCCC TGACCCCATG TCTCTGGAC TCAGGGCTG CTCTCCCCAC 1080
 ATTGGGCTGA CCGTGTCTCT CTAGTTGAAC CCTGGGAACA ATTTCCAAA CTGTCCAGGG 1140
 CGGGGTTGCT GTCTCAATCT CCTGGGCA CTTTCATCCT CAAGCTCAGG GCCATCCCT 1200
 TCTCTGACG TCTGACCAA ATTTAGTCCC AGAAATAAAC TGAGAAAGTG AAAAAAAAAA

70 Seq ID NO: 54 Protein sequence
 Protein Accession #: NP_036559
 1 11 21 31 41 51
 75 MATARPPWM VLCAITALL LGVTEHVLN NDVSCDHPSN TVPSGSNQLD GAGAGEDARS 60
 DSSSRING SDCHMTQFW QAALLRPNO LYCGAVLVHP QWLLTAHCR KKVFRVRLGH 120
 YSLSPVYESG QMQFGVKSI PHPGYSHPGH SNDLMLIKLN RRIRPTKDR PINVSSHCP 180
 AGTKCLVSGW GTTKSPQVHF PKVLQCLNIS VLSQKRCEDA YPRQIDTDF CAGDKAGRDS 240
 CQDSSGGLV CNGSLQGLV WGDYPCARPN RPYVTNLCK FTWIMQETIQ ANS

80 Seq ID NO: 55 DNA sequence
 Nucleic Acid Accession #: NM_002214
 Coding sequence: 681..2990
 1 11 21 31 41 51
 85 CCCAGAGCG CCTCCCCCTG TTGCTGGCAT CCGAGCTTC CTCCCTTGCC AGCCAGGAGC 60
 CTGCCGACTT GTCTTTGCCG GCTGCTCGC AGACGGGCT GCAAAGCTGC AACTAATGGT 120
 GTTGCCCTCC CTGCCACCT GTGGAAGCAA CTGCGCTGAT TGATGCGCCA CAGACTTTT 180

TCCCTCGAC CTGCGGGG TACCCTCCCA CAGATCCAGC ATCACCAGT GAATGTACAT 240
 TAGGOTGTT TCCCTCCAG CTTCGGGCTT TGTGTTGGT TGAATGTGTT TGGCTCTTCG 300
 CTAAGCTGAT TTATGACGCA GAAGCCCCAC CGGCTGGAGA GAAACAAAAG CTCCTTTCTT 360
 5 TGTCCCGGAG CAGGCTGGGG AGCCCTTGCA GAGCCCTCTC TCAGTCCGCC GCCGGGCCCT 420
 TGGCCGTGGA AGGAGGTGCT TCTCGGGGAC ACCGCGGGAC CCGCGGTGCC GAGCGGGGAG 480
 GGCCGTAGGG GCCGTGAGAT GCGAGGGGT GCCCGGGGCC GCTTACCTGC ACCGCTTGCT 540
 CCGAGCGCGG GGGTCCGCTT GCTAGGCTCG CGGAAAACCT CTTAGCGACA CTGCGCCGCG 600
 GGCCCGGAGG TCGCCCGGGA GGCAGAGCCC GCGTCCGGAA GGCAGCCAGG CCGCGGGGCG 660
 10 GGCGCGGGCT GTTTTGCAAT ATGTGCGGCT CGGCCCTGGC TTTTITACC GCTGCAITTG 720
 TCTGCTGCA AAAAGACCGG CAGGTTCCCG CCGGTTCTCT CTGGGCGACC TGGGTGTTT 780
 CACTTGTCT TGGACTGGGC CAAGGTGAAG ACAATAGATG TGCACTCTCA AATGCAGCAT 840
 CCTGTGCCAG GTGCTTGCG CTGGGTCCAG AATGTGGATG GTGTGTTCAA GAGGATTCCA 900
 TTTACGGTGG ATCAAGAAGT GAACGTTGTG ATATTGTTTC CAATTAATA AGCAAAAGCT 960
 15 GCTCAGTTGA TTCAATAGAA TACCCATCTG TGCACTGTTAT AATACCCACT GAAATGAAA 1020
 TTAATACCCA GTTGACACCA GGAGAAGTGT CTATCCAGCT GCGTCCAGGA GCCGAAGCTA 1080
 ATTTTATGCT GAAAGTTGAT CCTCTGAAGA AATATCCTGT GGATCTTTAT TATCTTGTG 1140
 ATGTCTCAGC ATCAATGCAC AATAATATAG AAAAATTAAA TTCGTTGGA ACGATTTAT 1200
 CTAGAAAAAT GGCATTTTTC TCCCGTGACT TTGCTCTTGG ATTTGGCTCA TACGTTGATA 1260
 20 AAACAGTTTC ACCATACATT AGCATCCACC CGGAAGGATG TCATAATCAA TGCAGTGACT 1320
 ACAATTTAGA CTGCTAGCCT CCGCATGGAT ACATCCATGT GCTGTCTTGG ACAGAGAAC 1380
 TCACTGAGTT TGAAGAGGAT GTTCATAGAC AGAAGATCTC TGGAAACATA GATACACCA 1440
 AAGGAGGTTT TGAAGCCTAT CTTCAGGCGAG CTGTCTGTGA AAGTCATATC GGATGCGGAA 1500
 AAGAGGCTAA AAGATTGCTG CTGCTGATGA CAGATCAGAC GTCTCATCTC GCTCTTGATA 1560
 25 GCAAAATTGC AGCAATAGAT GTGCCCAATG ACGGAAACCT TCATCTGAAA AACAAAGTCT 1620
 ACGTCAATC GACAAACCTG GAACACCCCT CACTAGGCCA ACTTTCAGAG AAATTAATAG 1680
 ACAACAACTA TAAATGTCAT TTTGCACTTC AAGGAAACCA ATTTCTATGG TATAAGGATC 1740
 TTTACCCCTT CTGCGGAGGC ACCATTGCTG GTGAAATAGA ATCAAGGCT GCAAACTCA 1800
 ATAAATTGGT AGTGAAGGCT TATCAGAAGC TCATTTTACA AGTGAAGTT CAGGTGAAA 1860
 30 ACCAGGTACA AGGCATCTAT TTTAACATTA CCGCCATCTG TCCAGATGGG TCCAGAAAGC 1920
 CAGGATGGA AGGATGCGA AAGCTGACGA GCAATGATGA AGTTCTTTTC AATGTAACAG 1980
 TTACAAAGAA AAAATGTGAT GTCAAGGAG GAAAAAACA TGCAATAATC AAACCTATTG 2040
 GTTTTAATGA AACCGCTAAA ATTCATATAC ACAGAAACCT CAGCTGTGAG TGTGAGGACA 2100
 ACAGAGGACC TAAAGGAAAG TGTGTAGATG AAACCTTTCT AGATTCCAAG TGTTCAGAT 2160
 35 GTGATGAGAA TAAATGTCAT TTTGATGAAG ATCAGTTTTC TTCTGAGAGT TGCAAGTCAC 2220
 ACAAGATCA GCCCTGTTGC AGTGGTCCAG GAGTTTGTGT TGTGGGAAA TGTTCATGTC 2280
 ACAAAATTAA GCTTGGGAAA AATGATGGA AATGATGGA AAAGGATGAC TTTTCTGTG 2340
 CATATCACA TGGAAATCTG TGTGCTGGGC ATGGAGAGTG TGAAGCAGGC AGATGCCAAT 2400
 40 GCTTCAGTGG CTGGGAAGCT GATCGATGCC AGTCCCTTC AGCAGCAGCC CAGCACTGTG 2460
 TCAATTCAA GGGCCAAGTG TGCAGTGGAA GAGGCACGTG TGTGTGTGGA AGGTGTGAGT 2520
 GCACCGATCC CAGGAGCATC GCGCGCTTCT GTGAACACTG CCCCACCTGT TATACAGCCT 2580
 GCAAGGAAAA TGGCAATTGT ATGCAATGCC TTCACCTCA CAATTTGTCT CAGGCTATAC 2640
 TTGATCAGTG CAAACCTCA TGTGCTCTCA TGAACAACA GCATTATGTC GACCAAACTT 2700
 CAGAATGTTT CTCAGGCCCA AGCTACTTGA GAATATTTT CATCATTTT ATAGTTACAT 2760
 45 TCTTGATTGG GTTGCTTAAA GTCTGATCA TTAGACAGGT GATACTACAA TGGAAATAGT 2820
 ATAAATTAAT GTCTCATCA GATTACAGAG TGTGAGCCTC AAAAAAGGAT AAGTTGATC 2880
 TGCAAGTGT TGGCAAGA GACGTACCTT ACCGACGTG GAGGCTGAA GAAATAAAA 2940
 TGGATATCAG CAAATTAAT GCTCATGAAA CTTTCAGGTG CAATCTTAAA AAAAAGATT 3000
 50 TTAACACTT AATGGGAAAC TGGAAATTGT AATAATTGCT CTAAGGATT ATAATTTAA 3060
 AAGTACAGG AGGAGACAAA TTGCTCACGG TCATGCCAGT TGCTGTTGT ACTCTGAAAC 3120
 GAAGACTGAC AAGTATCTC ATCATGATGT GACTACATA GCTGCTGACT TTTTCAGAGA 3180
 AATATGTTT TTACTACTGT TTGAGACTAG TGTGTTGTA GCATTTACT GTAATATA 3240
 ACTTATTAG ATCAGCATAG AATGTAGATC CTCTGAAGAG CACTGATTAC ACTTTACAGG 3300
 55 TACCTGTTAT CCTACGCTT CCGAGAGAGA ACAAATGCTG GAGAGAGTT AGCAATTGTT 3360
 CACTACAGG GTACAGTAAT CCTGCACTG GACATGTGAG GAAAAAATA ATCTGGCAAG 3420
 TATATTCTAA GGTGCGCAA CACTTCAACA GTTGTGTTT GAATAGACAA GAACAGCTAG 3480
 ATGAATAAAT GATTGTTGTT TCACCTTTTC AAGAGGTGAA CAGATACAC CTTAATCTTA 3540
 AAAGATTAT GCTTTTAAA GTGTGTAGTT TTAGCATGT GTGTTTATGG TTTGCTTAT 3600
 60 TTTGCAAGAT GGATACTAAT TCCAGCATTC TCTCTCTTT GCCTTTATGT TTTGTTTCT 3660
 TTTTACAGG ATAGTTTAT GTATGTCACA GATGACTGGA TTAATTAAGT GCTAAGTTAC 3720
 TACTGCCATA AAAAATAAT AATACAATGT CACTTTATCA GAATACTAGT TTTAAAAGCT 3780
 GAATGTTAA

Seq ID NO: 56 Protein sequence

Protein Accession #: NP_002205

65 1 11 21 31 41 51
 | | | | |
 MCGSALAPPT AAFVCLQND RGPASPLWAA NVFSLVLGLG QGEDNRCASS NAASCARCLA 60
 LGPECGMCVQ EDFISGSSRS ERCDIVENLI SKGCSVDSIE YPSVHVLIPT ENEINTQVTP 120
 70 GEVSIQLRPG AEFNFMKVH PLKYPVDLY YLVDVSASMH NNIEKLNSVG NDLSRKWAPP 180
 SRDFRLGFGS YVDKTVSPYI SIHPERIHQ CSDYNLDCMP PRGYIHVLSL TENITEFEKA 240
 VHRQKISGNI DTPEGGFDAM LQAACVESH GWRKEAKRLI LVMTDQTSHL ALDSKLAGIV 300
 VPDNGCHLK MNVYVKSTTM EHPSLGLLSE KLIDNNINVI FAVGKQFHW YKDLLPLPG 360
 TIAGEIESKA ANLANLVSEA YQKLISEVKV QVENQVQGIY FNITAI CPDG SRKPGMEGCR 420
 75 NVTSNDEVLF NVTVTKKCD VTGKNYAI KPIGFNETAK IHIHRNCSCQ CEDNRGPKGK 480
 CVDETFLDSK CFQDENKCH FDEDFSSSES CKSHKQFVPC SGRGVCVCGK CSCHKIKLKG 540
 VYGRYCEKDD PSCPYHGNL CAGHGECEAG RCQCFPSWEG DRQCPSAAA QHCVNSKQGV 600
 CSGRGTCVCG RCCTDPRSI GRFCEHCPTC YTACKENWNC MQCLHPHNLQ QAILDQCKTS 660
 CALMEQGHV DQTECFSSP SYLRIFPIIF IVTFLIGLLK VLIIRQVILQ WNSNKIKSSS 720
 80 DYRVASAKKD KLILQSVCTR AVTYRREKPB EIKMDISKLN AHETFRCNF

Seq ID NO: 57 DNA sequence

Nucleic Acid Accession #: NM_001719

Coding sequence: 123..1418

85 1 11 21 31 41 51
 | | | | |

5 GGGCGCAGCG GGGCCGCTCT GCAGCAAGTG ACCGACGGCC GGGACGGCG CCTGCCCCCT 60
 CTGCCACCTG GGGCGGTGGG GGGCCGGAGC CCGGAGCCCG GGTAGCCGT AGAGCCGGCG 120
 CGATGCACGT GGGCTCACTG GGAGCTGCGG GCGCGCACAG CTTCTGGGCG CTCTGGGCAC 180
 CCCTGTTCTT GCTGCGCTCC GCGCTGGCGG ACTTCAGCCT GGACAACGAG GTGCACCTCGA 240
 GCTTCATCCA CGCGGCGCTC CGCAGCCAGG AGCGGGCGGA GATGCAGCGC GAGATCTCTT 300
 CCATTTTGGG CTTGCCCCAC GCGCGCGGTC CGCACCTCCA GGGCAAGCAC AACTCGGCAC 360
 CCATGTTTCT GCTGAGCCTG TACAAAGGTA TGGCGGTGGA GAGGGGCGGC GGGCCCGGCG 420
 GCGAGGGCTT CTCTACCCCG TACAAGGCGG TCTTCAGTAC CCAGGGCCCC CCTCTGGCCA 480
 10 GCCTGCAAGA TAGCCATTTC CTCACCGAGG CCGACATGGT CATGAGCTTC GTCAACCTCG 540
 TGGAAACATGA CAAGGAATTC TTCCACCCAC GCTACCACCA TCGAGAGTTC CGGTTTGATC 600
 TTTCCAAAGAT CCCAGAAGGG GAAGCTGTGA CCGCAGCCGA ATTCCGGATC TACAAGGACT 660
 ACATCCGGGA ACCTCTCGAC AATGAGACTT TCCGGATCAG CGTTTATCAG GTGCTCCAGG 720
 AGCACTTGGG CAGGGAATCG GATCTCTTTC TGCTCGACAG CCGTACCCTC TGGGCTTCGG 780
 15 AGGAGGGCTG GCTGGTGTTC GACATCACAG CCACCAGCAA CCACTGGGTG GTCAATCCGC 840
 GGCACAACCT GGGCTGCGAG CTCTGGGTGG AGACGCTGGA TGGGCAAGGC ATCAACCCCA 900
 AGTTGGGCGG CTGATTGGGG GCGCACCGGC CCCAGAACAA CGAGCCCTTC ATGGTGGCTT 960
 TCTTCAAGGC CACGAGGCTC CACTTCGCGA GCATCCGGTC CAGGGGAGC AAACAGCGCA 1020
 GCCAGAACCG CAGGGAATCG CCCAAGAAC AGGAAGCCCT GCGGATGGCC AACGTGGCAG 1080
 20 AGAACACGAG CAGCGACCAG AGGCAGGCTT GTAAGAAGCA CGAGCTGTAT GTCACTCTCC 1140
 GAGACCTGGG CTGGCAGGAG TGGATCATCG CGCTGGAAGG CTAGCGCGCC TACTACTGTG 1200
 AGGGGGAGTG TGCTTCCCT CTGAACCTCT ACATGAACGC CACCAACCCAG GCCATCGTGC 1260
 AGACGCTGGT CCATCTCATC AACCCGGGAA CCGTGCCCAA GCGCTGCTGT GCGCCACGCG 1320
 AGCTCAATGC CATCTCGTCT CTCTACTTGG ATGACAGCTC CAACGTCTAT CTGAAGAAAT 1380
 25 ACAGAAACAT GGTGGTCCGG GCGTGTGGCT GCCACTAGCT CCTCGAGAA TTCAGACCTT 1440
 TTGGGGCCAA GTTTTCTCG ATCTCCATTT GCTGCGCTTG GCCAGGAACC AGCAGACCAA 1500
 CTGCGCTTTG TGAGACCTTC CCTCCCTTAT CCGCAACTTT AAAGGTGTGA GAGTATTAGG 1560
 AAACATGAGC AGCATATGCG TTTTGTATCG TTTTTCAGTG GCAGCATCCA ATGAACAAAG 1620
 TCCTCAAGTG TGTGACGCA AAACCTAGCA GGAAAAAATA ACAACGCATA AAGAAAAATG 1680
 30 GCGGGGCGAG GTCAATGGCT GGGAGTCTC AGCCATGCAC GGACTCGTTT CCAGAGGTAA 1740
 TTATGAGCGC CTACAGCCA GGCACCCGAG CCGTGGGAGG AAGGGGCGGT GGCAAGGGGT 1800
 GGGCACATTG GTGCTGTGCG GAAAGGAATA TTGACCCGGA AGTTCCTGTA ATAAATGTCA 1860
 CAATAAAACG AATGAATG

Seq ID NO: 58 Protein sequence

Protein Accession #: NP_001710

35 1 11 21 31 41 51
 MHVRLSLRAA PHSFVALWAP LFLRLSALAD FSLDNEVHSS FIHRLRSQRE RREMOREILS 60
 40 ILGLPHRPRP HLQGHNSAP MFMLDLYNAM AVEEGGGPGG QGFSYPYKAV PSTQGPPLAS 120
 LQDSHFILDA DMVMSFNLV EHDKEFFHPR YHIREFRFDL SKIPEGEAVT AAEFRYKYD 180
 IRRERFDNETF RISVYQLQSE HLGRESLPL LDSRTLWASE EGMVLFVDTA TSNHWVNP 240
 ENLGLQLSVE TLDGQSINPK LAGLIGRQFP QNKQPFMVAF FKATEVHFPS IRSTGSKQRS 300
 QNRSKTFPNQ EALRMNVAE NSSSDQRCAC KKHELYVSFR DLGWQDWIIA PEGYAAYYCE 360
 45 GECAPPLNSY MNATNRAIVQ TLVHFINEET VPKPCCAPTQ LNAISVLYPD DSNVILKRY 420
 RNMVVRACGC R

Seq ID NO: 59 DNA sequence

Nucleic Acid Accession #: NM_002821

Coding sequence: 150..3362

50 1 11 21 31 41 51
 AACTCCCGCC TCGGGACGCC TCGGGGTGGG GCTCCGGCTG CGGCTGCTGC TCGGGCGCCC 60
 GCGCTCCGGT GCGTCCGCTC CTGTGCGCG CCGCGGAGCA GTCTGCGGCC CGCGTGGGC 120
 55 CCTCAGCTCC TTTCTCTGAG CCGCGCGGGA TGGGAGCTGC GCGGGGATCC CCGGCCAGAG 180
 CCGCGCGGTT GCGCTCTGCT AGCGTCTTGC TGCTGCGGCT GCTGGGCGGT ACCCAGACAG 240
 CCATTGTCTT CATCAAGCAG CCGTCTCTCC AGGATGCACT GCAGGGGCGC CGGGCGCTGC 300
 TTGCTGTGA GGTGAGGCT CCGGGCGCGG TACATGTGTA CTGGCTGCTC GATGGGGCCC 360
 CTGTCCAGGA CACGGAGCGG GCTTTCGCTC AGGGCAGCAG CCTGAGCTTT GCAGCTGTGG 420
 60 ACCGGCTGCA GGAATCTGGC ACCTTCCGCT GTGTGGCTCG GGATGATGTC ACTGGAGAA 480
 AAGCCCGCAG TGCCAACGCC TCCTTCACCA TCAATGGAT TGAGGCAGGT CCTGTGTTCC 540
 TGAAGCATCC AGCTCCGGAA GCTGAGATCC AGCCACAGAC CCAGGTACCA CTCTGTGGCC 600
 ACATTGATGG GCACCTCGG CCCACCTACC AATGGTTCG AGATGGGACC CCGCTTTCTG 660
 ATGGTCAGAG CAACCACACA GTCAGCAGCA AGGAGCGGAA CCTGACGCTC CGGCCAGCTG 720
 65 GTCCTGAGCA TAGTGGGCTG TATTCTCTCT GCGCCACAG TGCTTTGGC CAGGCTTGCA 780
 GCAGCCAGAA CTTCACCTTG AGCATTTGCT ATGAAAGCTT TGCCAGGGTG GTGCTGGCAC 840
 CCCAGGAGCT GGTAGTAGCG AGGTATAGG AGGCCATGTT CCATTGCCAG TTCTCAGCCC 900
 AGCCACCCCG GAGCTCGAG TGGCTCTTGT AGGATGAGAC TCCCATCACT AACCGCAGTC 960
 GCGCCCCACA CTCTCGCAGA GCCACAGTGT TTGCCAACGG GTCTCTGCTG CTGACCCAGG 1020
 70 TCCGCGCCAG CAATGACGGG ATCTACCGCT GCATTGGCCA GGGCAGAGG GCGCCACCCA 1080
 TCATCTTGA AGCCACACTT CACCTAGCAG AGATTGAAGA CATGCCGCTA TTGAGCCAC 1140
 GGGTGTTTAC AGCTGGCAGC GAGGAGCTTG TGACCTGCTT TCCCCCAAG GGTCTGCCAG 1200
 AGCCACAGCT GTGTGGGGAG CACGCGGGAG TCCGGCTGCC CACCCATGGC AGGGTCTACC 1260
 AGAAGGGCCA CGAGCTGGTG TTGGCCAATA TTGCTGAAAG TGATGCTGGT GTCTACACCT 1320
 75 GCGACGCGGC CAACCTGGCT GGTGAGCGGA GACAGGATGT CAACATCACT GTGGCCACTG 1380
 TGCCCTCTCT GCTGAAGAAG CCGCAAGACA GCCAGCTGGA GGAGGGCAAA CCGGCTACT 1440
 TGGATTGCTT GACCCAGGCC ACACCAAAAC CTACAGTTGT CTGGTACAGA AACAGATGC 1500
 TCATCTCAGA GGACTCACGG TTCGAGGTCT TCAAGATGG GACCTTGCGC ATCAACAGCG 1560
 TGGAGGTGTA TGAAGGAGCA TGGTACCGTT GTATGAGCAG CACCCAGCG GGCAGCATCG 1620
 80 AGGCGCAAGC CCGTGTCCAA GTGCTGGAAA AGCTCAAGTT CACACCAACA CCGCAGCCAC 1680
 AGCAGTGCAT GCGATTGAC AAGGAGGCCA CCGTGCCTGT TTCAGCACA GCGGAGAGA 1740
 AGCCCACTAT TAAGTGGAA CCGGCAGATG GGAGCAGCCT CCCAGAGTGG GTGACAGACA 1800
 ACGCTGGGAG CCGTCAATTT GCGCGGGTGA CTGAGATGA CGCTGGCAAC TACACTTGCA 1860
 85 TTGCTCCAA CCGCGCGCAG GGCAGATTTC GTGCCCATGT CCAGCTCACT GTGGCAGTTT 1920
 TTATCACTT CAAGTGGAA CCAGAGCGTA CGACTGTGTA CCAGGGCCAC ACAGCCCTAC 1980
 TGCAGTGCGA GCGCCAGGG GACCCCAAGC CGCTGATTCG GTGGAAGGC AAGGACCGCA 2040

TCCTGGACCC CACCAAGCTG GGACCCAGGA TGCAATCTT CCAGAAATGGC TCCCTGGTGA 2100
 TCCATGACGT GGGCCCTGAG GACTCAGGCC GCTACACCTG CATTCGAGGC AACAGCTGCA 2160
 ACATCAGCA CACGGAGGCC CCCCTCTATG TCGTGGACAA GCCTGTGCCG GAGGAGTCGG 2220
 AGGGCCCTGG TAGCCCTCCC CAGCCCTCCC CCTACAAGA TGATCCAGAG CATTTGGTTG TCGGTGGTGT 2280
 CCGCTGTGGC CTACATCATT GCCGTGCTGG GCCTCATGTT CTACTGCAAG AAGCGCTGCA 2340
 AAGCCAGCG GCTCAGAGG CAGCCCGAGG GCGAGGAGCC AGAGATGGAA TGCTCAACG 2400
 GAGGGCCCTT GCAGAACCGG CAGCCCTCAG CAGAGATCCA AGAAGAATGT GCCTTGACCA 2460
 GCTTGGGCTC GGGCCCGCGG GCCACCAACA AACGCCACAG CACAAGTGAT AAGATGCACT 2520
 TCCCAAGGTC TAGCCTGCA GCTATCAGCA CGCTGGGGAA GAGTGAGTTT GGGGAGGTGT 2580
 TCCTGGCAAA GCGCTAGGCG TTGGAGGAGG GAGTGGCAGA GACCTGGTGA CTTGTGAAGA 2640
 GCGTGCAGAC GAAGGATGAG CAGCAGCAGC TGGACTTCCG GAGGAGTTTG GAGATGTTTG 2700
 GGAAGCTGAA CCAGCCCAAC GTGGTGCAGC TCCTGGGGCT GTGCCGGGAG GCTGAGCCCC 2760
 ACTACATGGT GCTGGAATAT GTGGATCTGG GAGACCTCAA GCAGTTCCTG AGGATTTCCA 2820
 AGAGCAGGA TGAAAAATTG AAGTACAGC CCTTCAGCAC CAAGCAGAAAG GTGGCCCTAT 2880
 GCACCCAGGT AGCCCTGGCG ATGGAGCACC TGTCACAA CAAGCTTTGT CATAAGGACT 2940
 TGGCTGGCGG TAACCTGCTG GTCACTGCC AGAGACAAGT AAGGTGTCT GCCTGGGCC 3000
 TCAGCAAGGA TGTGTACAA AGTGAGTACT ACCACTTCCG CCAGGCGCTG GTGCCGTGC 3060
 GCTGGATGTC CCCCGAGGCC ATCCTGGAGG GTGACTTCTC TACCAAGTCT GATGTCTGG 3120
 CCTTCGGTGT GCTGATGTC GAAGTGTGTT CACATGGAGA GATGCCCAT GTGGGCGAG 3180
 CAQATGATGA AGTACTGGCA GATTTCAGG CTGGGAAGGC TAGACTTCTC CAGCCGAGG 3240
 GCTGCCCTTC CAACTCTAT CGGCTGATG AGCGCTGCTG GCGCCTCAGC CCAAGGACC 3300
 GGCCTCCTT CAGTGAGATT GCCAGCGGCC TGGGAGACAG CACCGTGGAG AGCAAGCGGT 3360
 GAGGAGGGAG CCGGCTCAGG ATGGCTTGGG CAGGGAGAGA CATCTCTAGA GGAAGCTCA 3420
 CAGCATGATG GGCAGATCC CTGTCTCTCT GGGCCCTGAG GTGCCCTAGT GCAACAGGCA 3480
 TTGCTAGAGT CTGAGCAGG CCTGGCCTTT CCTCTCTTC CTACCCCTCA TCCTTTGGGA 3540
 GCGTGAATTG GACCCAACT GGGGAGTACT GCGCTTGGAG TGGGAGTGT CCGCTGCCAC 3600
 CTCTTCCTCT ATCAGGACA GTGTGGGTGC CACAGGTAAC CCAATTTCT GGCCTCAAC 3660
 TTCTCCCTT GACCGGCTCC AACTCTGCCA CTCTCTGCC AACTTTGCTT GGGGAGGCT 3720
 AGGCTTGGGA TGAGCTGGGT TTGTGGGAG TTCTTAATA TTCTCAAGT CTGGGCACAC 3780
 AGGGTAAATG AGTCTCTTCC CCACTGTGCC ACTTGGGGT CTAGACAGG ATTATAGAGG 3840
 ACACAGCAAG TGAGTCTCTC CCACTCTGGG CTGTGCCACA CTGACCCAGA CCAAGCTCT 3900
 CCCCACCTT CTCTCTTTC CTCTCTTAA GTGCTGGCA GATGAAGGAG TTTTCAGGAG 3960
 CTTTTCACAC TATATAAACC GCCCTTTTGT TATGCACCAC GGGCGGCTT TATATGTAAT 4020
 TGCAGCGTGG GGTGGGTGGG CATGGGAGGT AGGGGTGGGC CCTGGAGATG AGGAGGGTGG 4080
 GGCATCTCTA CCCACACTT TTATTGTGT GGTTTTGTG TTTTGTGTT TTTTGTGTT 4140
 TGTTTTGTG TTACACTCG CTGCTCTCAA TAAATAAGCC TTTTITA

Seq ID NO: 60 Protein sequence
 Protein Accession #: NP_002812

1 11 21 31 41 51
 | | | | |
 MGAARGSPAR PRRLLSVL LPLLLGGTQT AIVFIKQPSS QDALQRRAL LRCEVEAPGP 60
 VHVYMLLDGA PVQDTERRFA QSSLSFAAV DRLQDSGTFO CVARDDVTGE EARSANASFN 120
 IKWIEAGPVV LKHPASEAEI QPQTQVTLRC HIDGHPRTY QWPRDGTPLS DGQSNHTVSS 180
 KERNLTLRPA GPEHSLGYSC CAHSAFQAC SSQNTFLSIA DESFARVULA PQDVVVARYE 240
 EAMPHCQPSA QPPPSLQWLF EDETPITNRS RPPHLRRATV FANGSLLLTQ VRPRNAGTYR 300
 CIGGQQRGPP IILEATLHLA EIEDMPLFEP RVFTAGSEER VTCLPPKGLF EPSVWHEHAG 360
 VRLPTHGRVY QKHGELVLAN IAESDAGVYT CHAANLAGOR RQDVNITVAT VPSWLKIKPD 420
 SQLEBQPGY LDCLTQATPK PTVVWYRNQM LISEDSRFEV FKGNTLRINS VEVDGTWYR 480
 CMSSTPAGSI EAQARVQVLE KLFKTPPPQP QOCMEPDKEA TVPCSATGRE KPTIKMERAD 540
 GSSLFPMVTD NAGTLHFARV TRDDAGNYTC IASNGPQQI RAHVQLTVAV FITPKVEPER 600
 TTVYQGHIAL LQCEAQGDPK PLIQWKGKDR ILDPKLGPR MHIPQNGSLV IHDVAPEDSG 660
 RYTCIAGNSN NIKHTFAPLV VVDKEVPESB EPGSPPPYK MIQITGLSVG AAVAYIIAIVL 720
 GLMFPYCKRC KAKRLQKQPE GKEPEMECLN GGPIQNGQPS ABIQEEVALT SLGSGPAATN 780
 KRHSTSDMH FFRSLQFIT TLGKSEFGEV FLAKAQGLEB GVAETLVLVK SLQTKDEBQQ 840
 LDFRRELEMP GKLNHANVVR LGLLCRAEP HYMVLEYVDL GDLKQFLRIS KSKDKLKSQ 900
 PLSTKQKVAL CTQVALGMEH LSNNRFVHKD LAARNCLVSA QRQVKVSALG LSKDVYNSEY 960
 YHFRQANVPL RHMSPBALLE GDFSTKSDVW AFGVLMWEVF THGEMPHGGQ ADDEVLDLQ 1020
 AGKARLPQPE GCPSKLYRLM QRCWALSPKD RPSPEIASA LGDSTVDSKP

Seq ID NO: 61 DNA sequence
 Nucleic Acid Accession #: NM_006103
 Coding sequence: 29..406

1 11 21 31 41 51
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 CACCTGCACC CCGCCCGGGC ATAGCACCAT GCCTGCTGTG CGCCTAGGCC CGCTAGCCGC 60
 CGCCCTCTCT CTCAGCTGCG TGCTGTTCGG CTTCACCCCTA GTCTCAGGCA CAGGAGCAGA 120
 GAAGACTGGC GTGTGCCCGG AGCTCCAGGC TGACCAGAAC TGACGCAAG AGTGCGTCTC 180
 GGACAGCGAA TGGCCGACAC ACCTCAAGTG CTGCAGCGCG GGCTGTGCCA CCTTCTGCCT 240
 TCTCTGCCCA AATGATAAGG AGGGTTCCTG CCCCCAGTGT AACATTAACT TTCCCCAGCT 300
 CGGCTCTGTG CGGACCCAGT GCCAGGTGGA CAGCCAGTGT CCTGGCCAGA TGAATGCTG 360
 CCGCAATGGC TGTGGGAAGG TGTCTGTGT CACTCCCAAT TTCTGAGTCT CAGCCACCAC 420
 CAGGCTGAGC AGTGAGGAGA GAAAGTTTCT GCCTGGCCCT GCATCTGGTT CCAGCCACAC 480
 TGCCCTCCCC TTTTTCGGGA CTCTGTATTC CCTCTTGGGC TGACCACAGC TTCTCCCTTT 540
 CCCAACCAAT AAGTAACCA CTTTCAGCAA AAAAAAAAAA AAAA

Seq ID NO: 62 Protein sequence
 Protein Accession #: NP_006094

1 11 21 31 41 51
 | | | | |
 MPACRLGPLA AALLLSLLLF GPTLVSGTGA EKTGVCPQLQ ADQNTQECV SDSECADNLK 60
 CCSAGCATFC LLCPNDKEGS CPQVNIINFPQ LGLCRDQCQV DSQCPGQMKC CRNGCGKVSC 120
 VTFNF

Seq ID NO: 63 DNA sequence

Nucleic Acid Accession #: NM_001203

Coding sequence: 274..1782

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1      11      21      31      41      51
|      |      |      |      |
5  CGCGGGGCGC GGAGTCGGCG GGGGCTCGCG GGACGCGGGC AGTGC GGAGA CCGCGGCGCT 60
   GAGGAGCGGG GAGCGGGGAG CGCACGCGCG GGGTGGAGTT CAGCCTACTC TTTCTTAGAT 120
   GTGAAAGGAA AGGAAGATCA TTTCATGCCT TGTGTATAAA GGTTCAGACT TCTGCTGATT 180
   CATAACCATT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTACAGGCC 240
   TGCCATAAGT GAGAAGCAAA CTTCCTTGAT AACATGCTTT TGGGAAGTGC AGGAAAAATTA 300
10  AATGTGGGCA CCAAGAAAGA GGATGGTGAG AGTACAGCCC CCACCCCGCG TCCAAAGGTC 360
   TTGCGTTGTA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGCAGCACA 420
   GACGGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTTCGCTGT GGTCACTTCT 480
   GGTTCGCTAG GACTAGAAGG CTCAGATTTT CAGTGTGGG ACACCTCCAT TCCTCATCAA 540
   AGAAGATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAAGACCT ACACCTTACA 600
15  CTGCTCCCAT TGAAAAACAG AGATTTTGTT GATGGACCTA TACACCACAG GGCCTTACTT 660
   ATATCTGTGA CTGTCTGTAG TTGCTCTTGT GTCTTTATCA TATTATTTTG TTACTTCOAG 720
   TATAAAGAGC AAGAAACCAAG ACCTCGATAC AGCATTGGGT TAGAACAGGA TGAACCTTAC 780
   ATTCTCTCTG GCGAATCCCT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAGTGA 840
   TCAGGCTCCG CTCTGCTGCT CCAAGGACT ATAGCTAAGC AGATTCAGAT GGTGAACAG 900
20  ATTGAAAAAG GTGCTATAGG GGAAGTTTGG ATGGGAAAGT GCGTGGCGCA AAAGGTAGCT 960
   GTGAAGTGT TCTTCAACCA AGAGGAAGCC AGCTGGTTCA GAGAGACAGA AATATATCAG 1020
   ACAGTGTGTA TGAGGCATGA AAACATTTTG GGTTCATATG CTGCAGATAT CAAAGGGACA 1080
   GGTTCCTGGA CCGAGTGTGA CCTAATCACA GACTATCATG AAAATGGTTC CTTTATGAT 1140
   TATCTGAAGT CCACCAACCT AGACGCTAAA TCAATGCTGA AGTTAGCCTA CTCTTCTGTC 1200
25  AGTGGCTTAT GTCAATTACA CACAGAAATC TTAGTACTC AAGGCAACCC AGCAATTGCC 1260
   CATCGAGATC TGAAAGTAGA AAACATTCTG GTGAAGAAAA ATGGAACCTG CTGTATTGCT 1320
   GACCTGGGCG TGCGTGTAAA ATTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC 1380
   ACTCGAGTTG GCACCAACCG CTATATGCTC CCAGAAAGTGT TGGACGAGAG CTTGAACAGA 1440
   AATCACTTCC AGTCTTACAT CATGGCTGAC ATGTATAGTT TTGGCCTCAT CCTTTGGGAG 1500
30  GTTCTAGGGA GATGTGTATC AGGAGGTATA GTGGAAGAAT ACCAGCTTCC TTATCATGAC 1560
   CTAGTGCCCA GTGACCCCTC TTATGAGGAC ATGAGGGAGA TTGTGTGCAT CAAGAAGTTA 1620
   CGCCCTCAT TCCCAACCGC GTGGAGCAGT GATGAGTGTC TAAGGCAGAT GGGAAAACTC 1680
   ATGACAGAAT GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCCTGCG GGTAAAGAAA 1740
   ACCTTGCCA AAATGTGAGA GTCCAGGAC ATTAACCTCT GATAGGAGAG GAAAAGTAAG 1800
35  CATCTCTGCA GAAAGCCAAC AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAA 1860
   TAAGCATCCA CAGTACAAGC CTTGAACATC CTCTGCTTCC CAGTGGGTT CAGACCTCAC 1920
   CTTTCAGGGA GCGACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTG 1980
   TCTGTTTGTG GCGGAGAAA CCGTGGGTA ACTTGTTCAT GATATGATGC AT

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Seq ID NO: 64 Protein sequence

Protein Accession #: NP_001194

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1      11      21      31      41      51
|      |      |      |      |
45  MLLRSAGKLN VGTKEDGES TAPTPRPKVL RCKRHHCPE DSVNNICSTD GYCPTMIEED 60
   DSGLPVVTGG CLGLEGSDFG CRDTPIPHQR RSIECCTERN ECKDLHPTL PPLKNDPVD 120
   OPIHHRALLI SVTVCSLLLV LILFCYFRY KRQSTRPRYS IGLQEDETIY PPGESLRDLI 180
   EQSQSSGSGS GLPLLVQRTI AKQIQMVQKI GKRGYEVVM GKNRGKEKAV KVFTTEEAS 240
   WPRETRIYQT VLMRHENILG PIAADIRGTG SWTQLYLI TD YHENGSLVDY LKSTTLDAKS 300
   MLKLAYSSVS GLCHLHTEIF STQKPAIAH RDLKSKNLLV KNGTCCCLAD LGLVAKFISD 360
50  TNEVDIPPT RVGTGRYMPF EVLDESINRN HFQSYIMADM YSFLILMEV ARRCVSGGIV 420
   BEYQLPYHDL VPSDPSYEDM REIVCIKKLR PSFPNRWSSD ECLRQMGKLM TECWAHPAS 480
   RLTAIRVKKT LAKMSQSQDI KL

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Seq ID NO: 65 DNA sequence

Nucleic Acid Accession #: NM_006475.1

Coding sequence: 28..2538

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1      11      21      31      41      51
|      |      |      |      |
60  AACAGAAGTG CAACGGAGAG ACTCAAGATG ATTCCCTTTT TACCATGTT TTCTCTACTA 60
   TTGCTGCTTA TTGTAAACCC TATAAAGGCC AACATCATT ATGACAAGAT CTGGCTCAT 120
   AGTCGTATCA GGGGTCGGGA CCAAGGCCCA AATGTCTGTG CCCTTCAACA GATTTTGGGC 180
   ACCAAAAGA AATACTTCAG CACTGTGAAG AACTGTGATA AAAAGTCCAT CTGTGGACAG 240
   AAAACGACTG TTTTATATGA ATGTTGCCCT GGTATATGA GAATGGAAGG AATGAAAGGC 300
   TGCCACGACG TTTTGCCCAT TGACCATGTT TATGGCAGTC TGGGCATGTT GGGAGCCACC 360
65  ACAACGACG GCTATTCTGA CGCCTCAAAA CTGAGGGAGG AGATCGAGGG AAAGGGATCC 420
   TTCATTTACT TTGACCGAG TAATGAGGCT TGGGACAACT TGGATTCTGA TATCGTAGA 480
   GGTTTGGAGA GCAACGTGAA TGTGAATTA CTGAATGCTT TACATAGTCA CATGATTAAAT 540
   AAGAGAAATG TGACCAAGGA CTTAAAAAAT GGCATGATTA TTCCTTCAAT GTATAACAAAT 600
   TTGGGGCTTT TCATTAACCA TTATCTTAAT GGGGTGTGCA CTGTTAAATG TGCTCGAATC 660
70  ATCCATGGGA ACCAGATTGC AACAAATGGT GTTGTCCATG TCATTGACCG TGTGCTTACA 720
   CAAATGGTA CCTCAATTCA AGACTTCATT GAAGCAGAAG ATGACCTTTC ATCTTTTAGA 780
   GCAGCTGCCA TCACATCGGA CATATTGGAG GCCCTTGGAA GAGACGGTCA CTTACACACT 840
   TTTGCTCCCA CCAATGAGGC TTTTGAGAAA CTTCCACGAG GTGTCTAGA AAGGTTCTAG 900
   GGAGACAAGG TGGCTTCCGA AGCTCTTATG AAGTACCACA TCTTAAATAC TCTCCAGTGT 960
75  TCTGAGTCTA TTATGGGAGG AGCAGTCTTT GAGACGCTGG AAGGAAATAC AATTGAGATA 1020
   GGTGTGACG GTGACAGTAT AACAGTAAAT GGAATCAAAA TGTGGAACAA AAAGGATATT 1080
   GTGACAAATA ATGGTGTGAT CCAATTGATT GATCAGGTCC TAATTCCTGA TTCTGCCAAA 1140
   CAAGTTATTG AAGCTGCTGG AAAACAGCAA ACCACCTTCA CGGATCTTGT GGCCCAATTA 1200
   GGCTTGGCAT CTGCTCTGAG GCCAGATGGA GAATACACTT TGCTGGCACT TGTGAATTAAT 1260
80  GCATTTCTG CTGCTCTGAG CAGCATGGTT CAGCGCTCC TAAATTAAT TCTGCAGAAAT 1320
   CACATATTGA AAGTAAAGT TGGCCTTAAT GAGCTTTACA ACGGCAAAAT ACTGGAAGCC 1380
   ATCGAGGCA AACAGCTCAG AGTCTTCTGA TATCGTACAG CTGCTGCAT TGAATTTCA 1440
   TGATGGAGA AAGGGAGTAA GCAAGGAGGA AACGGTGGCA TTCACATATT CCGGAGATC 1500
   ATCAAGCCAG CAGAGAAATC CCTCCATGAA AAGTTAAATC AAGATAAGCG CTTTAGCACC 1560
85  TTCCTCAGCC TACTTGAAGC TGCAGACTTG AAAGAGCTCC TGACACAACC TGGAGACTGG 1620

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ACATTATTG TGCCAACCAA TGATGCTTT AAGGGAATGA CTAGTGAAGA AAAAGAAATT 1680
 CTGATACGGG ACMAAAATGC TCTTCAAAC ATCATTCTTT ATCACCCTGAC ACCAGGAGTT 1740
 TTCATTGGAA AAGGATTGTA ACCTGGTGT ACTAACATT TAAAGACCAC ACAAGGAAGC 1800
 5 AAAATCTTT TGAAAGAAGT AAATGATACA CTCTGGTGA ATGAATTGAA ATCAAAAGAA 1860
 TCTGACATCA TGACAACAAA TGGGTGTAAT CATGTTGTAG ATAACTTCCT CTATCCAGCA 1920
 GACACACCTG TTGGAATGA TCAACTGCTG GAAATACTTA ATAAATTAAT CAAATACATC 1980
 CAAATTAGT TTGTTCTGG TAGCACTTC AAAGAAATCC CCGTGAAGT CTATACAAT 2040
 AAAATTATAA CCAAAGTTGT GGAACCAAAA ATTAAGTGA TTGAAGSCAG TCTTCAGCCT 2100
 10 ATTATCAAAA CTGAAGGACC CACACTAACA AAAGTCAAAA TTGAAGTGA ACCTGAATTC 2160
 AGACTGATTA AAGAAGTGA AACATAACT GAAGTGATCC ATGGAGAGCC AATTATTAAA 2220
 AAATACACCA AAATCATTTA TGGAGTGCT GTGGAATAA CTGAAAAAGA GACACGAGAA 2280
 GAAAGATCA TTACAGTCC TGAATAAAA TACACTAGGA TTTCTACTGG AGGTGGAGAA 2340
 ACAGAAGAAA CTCTGAAGAA ATTGTTACAA GAAGAGGTCA CCAAGGTCAC CAAATTCATT 2400
 15 GAAGGTGGTG ATGGTCTTT ATTTGAAGAT GAAGAAATTA AAAGACTGCT TCAGGGAGAC 2460
 ACACCCGTGA GGAAGTTGCA AGCCCAACAA AAAGTTCAAG GTTCTAGAAG ACGATTAAAG 2520
 GAAGGTGCTT TCGAGTAAA ATCCAAAAAC CAGAAAAAAA TGTTTATACA ACCCTAAGTC 2580
 AATAACCTGA CCTTAGAAAA TTGTGAGAGC CAAGTTGACT TCAGGAAGT AAACATCAGC 2640
 ACAAGAAGC AATCATCAA TAATCTGAA CACAAATTTA ATATTTTTT TCTGAATGA 2700
 20 GAAACATGAG GGAATTTGT GAGTTAGCCT CCTGTGGTAA AGGAATTGAA GAAAAATAA 2760
 CACCTTACAC CTTTTCAT CTGACATTA AAAGTTCTGG CTAACTTGG AATCCATTAG 2820
 AGAAAAATCC TTGACACCA ATTCATTACA ATTCAAATCG AAGAGTTGT AACTGTTATC 2880
 CCATTGAAA GACCGAGCCT TGTATGTATG TTATGGATAC ATAAATGCA CGCAAGCCAT 2940
 TATCTCTCCA TGGGAAGCTA AGTTATAAAA ATAGGTGCTT GGTGTACAAA ACTTTTTATA 3000
 25 TCAAAAGGCT TTGCACATT CTATATGAGT GGGTTTACTG GTAAATTATG TTATTTTTA 3060
 CACTTAATT TGTACTCTCA GAATGTTTGT CATATGCTTC TTGCAATGCA TATTTTTTA 3120
 TCTCAACGT TTCAATAAAA CCATTTTTCA GATATAAAGA GAATTACTTC AAATTGAGTA 3180
 ATTCAGAAA ACTCAAGATT TAAGTTAAAA AGTGGTTTGG ACTTGGGAA

Seq ID NO: 66 protein sequence

Protein Accession #: NP_006466.1

1 11 21 31 41 51
 MIPFLPMFSL LLLLVNPN ANNHDKILA HSRIRGRDQG PNVCALQQL GTKKKYFSTC 60
 35 KNWYKKSICG QKTVLYECC PGYMRMEGMK GCPAVLPIDH VYGLGIVGA TTTQRYSDAS 120
 KLRSEIEGKG SFTYFAPSNE AWDNLDSDIR RGLSENVNVE LLNALHSHMI NKRLTKDLK 180
 NGMIIPMYN NLGFIINHYR NGVVTNVCAR IIBGNQIATN GVHVVIDRVL TQIGTSIQDF 240
 IEAEDDLSSP RAAATSDIL EALGRDGHFT LFPATNEAPE KLPRGVLERF MGDKVASEAL 300
 MKYHILATLQ CSESI MGAV PETLEGNTIE IGCDGDSITV NGIKOVNKKD IVTNNGVIHL 360
 40 IDQVLIPDSA RQVIELAGKQ QTTFTDLVAQ LGLASALRPD GEYTLAPVN NAFSDDTLSM 420
 VQRLLKILIL NHILKVKVGL NELYNGQILE TIGGKQLRVF VYRTAVCIEN SCMERKSKQG 480
 RNGALHIFRE IIKPAEKSLH EKLKQDKRFS TFLSLLEAAD LKELLTPQPD WTLFVPTNDA 540
 PKGMTSEKE ILIRDKNALQ NIILYHLTPG VPIGKGFEPP VTNILKTQSG SKIFLKEVND 600
 TLLVNEKLSK ESDIMTINGV IHVVDKLLVP ADTPVGNQDL LEILNKLIRY IQIKFVRGST 660
 45 FKEIPVTYVT TKIITKVVEP KIKVIEGSLQ PIKTEGPTL TKVKIEGEPE FRLIKEGETI 720
 TEVHGBPII KRYTKIDGV PVEITEKETR EERIITGPEI KYTRISTGGG ETEETLKLKL 780
 QEVTKVTKF IEGDGHLPF DEEIKRLQK DTPVRKLQAN KKVQSSRRRL REGRSQ

Seq ID NO: 67 DNA sequence

Nucleic Acid Accession #: EOS sequence

Coding sequence: 1-927

1 11 21 31 41 51
 ATGCGTGGGG GGTGCTCCGG GGGCCCCGCC GCGCGGAGCG GGCGTCTGCG GCTGGCGCGA 60
 55 CTAGCGCTGG TACTCTCGGG CTGGGTCTCC TCGTCTTCTC CCACCTCCTC GGCATCCTCC 120
 TTCTCCTCCT CGGCGCGGTT CCTGGCTTCC GCGGTGTCCG CCCAGCCCCC GCTGCCGGAC 180
 CAGTCCCCCG GTGCTCGGAG GTGCTCCGAG GCAGCGCGCA CAGTCAAGTG CGTTAACCGC 240
 AATCTGACCG AGGTGCCACG GGACCTGCCC GCCTACGTGC GCAACCTCTT CCTTACCGGC 300
 AACAGCTGG CCAGCAACCA CTTCCTTTAC CTGCGCGGGG ATGTGCTGGC CCAACTGCCC 360
 60 AGCCTCAGGC ACCTGGACTT AAGTAATAAT TCGTGTGTGA GCCTGACCTA CGTGTCTCTC 420
 CGCAACCTGA CACATCTAGA AAGCCTCCAC CTGGAGGACA ATGCCCTCAA GGTCTCTCAC 480
 AATGGCACCC TGGCTGAGTT GCAAGGTCTA CCCCACATTA GGGTTTTCTT GGACAACAAT 540
 CCCTGGGTCT GCGACTGCCA CATGGCAGAC ATGGTGACCT GGCTCAAGGA AACAGAGGTA 600
 GTGACGGGCA AAGACCGGCT CACCTGTGCA TATCCGGAAA AAATGAGGAA TCGGGTCTCT 660
 65 TTGGAATCA CAGATGCTGA CCGTGTGTGT GACCCGATTC TTCCCCATC CTGCACAAAC 720
 TCTTATGTCT TCGTGGGTAT TGTTTTAGCC CTGATAGGCG CTATTTTCTT CCTGGTTTTC 780
 TATTTGAACC GCAAGGGGAT AAAAAAGTGG ATGCATAACA TCAGAGATGC CTGCAGGGAT 840
 CACATGGAAG GGTATCATTA CAGATATGAA ATCAATGCGG ACCCCAGATT AACAAACCTC 900
 AGTCTCAACT CGGTCTCTCT CGAGTGA

Seq ID NO: 68 Protein sequence

Protein Accession #: EOS sequence

1 11 21 31 41 51
 MPGGCSRGA AGDGRLLRL LALVLLGWVS SSSPTSSASS FSSSAPPLAS AVSAQPPLEP 60
 75 QCPALCECSE AARTVKCVNR NLTEVPTDLP AYVRNLFLTQ NQLASNHFLY LPRDVLALPL 120
 SLRHLDLNN SLVSLTYVSP RNLTHLESLE LEDNALKVLH NGTLAEIQGL PHIRVFLDNN 180
 PMVDCOHMAD MVTWLKETEY VQKDRITCA YPERMNRVL LEINSAIDLDC DPILPPLSLQ 240
 SYVFLGIVLA LIGAIFLLVL YLNRKGIKKW MHNIRDACRD HMEGYHYRYE INADPRLTNL 300
 SSNSDVLE

Seq ID NO: 69 DNA sequence

Nucleic Acid Accession #: NM_000095.1

Coding sequence: 26..2299

1 11 21 31 41 51
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5	CAGCACCAG	CTCCCCGCA	CCGCCATGGT	CCCGACACC	GCCTGGCTTC	TTCTGCTCAC	60
	CCTGGCTGCC	CTGGGCGCGT	CCGGACAGGG	CCAGAGCCCG	TTGGGCTCAG	ACCTGGGCCC	120
	GCAGATGCTT	CGGGAACATC	AGGAAACCAA	CGCGGCGCTG	CAGGACGTGC	GGGACTGGCT	180
	GGGGCAGCAG	GTCAAGGAGA	TCACGTTCCCT	GAAAAACACG	GTGATGGAGT	GTGACGCGTG	240
	CGGATGACAG	CAGTCAGTAC	GCACCGGCGT	ACCCAGCGTG	CGGCCCCCTG	TCCACTGGCG	300
	GCCCGGCTTC	TGCTTCCCCG	GGTGGGCTTG	CATCCAGACG	GAGAGCGGCG	GCCGCTGGCG	360
	CCCCGCCCCC	GGGGGCTTCA	CGGGCAACGG	CTCGCACTGC	ACCGACGTCA	ACGAGTGCAG	420
	CGCCCACCCC	TGCTTCCCCC	GAGTCCGCTG	TATCAACACC	AGCCCGGGGT	TCGCTGCGA	480
10	GGCTTGGCGG	CGGGGTACCA	GCGGCCCCAC	CCACCAGGGC	GTGGGGCTGG	CTTTCGCCAA	540
	GGCCAAACAG	CAGGTTTGCA	CGGACATCAA	CGAGTGTGAG	ACCGGGCAAC	ATAACTGGCT	600
	CCCCAACTCC	GTGTGATACA	ACACCGGGGG	CTCCTTCCAG	TGCGGCGCGT	GCCAGCCCGG	660
	CTTCGTGGGC	GACCAGCGCT	CCGGCTGCCA	GCGCGGCGCA	CAGCGCTTCT	GCCCGGAGCG	720
	CTGCCCCAGC	GAGTGCCACG	AGCATGCAGA	CTGCGTCTTA	GAGCGGATG	GCTCGCGGTC	780
15	GTGCGTGTGT	CGGTTGGCT	GGGCGGCA	CGGATCCTC	TGTGGTCGCG	ACACTGACCT	840
	AGACGGCTTC	CCGACGAGA	AGCTGGGCTG	CCCGAGCCCG	CAGTGGCGTA	AGGACAACTG	900
	CGTGACTGTG	CCCAACTCAG	GGCAGGAGGA	TGTGGACCGC	GATGGCATCG	GAGACGCGTG	960
	CGATCCGGAT	GCCGACGGGG	ACGGGGTCCC	CAATGAAAAG	GACAACTGCC	CGCTGGTGCG	1020
	GAACCCAGAC	CAGCGCAAG	CGGACGAGGA	CAAGTGGGCG	GATGGTGCG	ACAACTGCCG	1080
20	GTCCCAAGAG	AACGACGACC	AAAAGGACAC	AGACCAGGAC	GGCGGGGGCG	ATCGTGCGCA	1140
	CGACGACATC	GACGGCGACC	GGATCCGCAA	CCAGGCGGAC	AACTGGCCCTA	GGTACCCCAA	1200
	CTCAGACCCG	AAGGACGATG	ATGGCGATGG	TATAGGGGAT	GCGTGTGACA	ACTGTCCCCA	1260
	GAAGAGCAAC	CCGGATCAGG	CGGATGTGGA	CCACGACTTT	GTGGGAGATG	CTTGTGACAG	1320
	CGATCAAGAC	CAGGATGGAG	ACGGACATCA	GGACTCTCGG	GACAACTGTC	CCACGCTGCC	1380
25	TAACAGTGCC	CAGGAGGACT	CAGACCACTG	TGGCCAGGGT	GATGCGCTCG	ACGACGACGA	1440
	CGACAATGAC	GGAGTCCCTC	ACAGTGGGGA	CAACTGCCCG	CTGGTGCTTA	ACCCCGGGCA	1500
	GGAGGACCGG	CCCAAGCTCAG	GCGTGGGCGA	CGTGTGCCAG	GACGACTTTG	ATGCAGACAA	1560
	GGTGGTAGAC	AAGATCGACG	TGTGTCCGGA	GAACGCTGAA	GTCACGCTCA	CCGACTTCAG	1620
	GGCCTTCCAG	ACAGTGGTGC	TGGACCCGGA	GGGTGACGCG	CAGATTGACC	CCAAGTGGGT	1680
30	GGTGTCAAC	CAGGGAAGGG	AGATCGTGCA	GACAATGAAC	AGCGACCCAG	GCCCTGGCTGT	1740
	GGGTTACACT	GCCTTCAATG	GCGTGGACTT	CGAGGGCAGC	TTCCATGTGA	ACACGGTCAC	1800
	GGATGACGAC	TATGCGGGCT	TCATCTTTGG	CTACCAGGAC	AGCTCCAGCT	TCTACGTGGT	1860
	CATGTGGAA	CAGATGGAGC	AAACGTATTG	GCAAGGCAAC	CCCTTCCGTC	CTGTGGCCGA	1920
	GCCTGGCATC	CAACTCAAGG	CTGTGAAGTC	TTCCACAGGC	CCCGGGGAAC	AGCTGCGGAA	1980
35	CGCTCTGTGG	CATACAGGAG	ACACAGAGTC	CCAGGTGCGG	CTGCTGTGGA	AGGACCCGCG	2040
	AAACGTGGGT	TGGAAGSACA	AGAAGTCTTA	TCGTTGGTTC	CTGCAGCACC	GGCCCCAAGT	2100
	GGGCTACATC	AGGGTGGCAT	TCTATGAGGG	CCCTGAGCTG	GTGGCCGACA	GCAACGTGGT	2160
	CTTGGACACA	ACCATCGCGG	GTGGCGCGCT	GGGGGTCTTC	TGCTTCTCCC	AGGAGAACAT	2220
	CATCTGGGCC	ACCTCGCGTT	ACCGCTGCAA	TGACACCATC	CCAGAGGACT	ATGAGACCCA	2280
40	TCAGCTGCGG	CAAGCCTAGG	GACCCAGGTC	AGGACCCGCG	GGATGACAGC	CACCTTCACC	2340
	CGCGCTGGAT	GGGGGCTCTG	CACCCAGCCC	AAGGGTGGCC	CGTCTGAGG	GGGAAGTGAG	2400
	AAGGGCTCAG	AGAGGACAAA	ATAAAGTGTG	TGTGACGGG			

Seq ID NO: 70 Protein sequence

Protein Accession #: NP_000086.1

45	1	11	21	31	41	51	
	MVPDTACVLL	LTLAALGASG	QGQSPLGSDL	GPQMLRELQE	TNAALQDVVD	WLRQQVREIT	60
	FLKNTVMECD	ACGMQOSVRT	GLPSVRPLLLH	CAPGFCFPGV	ACIQTESGGR	CGPCPAGFTG	120
50	NGSHCTDVNE	CNAHPCFPRV	RCINTSPGFR	CEACPFPGYSG	PTHQGVGLAF	AKANKQVCTD	180
	INECETGQHN	CVPNVNCINT	RGSFQCGPCQ	PGFVQDQASG	QQRGAQRFCP	DGSPSECEHE	240
	ADCVLERDGS	RSCVCRVWGA	GNGILCGRDT	DLGDFPDEKL	RCPEPQCRKD	NCVTVFNSGQ	300
	EDVDRIIDGD	ACDDPADGDI	VPNEKDNCEPL	VRNPDQRNTD	EDKWDGACDN	CRSQKNDQDK	360
	DTDDQGRGDA	CDDDIDGDR	RNQADNCPRV	PNSDQKDSDG	DGIGDADNDC	PQKSNPDQAD	420
55	VDHDFVGDAC	DSDDQDQDGD	HQDSRDNCPT	VPNSAQEDSD	HDGQGDACDD	DDNDGVDPDS	480
	RDNCRIVPNP	GQEDADRQGV	GDVQDDDFDA	DKVVDKIDVC	PENAEVTLTD	FRAFQTVVLD	540
	PEGDAQIDPN	WVVLNQGREI	VQTMNSDPGL	AVGYTAFNGV	DFEGTFPHVT	VTDDDYAGFI	600
	FQYQDSSSFY	VVMWQMBQET	YWQANPFRAV	AEPGIQLKAV	KSSTGFGBQL	RNALMHTGDT	660
	ESQVRLLMKD	PRNVGWKDKK	SYRWFLOHRP	QVGYIRVRFY	EGFELVADSN	VVLDTTMRGG	720
60	RLGVFCFSQE	NIWNLRLYR	CNDTIPEDYE	THQLRQA			

Seq ID NO: 71 DNA sequence

Nucleic Acid Accession #: NM_024626

Coding sequence: 71..919

65	1	11	21	31	41	51	
	GAGTCACCAA	GGAAGGCAGC	GGCAGCTCCA	CTCAGCCAGT	ACCCAGATAC	GCTGGGAACC	60
	TTCCCCAGCC	ATGGCTTCCC	TGGGGCAGAT	CCTCTTCTGG	AGCATAATTA	GCATCATCAT	120
	TATTCTGGCT	GGAGCAATTG	CACCTCATCAT	TGGCTTTGGT	ATTTCAGGGA	GACACTCCAT	180
70	CACAGTCACT	ACTGTGCGCT	CAGCTGGGAA	CATTGGGGAG	GATGGAAATCC	TGAGCTGCAC	240
	TTTTGAACCT	GACATCAAAC	TTTCTGATAT	CGTGATACAA	TGGCTGAAGG	AAGGTGTTTT	300
	AGGCTTGGTC	CATGAGTTCA	AAGAAGGCAA	AGATGAGCTG	TCGGAGCAGG	ATGAAATGTT	360
	CAGAGGCCGG	ACAGCAGTGT	TGTCTGATCA	AGTGATAGTT	GGCAATGCCT	CTTTGCGGCT	420
	GAAAAACGTC	CAACTCACAG	ATGCTGGCAC	CTACAAATGT	TATATCATCA	CTTCTAAAAG	480
75	CAAGGGGAAT	GCTAACCTTG	AGTATAAAAC	TGGAGCCTTC	AGCATGCGCG	AAGTGAATGT	540
	GGACTATAAT	GCCAGCTCAG	AGACCTTGGG	GTGTGAGGCT	CCCGATGGT	TCGCCAGGCC	600
	CACAGTGTGC	TGGGATCCCC	AAGTTGACCA	GGGAGCCAAC	TTCTCGGAAG	TCTCCAATAC	660
	CAGCTTTGAG	CTGAATCTTG	AGAATGTGAC	CATGAAGGTT	GTGTCTGTGC	TCTACAATGT	720
	TACGATCAAC	AACACATACT	CCTGTATGAT	TGAAAATGAC	ATTGCCAAAG	CAACAGGGGA	780
80	TATCAAAAGT	ACAGAAATCG	AGATCAAAA	GCGGAGTCAC	CTACAGCTGC	TAAACTCAAA	840
	GGCTTCTCTG	TGTGTCTCTT	CTTTCTTTGC	CATCAGCTGG	GCACTTCTGC	CTCTCAGCCC	900
	TTACTGTATG	CTAAAATAAT	GTGCTCTGGC	CACAAAAAAG	CATGCAAAAGT	CATTGTTACA	960
	ACAGGGATCT	ACAGAACTAT	TTCAACACCA	GATATGACCT	AGTTTTATAT	TTCTGGGAGG	1020
	AAATGAATTC	ATATCTAGAA	GTCTGGAGTG	AGCAAAACAG	AGCAAGAAAC	AAAAAGAAAG	1080
85	CAAAGCAGAG	AGGCTCCATC	ATGAACAAGA	TAAATCTATC	TTCAAGACA	TATTAGAAGT	1140
	TGGGAAAATA	ATTCAATGTA	ACTAGAGTCA	ACTGTGTCTG	GGCTAAGAAA	CCCTGGTTTT	1200

5 GAGTAGAAAA GGGCGTGGAA AGAGGGGAGC CAACAAATCT GTCTGCTTCC TCACATTAGT 1260
 CATTOGCCAA TAAGCATTCT GTCTCTTTGG CTGCTGCCTC AGCACAGAGA GCCAGAACTC 1320
 TATCGGGCAC CAGGATAACA TCTCTCAGTG AACAGAGTTG ACAGAGCCTA TGGGAAATGC 1380
 CTGATGGGAT TATCTTCAGC TTGTTGAGCT TCTAAGTTTC TTTCCTTCA TTCTACCCCTG 1440
 CAAGCCAAGT TCTGTAAAGG AAATGCCTGA GTTCTAGCTC AGGTTTTCTT ACTCTGAATT 1500
 TAGATCTCCA GACCTTGCCT GGCCACAATT CAATTAAGG CAACAAACAT ATACCTTCCA 1560
 TGAAGCACAC ACAGACTTTT GAAAGCAAGG ACAATGACTG CTTGAATTGA GGCCTTGAGG 1620
 AATGAAGCTT TGAAGGAAAA GAATACCTTG TTTCAGCCCT CCTTCCACA CTCTTCATGT 1680
 10 GTTAACCACT GCCTTCTCGG ACCTTGGAGC CACGGTGACT GTATTACATG TTGTTATAGA 1740
 AAACCTGATT TAGAGTCTGT ATCGTTCAAG AGAATGATTA AATATACATT TCCTAAAAAA 1800
 AAAAAAAAAA A

Seq ID NO: 72 Protein sequence

Protein Accession #: NP_078902

15 1 11 21 31 41 51
 MASLGQILFW SIISIIIIILA GAIALIIGPG ISGRHSITVT TVASAGNIGE DGILSCTFEP 60
 DIKLSDIVIQ WLKEGVLGIV HEFKEGKDEL SEQDEMFRGR TAVFADQVIV GNASLRLKNV 120
 20 QLTDAGTYKC YIITSKGKGN ANLEYKTGAF SMPEVNVVDYN ASSETLRCEA PRWFPQPTVV 180
 WASQVQGAN FSEVSNSTPE LNSENVIMKV VSVLYNVITN NTYSCHIEND IAKATQDIKV 240
 TESSIKRRSH LQLLNSKASL CVSSFFAISW ALLPLSPYLM LK

Seq ID NO: 73 DNA sequence

Nucleic Acid Accession #: XM_057014

Coding sequence: 143..874

25 1 11 21 31 41 51
 GGGAGGGGAG GAGGCGCGCG GGTGAAAGGC GCATTGATGC AGCCTCGCGC GGCCTCGGAG 60
 CGCGGGCGAG CCAGACGCTG ACCACGTTCCT TCTCCTCGGT CTCCTCGGCC TCCAGCTCGG 120
 30 CGCTGCCCGG CAGCGGGGAG CCATGCGGACC CCAGGGCCCC CGCGCTCCCG CGCAGCGGCT 180
 CGCGGGCTTC CTGCTGCTCC TGCTGCTGCA GCTGCCCGCG CGCTCGAGCG CCTCTGAGAT 240
 CCCCAGGGGG AAGCAAAAGG CGCAGCTCCG GCAGAGGGAG GTGGTGGACC TGTATAATGG 300
 AATGTGCTTA CAAGGGCCAG CAGGAGTGCC TGGTCTGAGC GGGAGCCCTG GGGCCAAATG 360
 35 CATTCGGGTG ACACCTGGGA TCCAGGTGCG GGATGGATTG AAAGGAGAAA AGGGGGAATG 420
 TCTGAGGGAA AGCTTTGAGG AGTCTCTGAC ACCCAACTAC AAGCAGTGTT CATGGAGTTC 480
 ATTGAATTAT GGCATAGATC TTGGGAAAAAT TGCGGAGTGT ACATTTACAA AGATGCGTTC 540
 AAATAGTGCT CTAAGAGTTT TGTTCAGTGG CTCACTTCGG CTAAAAATGCA GAAATGCATG 600
 CTGTCAAGCT TGTATTATCA CATTCAATGG AGCTGAATGT TCAGGACCTC TTCCCATTTGA 660
 40 AGCTATAAAT TATTGGACCC AAGGAAGCCC TGAAATGAAT TCAACAATTA ATATTCTATG 720
 CACTTCTTCT GTGGAAGGAC TTGTGGAAGG AATTGGTGCT GGATTAGTGG ATGTGTCTAT 780
 CTGGGTGGCG ACTTGTTCAG ATTACCCAAA AGGAGATGCT TCTACTGGAT GGAATTCAAT 840
 TTCTCGCATC ATTATTGAAG AACTACCAAA ATAAATGCTT TAATTTTCAT TTGTACCTTC 900
 TTTTATTAT ATGCTTGGGA ATGGTTCAC TAAATGACAT TTTAAATAAG TTTATGTATA 960
 45 CATCTGAATG AAAAGCAAAG CTAAATATGT TTACAGACCA AAGTGTGATT TCACACTGTT 1020
 TTTAAATCTA GCATTATTTCA TTTTGCTTCA ATCAAAAGTG GTTTCAATAT TTTTITTAGT 1080
 TGGTTAGAAT ACTTCTTCTA TAGTCACATT CTCTCAACCT ATAATTGGGA ATATTGTTGT 1140
 GGTCTTTTGT TTTTCTCTCT AGTATAGCAT TTTTAAAAAA ATATAAAAGC TACCAATCTT 1200
 TGTACAATTT GTAAATGTTA AGAATTTTTT TTATATCTGT TAAATAAAAA TTATTTCCAA 1260
 50 CAACCTTAAA AAAAAAAAAA AAAA

Seq ID NO: 74 Protein sequence

Protein Accession #: XP_057014

55 1 11 21 31 41 51
 MRPQGPAAAP QRLRGLLLLL LLQLPAPSSA SEIPKGRQKA QLRQREVVDL YNGMCLOGPA 60
 GVPGRDGSFG ANGIPTGPGI PGRDFKGEK GECLRESFEE SWTPNYKQCS WSSLNYGIDL 120
 60 GLIABCTFTK MRSNSALRVL FSGSLRLKCR NACQQRWYFT PNGAECSSPL PIEALIYLDQ 180
 GSPFMNSTIN IHRTSSEVEGL CEGIGAGLVD VAIWVGTCSD YFKGDASTGW NSVSRIIEER 240
 LPK

Seq ID NO: 75 DNA sequence

Nucleic Acid Accession #: BC010423

Coding sequence: 248..1780

65 1 11 21 31 41 51
 CACAGCGTGG GAAGCAGCTC TGGGGGAGCT CGGAGCTCCC GATCACGGCT TCTTGGGGGT 60
 AGCTACGGCT GGGTGTGTAG AACGGGGCCG GGGCTGGGGC TGGGTCCCTT AGTGAGAGCC 120
 CAAGTGGGAG AGGCAAGAAC TCTGCAGCTT CCTGCCCTCT GGGTCAGTTC CTTATTCAAG 180
 70 TCTGCAGCGG GCTCCAGAGG AGATCTCGGT GGAACCTCAG AAACGCTGGG CAGTCTGCCT 240
 TTCAACCATG CCCCCTGTCC TGGGAGCCGA GATGTGGGGG CCTGAGGCCT GGCTGCTGCT 300
 GCTGCTACTG CTGGCATCAT TTACAGGCCG GTGCCCGCGG GGTGAGCTGG AGACCTCAGA 360
 CGTGTAACT GTGGTGTCTG GCCAGGACGC AAAACTGCCCT TGCTTCTACC GAGGGGACTC 420
 CGGCGAGCAA GTGGGGCAAG TGGCATGGGC TCGGGTGGAC CGGGGCGAAG GCGCCAGGA 480
 75 ACTAGCGCTA CTGCACTCCA AATACGGGCT TCATGTGAGC CCGGCTTACG AGGGCCGCGT 540
 GGAGCAGCCG CGGCCCCCAG GCAACCCCTT GGACGGCTCA GTGCTCTGCG GCAACGCACT 600
 CAGGCGGAT GAGGCGAGT ACGAGTGCCG GGTCAACACC TTCCCGCGCG GCAGCTTCCA 660
 GCGCGGGCTG CCGCTCCGAG TGCTGTGTCC TCCCTTGCCC TCACTGAATC CTGTGCCAGC 720
 ACTAGAAGAG GGCCAGGGCC TGACCTTGGC AGCCTCTGCG ACAGCTGAGG GCAGCCAGCG 780
 80 CCCCAGCGTG ACCTGGGACA CGGAGGTCAA AGGCACAACG TCAGCGGTTT CCTTCAAGCA 840
 CTCCCGCTCT GCTGCGGTCA CCTCAGATT CCACCTGGTG CTAAGCCGCA GCATGAATGG 900
 CGAGCCACTG ACTGTGTGG TGTCCCATCC TGGCTGTCTC CAGGACCAAA GGATCACCCTA 960
 CATCTCCAC GTGTCTCTCC TTGCTGAGGC CTCTGTGAGG GGCCTTGAAG ACCAAAATCT 1020
 GTGGCACATT GGCAGAGAG GAGCTATGCT CAAGTGCCTG AGTGAAGGGC AGCCCTCTCC 1080
 85 CTCATACAACT TGGACACGGC TGGATGGGCC TCTGCCAGT GGGGTACGAT TGGATGGGGA 1140
 CACTTTGGGC TTTCCCCAC TGACCACTGA GCACAGGGC ATCTACGCTT GCCATGTCAG 1200

5	CAATGAGTTC	TCCTCAAGGG	ATTCTCAGGT	CACGTGCGAT	GTTCTTGACC	CCCAGGAAGA	1260
	CTCTGGGAAG	CAGGTGGACC	TAGTGTGAGC	CTCGTGGGTG	GTGGTGGGTG	TGATCGCCGC	1320
	ACTCTTGTTC	TGCTTCTG	TGGTGGTGGT	GGTGTCTCATG	TCCCGATACC	ATCCGGCCAA	1380
	GGCCCCAGCAG	ATGACCCAGA	AATATGAGGA	GGAGCTGACC	CTGACCCAGG	AGAACTCCAT	1440
	CCGGAGGCTG	CATTCCCATC	ACACGGACCC	CAGGAGCCAG	CCGGAGGAGA	GTGTAGGGCT	1500
	GAGAGCCGAG	GGCCACCTCG	ATAGTCTCAA	GGACAACAGT	AGCTGCTCTG	TGATGAGTGA	1560
	AGAGCCCGAG	GGCCGAGTTT	ACTCCACGCT	GACCAAGGTT	AGGGAGATAG	AAACACAGAC	1620
	TGAACCTCTG	TCTCCAGGCT	CTGGGCGGCG	CGAGGAGGAG	GAAGATCAGG	ATGAAGGCAT	1680
10	CAAAACAGGCC	ATGAACCAAT	TGTTTCAGGA	GAATGGGACC	CTACGGGCCA	AGCCACAGGG	1740
	CAATGGCATC	TACATCAATG	GGCGGGGACA	CCTGTCTGTA	CCCAGGCTTG	CCTCCCTTCC	1800
	CTAGGCGCTG	CTCCTTCTGT	TGACATGGGA	GATTTTAGCT	CATCTTGGGG	GCCTCCCTAA	1860
	ACACCCCATC	TTCTTGCGGA	AGATGCTCCC	CATCCCACTG	ACTGCTTGAC	CTTTACCTCC	1920
	AACCCCTCTG	TTCAATCGGA	GGGCTCCACC	AATTGAGTCT	CTCCCAACAT	GCATGCAGGT	1980
	CACGTGTGTG	TGTCATGTGT	GCCTGTGTGA	GTGTTGACTG	ACTGTGTGTG	TGTGGAGGGG	2040
15	TGACTGTCCG	TGGAGGGGTG	ACTGTGTCCG	TGGTGTGTAT	TATGCTGTCA	TATCAGAGTC	2100
	AAGTGAATCT	TGTGTATGTG	GCCACGGGAT	TTGAGTGGTT	GCGTGGGCAA	CACGTTCAGG	2160
	GTTTGGCGTG	TGTGTCTATG	GGCTGTGTGT	GACCTCTGCC	TGAAAAGCA	GGTATTTTCT	2220
	CAGACCCAGG	AGCATATTAT	ATGATGCAGA	GTTTGGAGGA	GAGAGGTGGA	GACTGTGGCT	2280
20	CAGACCCAGG	TGTGCGGGCA	TAGCTGGAGC	TGGAATCTGC	CTCCGCTGTG	AGGGAACCTG	2340
	TCTCTCAACA	CTTCCGAGCC	ATGGGGGCAA	GTGTGAAGCA	GCCAGTCCCT	GGGTGAGCCA	2400
	GAGGCTTGAA	CTTCTACAGA	AGCCCTCTGC	CCTCTGGTGG	CCTCTGGGCC	TGCTGCATGT	2460
	ACATATTTTC	TGTAAATATA	CATGCGCCGG	GAGCTTCTTG	CAGGAATACT	GCTCCGAATC	2520
	ACTTTTAAAT	TTTTTCTTTT	TTTTTCTTGG	CCCTTTCCAT	TAGTTGTATT	TTTTATTAT	2580
25	TTTTATTATT	ATTTTCTTTT	AGAGTTTGAG	TCCAGCTCTG	ACGATATAGC	CAGACCTGT	2640
	CTGTAAAAAA	ACCAAAACCC	AAAAAAAATA	AAAAAAAATA			

Seq ID NO: 76 Protein sequence

Protein Accession #: AAH10423

30	1	11	21	31	41	51	
	MPLSLGAEHW	GPEAWLLILL	LLASFTGRCP	AGELETSDDV	TVVLQDQAKL	PCPYRGDSGB	60
	QVQGVAVARV	DAGEGAQELA	LLHSKYGLHV	SPAYEGRVEQ	PPPPRNPLDG	SVLLRNAVQA	120
	DEGEYECRVS	TPFAGSFQAR	LRLRLVLPPL	PSLNPGPALE	EQGLTLAAS	CTAEGSPAPS	180
35	VTWDTVEKGT	TSSRSFKHSR	SAAVTSEPHL	VPSRSMNQRP	LTCVVSHPLG	LQDQRITHIL	240
	HVSFLAEASV	RGLDQNLNH	IGREGAMKLC	LSEGGPPPSY	NWTRLDGFLP	SGVRVDGDTL	300
	GFPLITTEHS	GIYVCHVNSE	FSSRDSQVTV	DVLDDQEDSG	KQVDLVASAV	VVVGVIALL	360
	FCLLVVVVVL	MSRYHRRKAQ	QMTQKYEEEL	TLTRENILRR	LHSHHTDPRS	QPESEVGLRA	420
	EGHPDPLKDN	SSCSVMSEEP	EGRSYSTLT	VREIETQTEL	LSPGSGRAEB	EEDQDEGIKQ	480
40	AMNHFPVQENG	TLRAKPTGNG	IYINGRGHLV				

Seq ID NO: 77 DNA sequence

Nucleic Acid Accession #: NM_003474.2

Coding sequence: 37..3036

45	1	11	21	31	41	51	
	CACCTAACGCT	CTTCTAGTCT	CCCGGGCCAA	CTCGGACAGT	TTGCTCATTT	ATTGCAACGG	60
	TCAAGGCTGG	CTTGTGCCAG	AACGGCGCGC	GCGCGACGCA	CGCACACACA	CGGGGGGAAA	120
	CTTTTAAATA	AATGAAAGGC	TAGAAGAGCT	CAGCGCGCGC	GCGGGCCGTG	CGCGAGGGCT	180
50	CCGGAGCTGA	CTGCGCAGG	CAGGAAATCC	CTCGGTGCGC	GACGCCCCGG	CCCGCTCGGC	240
	GCCCCGCTGG	GATGTTGTCG	CGCTGCGCGC	CGGGCCCCGAG	AGCTGCTGCA	CTGAAGGCGG	300
	GCGACGATGG	CAGCGCGCCC	GCTGCGCGTG	TCCCGCGCCC	GCGCCCTCCT	GCTGCGCCGT	360
	CGCGGTGCTC	TGCTGCGGCC	CTGCGAGGCC	CGAGGGGTGA	GCTTATGGAA	CGAAGGAAGA	420
	GCTGATGAAG	TGTGTCAGTG	CTCTGTTGCG	AGTGGGGACC	TCTGGATCCC	AGTGAAGAGC	480
55	TTGCACTCCA	AGAATCATCC	AGAGTGTCTG	AATATTGCGC	TACAACGGGA	AAGCAAGAAA	540
	CTGATCATAA	ATCTGGAAGG	AAATGAAGGT	CTCATTGCCA	GCAGTTTCAC	GGAAACCCAC	600
	TATCTGCAAG	ACGGTACTGA	TGTCTCCCTC	GCTCGAATTT	ACACGGTAAT	TCTGGGTAC	660
	TGTTACTACC	ATGGACATGT	ACGGGGATAT	TCTGATTCAG	CAGTCAGTCT	CAGCACTGCT	720
	TCTGCTCTCA	GGGGACTTAT	TGTGTTTGAA	AATGAAAGCT	ATGTCTTAGA	ACCAATGAAA	780
60	AGTGCACACA	ACAGATACAA	ACTCTTCCCA	GCGAAGAAGC	TGAAAAGCGT	CCGGGGATCA	840
	TGTGGATCAC	ATCACACAC	ACCAAACTTC	GCTGCAAGAA	ATGTGTTTCC	ACCACCTCT	900
	CAGACATGGG	CAAGAAGGCA	TAAAGAGAG	ACCTCAAGG	CAACTAAGTA	TGTGGAGCTG	960
	GTGATCGTGG	CAGACAACCG	AGAGTTTCAG	AGGCAAGGAA	AAGATCTGGA	AAAAGTTAAG	1020
	CAGCGATTAA	TAGAGATTGC	TAATCAAGTT	GACAAATTTT	ACAGACCACT	GAACATTGGG	1080
	ATCGTGTGG	TAGGCGTGGG	AGTGTGGAAT	GACATGGACA	AATGCTCTGT	AAGTCAGGAC	1140
65	CCATTCAACA	GCCCTCATGA	ATTTCTGGAC	TGGAGGAAGA	TGAAGCTTCT	ACCTCGCAAA	1200
	TCCCATGACA	ATGCGCAGCT	TGTCAGTGGG	GTTTATTTCC	AAGGGACCC	CATCGGCATG	1260
	GCCCCAATCA	TGAGCATGTG	CACGGCAGAC	CAGTCTGGGG	GAATGTGCAT	GGACCATTTA	1320
	GACAATCCCC	TGCTGTCAGC	CGTGACCTTG	GCACATGAGC	TGGGCCACAA	TTTCGGGATG	1380
	AATCATGACA	CACCTGACAG	GGGCTGTAGC	TGTCAAATGG	CGGTTGAGAA	AGGAGGCTGC	1440
70	ATCATGAACG	CTTCCACCGG	GTACCCATTT	CCCATGGTGT	TCAGCAGTTG	CAGCAGGAAG	1500
	GACTTGGAGA	CCAGCTTGGG	GAAAGGAATG	GGGTTGTGCC	TGTTTAACTT	GCCGGAAGTC	1560
	AGGGAGTCTT	TCCGGGGCCA	GAAGTGTGGG	AACAGATTGG	TGGAAGAAGG	AGAGGAGTGT	1620
	GACTGTGGGG	AGCCAGAGGA	ATGTATGAAT	CGCTGCTGCA	ATGCCACCA	CTGTACCTTG	1680
75	AAGCCGAGCG	CTGTGTGCGC	ACATGGGCTG	TGCTGTGAAG	ACTGCCAGCT	GAAGCTTGCA	1740
	GGAACAGCGT	CCAGGGACTC	CAGCAACTCC	TGTGACCTCC	CAGAGTTCTG	CACAGGGGCC	1800
	AGCCCTCACT	GCCCAGCCAA	CGTGTACCTG	CAGGATGGGC	ACTCATGTCA	GGATGTGGAC	1860
	GGCTACTGCT	ACAATGGCAT	CTGCCAGACT	CAAGGACGCG	AGTGTGTGAC	ACTCTGGGGA	1920
	CCAGGTGCTA	AACTGCCCCC	TGGGATCTGC	TTTGAGAGAG	TCAATTTCTG	AGGTGATCCT	1980
	TATGGCAACT	GTGGCAAGGT	CTCGAAGAGT	TCCTTTGCCA	AATGCGAGAT	GAGAGATGCT	2040
80	AAATGTGGAA	AAATCCAGTG	TCAAGGAGGT	GCCAGCCGCG	CAGTCATTGG	TACCAATGCC	2100
	GTTTCCATAG	AAACAACAT	CCCCCTGCAG	CAAGGAGGCC	GGATTCCTGT	CCGGGGGACC	2160
	CACGTGTACT	TGGGCGATGA	CATGCGGGAC	CCAGGGCTTG	TGCTTGACAG	CACAAAGTGT	2220
	GCAGATGGAA	AAATCTGCGT	GAATCGTCAA	TGTCAAATAA	TTAGTGTCTT	TGGGGTTTAC	2280
	GAGTGTGCAA	TGCAGTGCCA	CGGCAGAGGG	GTGTGCAACA	ACAGGAAGAA	CTGCCACTGC	2340
85	GAGGCCCACT	GGGCACCTCC	CTTCTGTGAC	AAGTTTGCTT	TTGGAGGAAG	CACAGACAGC	2400

	GGCCCCATCC	GGCAAGCAGA	TAACCAAGGT	TTAACCATAG	GAATTCCTGGT	GACCATCCTG	2460
	TGTCCTCTTG	CTGCCGGAAT	TGTGGTTTAT	CTCAAAAGGA	AGACCTTGAT	ACGACTGCTG	2520
	TTTACAAATA	AGAAGACCAC	CATTGAAAAA	CTAAGGTGTG	TGCGCCCTTC	CCGCGCCACC	2580
5	CGTGGCTTCC	AACCTGTGCA	GGCTCACCTC	GGCCACCTTG	GAAAAGGCCT	GATGAGGAAG	2640
	CGCCAGGATT	CTTACCCACG	GAAGGACAAT	CCCAGGAGAT	TGCTGCAGTG	TCAGAAATGTT	2700
	GACATCAGCA	GACCCCTCAA	CGCCCTGAAT	GTCCCTCAGC	CCCACTCAAC	TCAGCGAGTG	2760
	CTTCTCCCC	TCCACCGGGC	CCCAGTGCA	CCTAGCGTCC	CTGCCAGACC	CTGCCAGGCC	2820
	AAGCTGCAC	TTAGGCAGGC	CCAGGGGACC	TGTAAGCCAA	ACCCCTCTCA	GAAGCTCTG	2880
10	CCTGCAGATC	CTCTGGCCAG	AACAACCTCG	CTCACTCATG	CCTTGGCCAG	GACCCAGGGA	2940
	CAATGGGAGA	CTGGGCTCCG	CCTGGCACCC	CTCAGACCTG	CTCCACAATA	TCCACACCAA	3000
	GTGCCCAGAT	CCACCCACAC	CGCCTATATT	AAGTGAGAAG	CCGACACCTT	TTTTCAACAG	3060
	TGAAGACAGA	AGTTTGCAC	ATCTTTCAGC	TCCAGTTGGA	GTTTTTTGTA	CCAACTTTTA	3120
	GGATTTTTTT	TAATGTTTAA	AACATCATT	CTATAAGAAC	TTTGAGCTAC	TGCCGTCACT	3180
15	GCTGTGCTGT	GCTATGCTGC	TCTGTCTACT	TGCACAGGTA	CTTGTAATTT	ATTAATTTAT	3240
	GCAGAAATGT	GATTACAGTG	CAGTGGCGTG	TAGTAGGCAT	TTTTACCATC	ACTGAGTTTT	3300
	CCATGGCAGG	AAGGCTTGTT	GTGCTTTTAG	TATTTTAGTG	AACCTGAAAT	ATCCTGCTTG	3360
	ATGGGATTTCT	GGACAGGATG	TGTTTGCTTT	CTGATCAAGG	CCTTATTGGA	AAGCAGTCCC	3420
	CCAACTACCC	CCAGCTGTGC	TTATGTTACC	AGATGCACTC	CAAGAGATCC	CAAGTAGAAT	3480
20	CTCAGTTGAT	TTTCTGGATT	CCCCATCTCA	GGCCAGAGCC	AAGGGGCTTC	AGGTCAGGCC	3540
	TGTGTTTGGC	TTTCAGGGAG	GCCCTGTGCC	CCTTGACAAC	TGCGAGGCAG	GCTCCCAGGG	3600
	ACACCTGGGA	GAAATCTGCG	TTCTGGCCAG	GAAGCTTTGG	TGAGAACCTG	GGTTGCAGAC	3660
	AGGAATCTTA	AGGTGTAGCC	ACACCAGGAT	AGAGACTGGA	ACACTAGACA	AGCCAGAACT	3720
	TGACCTTGAG	CTGACCAGCC	GTGACATGT	TTGGAAGGGG	TCTGTAGTGT	CACTCAAGGC	3780
25	GGTGCTTGAT	AGAAATGCCA	AGCACTTCTT	TTTCTCGCTG	TCCTTTCTAG	AGCACTGCCA	3840
	CCAGTAGGTT	ATTTAGCTTG	GGAAAGGTGG	TGTTTCTGTA	AGAAACCTAC	TGCCCAGGCA	3900
	CTGCAAAACG	CCACCTCCCT	ATACTGCTTG	GAGCTGAGCA	AATCACCACA	AACTGTAATA	3960
	CAATGATCCT	GTATTAGAG	AGATGAGGAC	TTTCCATGGG	ACCAACAATA	TTTTCAGATG	4020
	TGAACCATTA	ACCACTCTTA	GTCAATCAAG	TCTGTTTACT	GCAAGGTTCA	ACTTATTAAC	4080
30	AATTAGGCAG	ACTCTTTATG	CTTGCAAAAA	CTACAACCAA	TGGAATGTGA	TGTTTCATGG	4140
	TATAGTTTAT	GTCTGCTATC	ATTATTGCTA	GATATTGGAC	AAAGAACCTT	CTCTATGGGG	4200
	CATCCTCTTT	TTTCAACTTG	GCTGCAGGAA	TCTTTAAAG	ATGCTTTTAA	CAGAGTCTGA	4260
	ACCTATTCTT	TAAACACTTG	CAACCTACCT	GTTGAGCATC	ACAGAAATGT	ATAAGGAAAT	4320
	CAACTGTGCT	TAACTATTAT	TAAATATTAT	GAGATGTGGC	TTGGGCAGCA	TCCCTTTGAA	4380
35	CTCTTCACTC	TTCAAAATGCC	TGACTAGGGA	GCCATGTTTC	ACAAGGTCTT	TAAAGTGACT	4440
	AATGGCATGA	GAAATACAAA	AATACTCAGA	TAAGGTAAAA	TGCCATGATG	CCTCTGTCTT	4500
	CTGGACTGGT	TTTCACTTAT	GAAGACAATT	GACAACAGTT	ACATAATTCA	CTCTGAGTGT	4560
	TTTATGAGAA	AGCCTCTTTT	TGGGGTCAAC	AGTTTCTCTA	TGCTTTGAAA	CAGAAAAATA	4620
	TGTACCAAGA	ATCTTGGTTT	GCCCTCCAGA	AAACAAAACT	GCAITTCAC	TTCCCGGTGT	4680
40	TCCCACTGT	ATCTAGGCAA	CATAGTATTC	ATGACTATGG	ATAAACTAAA	CACGTGACAC	4740
	AAACACACAC	AAAAGGGAAC	CCAGCTCTAA	TACATTCCAA	CTCGTATAGC	ATGCATCTGT	4800
	TTATTTCTATA	GTTATTAAAT	TCTTTAAAT	GTAAAGCCAT	GCTGGAAAT	AATACTGCTG	4860
	AGATACATAC	AGAAATTACTG	TAACTGATTA	CACCTTGGTA	TTGTACTAAA	GCCAAACATA	4920
	TATATCTAT	TAAAAAGGTT	TACAGAAATT	TATGGTGCAT	TAOGTGGGCA	TTGTCTTTTT	4980
45	AGATGCCCAA	ATCCTTAGAT	CTGGCATGTT	AGCCCTTCTC	CCAATTATAA	GAGGATATGA	5040
	ACCAAAAAAA	AAAAAAA	AA				

Seq ID NO: 78 Protein sequence

Protein Accession #: NP_003465

	1	11	21	31	41	51	
50	MAARPLPVSP	ARALLLALAG	ALLAPCEARG	VSLWNEGRAD	EVVSASVRSR	DLNIPVKSFD	60
	SKNHPEVLNI	RLQRESKELI	INLERNELI	ASSFTETHYL	QDGTDVSLAR	NYTVILGHY	120
	YHGHVRYGSD	SAVSLKTCG	LRGLIVFENE	SYVLEPMKSA	TNRKLEFPAP	KLKSVRSGSG	180
55	SHHNTFNLA	KNVFPFSPQ	WARRHKRETL	KATKYVELVI	VADNREFRQ	GKDLKVKQR	240
	LIEIANRVDK	PYRLNIRIV	LVGVEVNDM	DKCSVSQDPF	TSLEHFLDWR	KMKLLPRKSH	300
	DNAQLVSOVY	PQQTIGMAP	IMSMCTADQS	GGIVMDHSDN	PLGAAVTLAH	ELGHNFGMNH	360
	DTLDRGCSQ	MAVEKGGCTM	NASTGYPPFM	VPSSCSKRLD	ETSLEKGMV	CLPNLPEVRE	420
	SFGQKCGN	FVEGEECD	GEPEECNRC	CNATTCTLKP	DAVCAHGLCC	EDCQLKPAGT	480
60	ACRDSNSCD	LPEFTGASP	HCPANVYLHD	GHSQDQVDGY	CYNGICQTHE	QQCVTLWPG	540
	AKPAPGICPE	RVNSAGDPY	NCGRVSKSEF	AKCEMRDAKC	GKIQCQGGAS	RPVIGTNAV	600
	IETNIPLOQG	GRILCRGTHV	YLGDDMPDPG	LVLGATKCAD	GKICLNRCQ	NISVFGVHEC	660
	AMQCHRGVVC	NNRNCHCEA	HWAPPPCKDF	GFGGSTDSGP	IRQADNQLT	IGILVTILCL	720
	LAAGFVVYLK	RKTLIRLLFT	NKKTITIEKL	CVRPSRPPRG	FQPCQAHGLH	LGRGLMRKFP	780
65	DSYPPKDNPR	RLLOQCNVDI	SRPLNGLNVP	QPQSTQVLP	PLHRAPRAPS	VPARPLPAKP	840
	ALRQAQGTCK	PNPPQKPLPA	DPLARTTRLT	HALARTPGQW	ETGLRLAPLR	PAPQYPHQVP	900
	RSTHTAYIK						

Seq ID NO: 79 DNA sequence

Nucleic Acid Accession #: NM_003714

Coding sequence: 135..1043

	1	11	21	31	41	51	
70	GAGGAGGAGG	GAAAAGCGGA	GCAAAAAGGA	AGAGTGGGAG	GAGGAGGGGA	AGCGGCGAAG	60
	GAGGAAGAGG	AGGAGGAGGA	AGAGGGGAGC	ACAAAGGATC	CAGGTCTCCC	GACGGGAGGT	120
75	TAATACCAAG	AACCTGTGT	GCCGAGCGGC	TGGCCAGATT	CATGACCCCTG	GCTTTGGTGT	180
	TGGCCACCTT	TGACCCGCGC	CGGGGACCG	ACGCCACCAA	CCCACCCGAG	GGTCCCCAAG	240
	ACAGGAGCTC	CCAGCAGAAA	GGCCGCCCTG	CCCTGCAGAA	TACAGCGGAG	ATCCAGCACT	300
	GTTTGTGCAA	CGCTGGCGAT	GTGGGGTGTG	GCCTGTTTGA	ATGTTTTCAG	AACAACTCTT	360
80	GTGAGATTGG	GGGCTTACAT	GGGATTGCA	TGACTTTTCT	GCACAACTCT	GGAAATTTTG	420
	ATGCCACGGG	CAAGTCATT	ATCAAGACG	CCTTGAAATG	TAAAGCCCA	GCTCTGCGGC	480
	ACAGGTTGGG	CTGCATTAAG	CGGAAGTGCC	CGGCCATCAG	GGAAATGGTG	TCCCACTTGC	540
	AGCGGGGAATG	CTAOCCTCAAG	CACGACCTGT	GCGCGGCTGC	CCAGGAGAAC	ACCGGGGTGA	600
	TAGTGGAGAT	GATCGATTTC	AAGGACTTGC	TGCTGCACGA	ACCCTAAGTG	GACCTCGTGA	660
85	ACTTGTCTGT	GACCTGTGGG	GAGGAGGTGA	AGGAGGCCAT	CACCCACAGC	GTGCAAGTTC	720
	AGTGTGAGCA	GAACTGGGGA	AGCCTGTGCT	CCATCTGTAG	CTTCTGCACC	TGGCCATACC	780

5 AGAAGCCTCC CACGGCGCCC CCGAGCGGCC AGCCCCAGGT GGACAGAAC AAGCTCTCCA 840
 GGGCCCAACA CGGGGAAGCA GGACATCACC TOCCAGAGCC CAGCAGTAGG GAGACTGGCC 900
 GAGGTGCCAA GGGTGAGCGA GGTAGCAAGA GCCACCCAAA CGCCCATGCC CGAGGCAGAG 960
 TCGGGGGCCT TCGGGCTCAG GGACCTTCCG GAAGCAGCGA GTGGGAAGAC GAACAGTCTG 1020
 AGTATTCTGA TATCCGAGG TGAAATGAAA GGCCCTGGCCA CGAAATCTTT CCTCCACGCC 1080
 GTCCATTTC TATCTATGG ACATTCCAAA ACATTACCA TTAGAGAGGG GGGATGTAC 1140
 ACGCAGGATT CTGTGGGGAC TGTGGACTTC ATCGAGGTGT GTGTTCGCGG AACGGACAGG 1200
 TGAGATGGAG ACCCTTGGGG CCGTGGGGTC TCAGGGGTGC CTGGTGAATT CTGCATTAC 1260
 10 AGCTACTCAA GGGAGCGCGC CCGGTTATC CTCTACCTT TGTCTTCTT CCATCTGTGG 1320
 AGTCAGTGGG TGTGGCGCGC TCTGTGTGG GGGAGGTGAA CCAGGGAGGG GCAGGGCAAG 1380
 GCAGGGCCCC CAGAGCTGGG CCACACAGTG GGTGCTGGGC CTGCCCCGA AGCTTCTGGT 1440
 GCAGCAGCCT CTGGTGTGT CTCCGCGGAA GTCCGGCGG CTGGATTCCA GGACAGGAGT 1500
 GAATGTAAA TAAATATCG CTTAGAATGC AGGAGAAGGG TGGAGAGGAG GCAGGGCGCC 1560
 15 AGGGGGTCT TGGTGCCAAA CTGAAATTCA GTTCTTGTG TGGGGCCTTG CGGTTCAAG 1620
 CTCTTGGCGA GGGTGGAGGG AGGAGTGTCA TTTCTATGT TAAATTCTGA GCCATTGTAC 1680
 TGTCTGGGCT GGGGGGGACA CTGTCCAAGG GAGTGGCCCC TATGAGTTTA TATTTAAACC 1740
 ACTGCTTCAA ATCTCGATT CACTTTTTT ATTTATCCAG TTATATCTAC ATATCTGTCA 1800
 TCTAAATAAA TGGCTTTCAA ACAAGCAAC TGGGTCTTA AAACCACTC AAAGGGGGTT 1860
 20 TAAAAAATA AAAACAGCC CATCTTTGA GGCTGATTT TCTTTTTTT AAGTCTTAT 1920
 TTAAGAGCTA TCAACAGCG ACATAGCCAT ACATCTGACT GCCTGACATG GACTCCTGCC 1980
 CACTTGGGG AAACTTTATA CCCAGAGGAA AATACACACC TGGGGAGTAC ATTTGACAAA 2040
 TTTCCCTTAG GATTTCGTTA TCTCACCTTG ACCCTCAGCC AAGATTGGTA AAGCTGGCTC 2100
 CTGGCGATT CAGGAGACCC AGCTGGAAAC CTGGCTTCTC CATGTGAGGG GATGGGAAAG 2160
 25 GAAAGAAGAG AATGAAGACT ACTTAGTAAT TCCCATCAGG AAATGCTGAC CTTTACATA 2220
 AAATCAAGGA GACTGCTGAA AATCTCTAAG GGACAGGATT TTCCAGATCC TAAATTGAAA 2280
 TTAGCAATA AGGAGAGGAG TCCAAGGGGA CAAATAAAGG CAGAGAGAGA GAGAGAGAGA 2340
 GGGAGAGGAA GAAAGAGAG AGAGAAAAGA GCCTCGTGCC

Seq ID NO: 80 Protein sequence

Protein Accession #: NP_003705

1 11 21 31 41 51
 MCAERLQFM TLALVLATFD PARGTDATNP PEGPQDRSSQ QKRLSLQNT ABIQHCLVNA 60
 GDVGGGVFEC FENNSCEIRG LHGICMTFLH NAGKFDAGQK SPIKDALKCK AEALRHRFGC 120
 35 ISRKCPAIRE MVSQLORECY LKHDLCAAAQ ENTRVIVEMI HFKDLLLEFP YVDLVNLLLT 180
 CGSEVKEAIT HSYVQCEQN WSLCSILSP CTSAIQKPPF APPERQPVQD RTKLSRAHHG 240
 EAGHHLPEPS SRETGRGAKG ERGSKSHPNH HARGRVGGLG AQGPSGSSSEW EDEQSEYSID 300
 RR

Seq ID NO: 81 DNA sequence

Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
 AATCATGTTT TTGGAATAAA AATGGTAAAT GTTTTTTTTT TTTTTTTTTT GTTAGTAATG 60
 45 GAAGTATTC ATTATTTTAA ATTTTATGTA TGTACAGACA AGAGCTATAT GGGAAAGTAG 120
 CTATTACAGA CCCATTATAG TTTCATCATT TATAACCAGG GTTGGTAGTA AAGCAACAGA 180
 AATACATCTT CAATGCAGAC TTGCTCCCAQ CATCTCTTC CTTCATCCCT TGACCATATT 240
 GCATCTGGGA GAGGAAGAAG ACATCCTCAG CCCACCACCC CTTCCTCCTC AATGTGGAGT 300
 50 GAGTGTGGG TCAACTGATA AGCAGTGACG ACTCTTCATT TTGCTTTGTT GGTGCTTGG 360
 AGGCATGTGA GGGCAGCGCC TCAAAATCCA GAGACCTTGC CTTCAGGATT TGAGGTGGGC 420
 AAAGATGTGA AAGAGACCTT TTAGCCACTC AGTGTATCA AAAGCAATCA CCAAGAAAGT 480
 TTTTGCATCT GGCATTGTGT TGGGACGTC ATCAGCAGTA CCGTACGGTC TCCTTACTCG 540
 ACAAGTATTT AGACCTTGT AACAGCAGTG TACACCCGGT GGAAAACTCC TATCTAATG 600
 55 CATGGCAGAA TTGTAAACAT TTCCTCCTTC ACCAAATTTG TGGATGGAAT AAACATGTAG 660
 CCTTAAACTT TATTTGGCTT TCCGGTCTTG CCACTGCGGG GCCCAAAAC TTTCAGAAGT 720
 AGGAATCCTG TGCGATCTGC TAATGTGTAT TGGAGAGAAAG AGTAGAGGTG ACAGTATCTA 780
 TGGGTGCAGT ACCAGAACTA TTACGAAATG TTCCAGCTGC GATTTCAGAG GAATCCCCCC 840
 TGACCCCTGG ACGTGGTTCT CTTATTTTCA TCACCTGTG CCG

Seq ID NO: 82 DNA sequence

Nucleic Acid Accession #: XM_061091.1

Coding sequence: 1..2481

1 11 21 31 41 51
 65 ATGCCAAATA CTTCAGGAAC AACCAAGGAT GAAATTTGGC TTCTCCAAGA GCGCCCCGGG 60
 CACCGAGCGC TGTGCGCGGC TCTCCTTCCG GTGAGTCCCA GCCCGAGATT GGCTCTGGCG 120
 CCGGGTACC CGCCAGTGCC GGCTGCGGAT GACCGATTCA CGCTCCCGAT GATTGGAGGT 180
 CAGATGCATG GTGAGAAGGT AGATCTCTGG AGCCTTGGTG TTCTTTGCTA TGAATTTTAA 240
 70 GTTGGGAAGC CTCCCTTTGA GGCAGAACGAA GTCCATGTAA GCAAGAAAC CATCGGGAAG 300
 ATTTCACTG CACGCAAAAT GATGTGGTGC TGGCTGCAG TGGACATCAT GTTCTGTGTA 360
 GATGGGTCTA ACAGCGTCCG GAAAGGGAGC TTTGAAAGGT CCAAGCACTT TGCCATCACA 420
 GTCTGTGACG GTCTGGACAT CAGCCCCGAG AGGGTCAGAG TGGGAGCATT CCAGTTCAGT 480
 TCCACTCTC ATCTGGAATT CCCCTTGGAT TCATTTTCAA CCCAACAGGA AGTGAAGGCA 540
 75 AGAATCAAGA GGAATGGTTT CAAAGGAGGG CGCACGGAGA CGGAACCTGC TCTGAAATAC 600
 CTTCTGCACA GAGGGTTGCC TGGAGGCAGA AATGCTTCTG TGCCCCAGAT CCTCATCATC 660
 GTCACTGATG GGAAGTCCCA GGGGATGTG GCACTGCCAT CCAAGCAGCT GAAGGAAAGG 720
 GGTGTCACTG TGTGTGCTGT GGGGGTCAGG TTTCACAGT GGGAGGAGCT GCATGCACTG 780
 GCCAGCGAGC CTCAGAGGCA GCACGTGCTG TTGGCTGAGC AGGTGGAGGA TGCCACCAAC 840
 80 GGCCTCTTCA GCACCTTCAG CAGCTCGGCC ATCTGTCTCA GCGCAACGCC AGCTGGGAGC 900
 CCGAGCTTG TCTTCATGGA GCGGTTAATG GGCATCTCTC TGATAGGCC CTGTGACTCG 960
 CAGCCCTGCC AGAATGGAAG CACATGTGTT CCAGAAGGAC TGGACGGCTA CCAATGCCCTC 1020
 TGCCCGCTGG CTTTGGAGG GGAGGCTAAC TGTGCCCTGA AGCTGAGCCT GSAATGCAGG 1080
 GTGACCTCC TCTTCTGCTG GGACAGCTCT GCGGGCACCA CTCTGGAAGG CTTCTGCGG 1140
 85 GCGAAAGTCT TGTGAAGCG GTTGTGCGG GCGGTGCTGA GCGAGGACTC TCGGGCCCGA 1200
 GTGGGTGTGG CCACATACAG CAGGGAGCTG CTGGTGGCGG TGCTGTGGG GAGTACCAG 1260

5 GATGTGCTG ACCTGGTCTG GAGCCTGAT GGCATTCCCT TCCGTGGTGG CCCCACCTG 1320
 ACGGGCAGTG CCTTGCAGCA GCGGCGAGAG CGTGGCTTCG GGAGCGCCAC CAGGACAGGC 1380
 CAGGACCGGC CACGTAGAGT GGTGGTITTTG CTCACTGAGT CACACTCCGA GGATGAGGTT 1440
 GCGGGCCGCG CGGTTCACGC AAGGGCGCGA GAGCTGCTCC TGCTGGGTGT AGGCAGTGAG 1500
 GCGGTGGGGG CAGAGCTGGA GGAGATACA GGCAGCCCAA AGCATGTGAT GGCTACTACTG 1560
 GATCCTCAGG ATCTGTTCAA CCAATCCCT GAGCTGCAGG GGAAGCTGTG CAGCGGCGAG 1620
 CGGCCAGGGT GCGGACACA AGCCCTGGAC CTCGTCTTCA TGTGGACAC CTCGCTCTCA 1680
 GTAGGGCCCG AGAATTTTGC TCAGATGAG AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT 1740
 10 GAGGTGAACC CTGACGTGAC ACAGGTCCGC CTGGTGGTGT ATGGCAGCCA GGTGCAGACT 1800
 GCCTTCCGGG TGGACACAA ACCCAACCGG GCTGCGATGC TGGGGCCAT TAGCCAGGCC 1860
 CCCTACCTAG GTGGGTGGG CTCAGCCGGC ACCGCCCTGC TGCACATCTA TGACAAAGTG 1920
 ATGACCGTCC AGAGGGGTGC CCGGCTGGT GTCCCAAGG CTGTGGTGGT GCTCAGAGGC 1980
 GGGAGAGGGG CAGAGGATGC AGCGTTCTCT GCCCAGAAGC TGAGGAACAA TGGCATCTCT 2040
 15 GTCTTGGTGG TGGCGTGGG GCCTGTCTTA AGTGAGGGTC TGGGAGGCT TGCAGGTCCC 2100
 CGGATTTCCC TGATCCAGT GGCAGCTTAC GCCGACCTGC GGTACACCA GACCGTGTCT 2160
 ATTGAGTGGC TGTGTGGGA AGCCAAGCAG CCAGTCAACC TCTGCAACCC CAGCCCGTGC 2220
 ATGAATGAGG GCAGCTGGCT CCTGCAGAT GGGAGCTACC GCTGCAAGTG TCGGGATGGC 2280
 TGGGAGGGCC CCCACTGCGA GAACCGTGAG TGGAGCTCTT GCTCTGTATG TGTGAGCCAG 2340
 20 GGTAGGATTC TTGAGAGGCC CCTGAGGCAC ATGGCTCCCG TGCAGGAGGG CAGCAGCCGT 2400
 ACCCTCCCA GCACTACAG AGAAGGCCTG GGCACGTAAA TGGTGCTTAC CTCTGGAAT 2460
 GTCTGTGCCC CAGTCTCTTA G

Seq ID NO: 83 Protein sequence

Protein Accession #: XP_061091.1

25 1 11 21 31 41 51
 MENTSGTTRI EIMLLQEPFG HRLVAALLP VSPSPELALA PGYPPVPAAD DRFTLPMIGG 60
 QMHGEKVDLW SLOVLCYEPL VGKPPFEANE VHSVETIGK ISAASKMMWC SAAVDIMPLL 120
 30 DGSNSVKGGS PERSKHFAIT VCDGLDISPE RVRVGAFQFS STPHLEFPID SFSTQQEVIA 180
 RIKRMVFKGG RTETELALKY LLHRGLPFGGR NASVPQILII VTGDKSQGDV ALPSQKLKER 240
 GVTTFVGVVR FTRNEELHAL ASEPRGQHV LLAQVEDATN GLPSTLSSSA ICSSATPAGS 300
 PELVFMERLM GISLIGPCDS QPCQNGGTCV PEGLDGYQCL CPLAFGGEAN CALKLSLECR 360
 VDLLFLDSS AGTTLDFLR AKVFKREVR AVLSZDSRAR VGVATYSREL LVAVPVGEYQ 420
 35 DVPLVWSLD GIPPRGGPTL TGSALRQAAE RFGSATRTG QDRPRRVVVL LTESHSEDEV 480
 AGPARHARAR ELLLLGVGSE AVRAELEBIT GSPKHVMVYS DPQDLNQP ELQGLKLSRQ 540
 RFGCRTQALD LVFPLDTSAS VGPENFAQMQ SFVRSALQF EVNPDVTQVG LVVYGSQVQT 600
 AFGDLTKPTR AMLRAISQA PYLGGVGSAG TALLHIYDKV MTVQGRARPG VPKAVVVLTG 660
 GRGAEDAAVP AQKLRNNGIS VLVVGVGPVL SEGLRRLIAGP RDSLIHVAAY ADLRYHQDVL 720
 40 IEWLCEBAKQ PVNLCKPSPC MNEGSCVLQN GSYRCKCRDG WEGPHCENTRE WSSCSVCVSQ 780
 GWILETFLRH MAPVQEGSSR TPPSMYREGL GTEMVPTFWN VCAEFG

Seq ID NO: 84 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..2424

45 1 11 21 31 41 51
 ATGCCCCCTT TCTGTGTGCT GGAGGCGGTC TGTGTTTTCC TGTITTTCCAG AGTGCCCCCA 60
 TCTCTCCCTC TCCAGGAAGT CCATGTAAGC AAAGAAACCA TCGGGAAGAT TTCAGCTGGC 120
 50 AGCAAAATGA TGTGGTGCTC GGCTGCAGTG GACATCATGT TTCTGTTAGA TGGGTCTAAC 180
 AGCGTGGGGA AAGGAGGCTT TGAAAGGTCC AAGCATTCTT CCATCAGAGT CTGTGACGGT 240
 CTGACATATCA GCCCCGAGAG GGTGAGAGTG GGAGCATTCC AGTTCAGTTC CACTCTCAT 300
 CTGGAATTCC CCTTGGATTC ATTTTCAACC CAACAGGAAG TGAAGGCAAG AATCAAGAGG 360
 55 ATGTTTTTCA AAGGAGGGCG CACGAGAGCG GAACCTGTCT TGAAATACCT TCTGCACAGA 420
 GGGTGTGCTG GAGGACAGAA TGCTTCTGTG CCCGAGATCC TCATCATCGT CACTGATGGG 480
 AAGTCCCAGG GGGATGTGGC ACTGCCATCC AAGCAGCTGA AGGAAGAGGGG TGTCACGTGG 540
 TTTGCTGTGG GGGTCAGGTT TCCGAGGTGG GAGGAGCTGC ATGCAGTGGC CAGCGAGGCT 600
 AGAGGGGAGC AGCTGCTGTT GGCTGAGCAG GTGGAGGATG CCACCAACGG CCTCTTCAGC 660
 60 ACCCTCAGCA GCTCGGCCAT CTGCTCCAGC GCCACGCCAG ACTGCAGGGT CGAGGCTCAC 720
 CCCTGTGAGC ACAGGACGCT GGAGATGGTC CGGAGTTGCG CTGGCAATGC CCCATGCTGG 780
 AGAGGATCGC GCGGAGCCCT TGCGGTGCTG GCTGCACACT GTCCCTTCTA CAGCTGGAAG 840
 AGAGTGTTC TAACCCACCC TGCCACCTGC TACAGGACCA CCGGCCAGG CCGCTGTGAC 900
 TCGCAGCCCT GCCAGATGAG AGGCACATGT GTTCCAGAG GACTGGAAGG CTACAGTGC 960
 65 CTCTGCCCGC TGGCCTTTGG AGGGGAGGCT AACTGTGCCC TGAAGCTGAG CTTGGAATGC 1020
 AGGGTGGACC TCTCTTCTCT GCTGGACAGC TCTGCGGSCA CCACCTGGA CCGCTTCTCTG 1080
 CCGGCCAAG TCTTCTGTGA GCGGTTTGTG CCGGCCGTGC TGAGCGAGGA CTCTCGGGCC 1140
 CGAGTGGGTG TGGCCACATA CAGCAGGGAG CTGCTGTGGG CGGTGCTGTG GGGGGAGTAC 1200
 CAGGATGTGC CTGACCTGGT CTGAGGCTTC GATGGCATTG CCTTCCGTGG TGGCCCCACC 1260
 CTGACGGGCA GTGCTTGGG GCAGGCGGCA GAGGTGGCT TCGGGAGCGC CACCAAGACA 1320
 70 GGCCAGGACC GGCCACGTAG AGTGGTGGTT TTGCTCACTG AGTCACTC CGAGGATGAG 1380
 GTTGGCGGCC CAGCGCGTCA CGCAAGGGCG CGAGAGCTGC TCCTGCTGGG TGTAGGCAGT 1440
 GAGGCGGTGC GGGCAGAGCT GGAGGAGATC ACAGGCAGCC CAAAGCATGT GATGGTCTAC 1500
 TCGATCCTC AGGATCTGTT CAACCAATC CCTGAGCTGC AGGGGAAGCT GTGCAGCCGG 1560
 CAGCGGCCAG GTGCGCGGAC ACAAGCCCTG GACCTGTCT TCAATGTTGA CACCTGTGCG 1620
 75 TCAGTAGGGC CCGAATATT TGCTCAGATG CAGAGCTTTG TGAGAAGCTG TGCCCTCCAG 1680
 TTTGAGGTGA ACCCTGACGT GACACAGGTC GGCCTGGTGG TGTATGGCAG CCAGGTGCAG 1740
 ACTGCTTTCG GCTGTGACAC CAACCCACCC CGGGCTGCGA TGCTGCGGGC CATTAGCCAG 1800
 GCGCCCTACC TAGTGGGGT GGGCTCAGCC GGCACCGCCC TGCTGCACAT CTATGACAAA 1860
 GTGATGACCG CTCAGAGGCT TGCCCGGCTT GGTGTCCCA AAGCTGTGGT GGTGCTCA 1920
 80 GCGGGAGAG GCGCAGAGGA TGCAGCCGTT CCTGCCAGA AGCTGAGGAA CAATGGCATC 1980
 TCTGTCTTGG TGTGGGCGT GGGGCGCTTC CTAAGTGAGG GTCTGCGGAG GCTTGCAGGT 2040
 CCGCGGATT CCTGATCCA GGTGGCAGCT TACGCGAGCC TGCGGTACCA CCAGGACGTG 2100
 CTCATTGAGT GGTGTGTGG AGAAGCCAG CAGCCAGTCA ACCTCTGCAA ACCCAGCCCG 2160
 TGCATGAATG AGGCAGCTG GTCCTGCAAG AATGGGAGCT ACCGCTGCAA GTGTGGGAT 2220
 85 GGCTGGGAGG GCGCCCACTG CGAGAACCGT GAGTGGAGCT CTTGCTCTGT ATGTGTGAGC 2280
 CAGGGATGGA TTCTTGAGAC GCCCTGAGG CACATGGCTC CCGTGACAGA GGGCAGCAGC 2340

CGTACCCCTC CCAGCAACTA CAGAGAAGGC CTGGGCACTG AATGGTGCC TACCTTCTGG 2400
AATGTCGTG CCCAGGTCC TTAG

Seq ID NO: 85 Protein sequence

Protein Accession #: Eos sequence

1 11 21 31 41 51
MPPFLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN 60
SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QOEVKARIKR 120
MVPKGGRTET ELALKYLLER GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKERGVTV 180
FAVGVRFPFRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
PCEHRTLEMW REFAGNAPCW RGSRRTLAVL AAHCFFYSWK RVFLTHPATC YRTTCPPGCD 300
SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360
RAKVVFVRFPV RAVLSSEDSRA RVGVATYSRE LLVAVPVGEY QDVVDLWVSL DGIFPRGGPT 420
LTGSALRQAA ERGPGSATRT QQDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVS 480
EAVRAKLEBI TGSFHVVMVY SDPQDLFNQI PELQGLKCSR QRPQCRTQAL DLVFLMDTSA 540
SVGPENFAQM QSFVRSQALQ FEVNPVDVTQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
APYLGGVGSA LTHLHLYDK VMTVQRGARP GVPKAVVVLV GGRGAEDAAV PAQKLRRNGI 660
SVLVVVGVPV LSEGLRLRAG PRDSLIEHVA YADLRVHQDV LIEMLCSEAK QPVNLCKPSP 720
CWNBSGCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETPLR HMAFVQBSGS 780
RTFSPNYREB LGTEMVTFW NVCAPGE

Seq ID NO: 86 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 89..2356

1 11 21 31 41 51
GCCCCCTGGC CCGAGCCGCG CCGGGTCTG TGAGTAGAGC CGCCCCGGCA CCGAGCGCTG 60
GTGCGCCGTC TCCCTCCGTT ATATCAACAT GCCCCCTTTC CTGTTGCTGG AAGCCGCTG 120
TGTTTTCTG TTTTCCAGAG TGCCCCCATC TCTCCCTCTC CAGGAAGTCC ATGTAAGCAA 180
AGAAACCATC GGAAGATTAT CAGCTGCCAG CAARAATGAT TGGTGTCTCG CTGCAGTGGA 240
CATCATGTTT CTGTAGATG GGTCTAACAG CGTCGGGAAA GGGAGCTTTG AAAGGTCCAA 300
GCACCTTTGC ATCAGCTCT GTGACGGTCT GGACATCAGC CCGAGAGGGG TCAGAGTGGG 360
AGCATTCAG TTAGTTCCT CTCTCATCT GGAATCCCC TTGATTATCAT TTTCAACCCA 420
ACAGGAAGTG AAGCAAGAA TCAAGAGGAT GGTTTTCAAA GGAGGGCGCA CGGAGACGGA 480
ACTTGCTCTG AAATACCTTC TGACAGAGG GTTGCTGGA GGCAGAAATG CTTCTGTGCC 540
CCAGATCCTC ATCATCTGCA CTGATGGGAA GTTCCAGGGG GATGTGGCAC TGCCATCCAA 600
CGAGCTGAAG GAAAGGGGTG TCACTGTGTT TGCTGTGGGG GTACAGTTTC CCAGTGCGGA 660
GGAGCTGCAT GCATGCGCCA GCGAGCCTAG AGGGCAGCAC GTGCTGTGG CTGAGCAGGT 720
GGAGGATGCC ACCAACGGCC TCTTCAGCAC CTTACAGCAG TCGGCAATCT GCTCCAGCGC 780
CACGCCAGAC TGACGGGTG AGGCTCACCC CTGTGAGCAC AGGACGCTGG AGATGCTCCG 840
GGAGTTCCGT GGCATATGCC CATGCTGGAG AGGATCGCGG CGGACCCCTG CGGTGCTGGC 900
TGACACCTGT CCTTCTCA GCTGGAAGAG AGTGTTCCTA ACCCAACCTG CCACCTGCTA 960
CAGGACCAAC TGCCCGAGCC CCTGTGACTC GCAGCCCTGC CAGAAATGGAG GCACATGTGT 1020
TCCAGAGGSA CTGAGCGGT ACCAGTGCT CTGCGCGCTG GCCTTTGGAG GGGAGGCTAA 1080
CTGTGCCCTG AAGCTGAGCC TGAATGCAG GGTGACCTC CTCCTCTGTC TGGACAGCTC 1140
TGCGGGCACC ACTCTGAGG GCTTCTGCG GGCCAAAGTC TTCTGTAAGC GGTTTGTGCG 1200
GGCGGTGCTG AGCGAGGACT CTGCGGCGCG AGTGGGTGTG GCCACATACA GCAGGAGACT 1260
GCTGTGGGCG GTGCTGTGG GGGAGTACCA GGATGTGCCT GACCTGTGCT GGAGCCTCGA 1320
TGGCATTCCT TTCTGTGCT GCGCCACCT GACGGGCAGT GCCTTGGGCG AGGCGGCGA 1380
GCTGTGCTTC GGGAGCGCCA CCAGGACAGG CCAGGACCGG CCACTAGAG TGGTGGTTTT 1440
GCTCACTAGT TCACACTCCG AGGATGAGGT TGCGGGCCCA GCGGTTCAG CAAGGGGCGG 1500
AGAGCTGCTC CTGCTGGGT TAGGCAGTGA GCGGTGCGG GCAGAGCTGG AGGAGATCAC 1560
AGGACGCCCA AAGCATGTGA TGGTCTACTC GGATCTCTAG GATCTGTTC ACCAAATCCC 1620
TGAGCTGCAG CCGAAGCTGT GCAGCGGCA GCGGCCAGGG TGCGGACAC AAGCCCTGGA 1680
CCTGCTCTTC ATGTGTGACA CCTGTGCTC AGTAGGGCCC GAGAAATTTG CTCAGATGCA 1740
GAGCTTTGTG AGAAGCTGTG CCTTCCAGTT TGAGGTGAAC CCTGACGTGA CACAGGTCCG 1800
CTGTGTGTG TATGTGAGCC AGGTGCAGAC TGCTTCCGG CTGGACACCA AACCCACCCG 1860
GGCTGCGATG CTGCGGCGCA TTAGCCAGGC CCCCTACTTA GGTGGGGTGG GCTCAGCCGG 1920
CACCGGCCCT CTGCATCTC ATGACAAAGT GATGACCGTC CAGAGGGGTG CCGGCGCTGG 1980
TGTCGCCAAA GCTGTGTGG TGCTCAGAG CCGGAGAGGC GCAGAGGATG CAGCCGTTC 2040
TGCCAGAAAG CTGAGGAACA ATGGCATCTC TGTCTTGGTC GTGGGCGTGG GGCCTGTCTC 2100
AAGTGAGGGT CTGCGGAGGC TTGAGGTCC CCGGATTCCT CTGATCCAG TGGCAGCTTA 2160
CGCCGACCTG CGGTACCAAC AGGACGTGCT CATGTAGTGG CTGTGTGGAG AAGCCAGCA 2220
GCCAGTCAAC CTCTGCAAC CCAGCCCGTG CATGAATGAG GGCAGCTGCG TCTGTGAGAA 2280
TGGGAGCTAC CGCTGCAAGT GTCGGATGG CTGGGAGGGC CCCCCTGCG AGAACCGATT 2340
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AGCAACTACA GAGAAGGCTT GGGCACTGAA ATGGTGCTTA CCTCTGGAA TGTCTGTGCC 2460
CCAGGTCTCT AGAATGTCTG CTTCGCGCG TGCCAGGAC CACTATTCTC ACTGAGGGAG 2520
GAGGATGTCC CAACTGCAG CATGCTGCTT AGAGACAAGA AAGCAGCTGA TGTCAACCCAC 2580
AAACGATGTT GTTGAAGAT TTTGATGTGT AAGTAAATAC CCACTTCTG TACCTGTCTG 2640
GCCTTGTGTA GGCATGTGCA TCTGCCACCT TTCCCTTGAG GATAAACAA GGGTCTCTGA 2700
GACTTAAATT TAGGGGCTG ACCTTCTTT GCACACAATC AATGCTCGCC AGAATGTGT 2760
TGACACAGTA ATGCCAGCA GAGGCCCTTA CTAGAGCATC CTTGGAGCG

Seq ID NO: 87 Protein sequence

Protein Accession #: Eos sequence

1 11 21 31 41 51
MPPFLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN 60
SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QOEVKARIKR 120
MVPKGGRTET ELALKYLLER GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKERGVTV 180
FAVGVRFPFRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
PCEHRTLEMW REFAGNAPCW RGSRRTLAVL AAHCFFYSWK RVFLTHPATC YRTTCPPGCD 300
SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360

RAKVFPKRV RAVLSSEDSRA RVGVATYSRE LLVAVFVGEY QDVPLVWSL DGIPFRGGPT 420
 LTGSALRQAA ERGFGSATRT GQDRPRRVVV LLTSEHSEDE VAGPARHARA RELLLLVGVS 480
 EAVRAEGLSI TGSPKHMVY SDPQDLFNQI PELQGLCSR QRPGRCTQAL DLVFMIDTSA 540
 SVGPENPAQM QSFVRSALQ FEVNPDTVQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
 APYLGGVGA GTALLHYDK VMTVQGRARP GVFKAVVVL T GGRGAEDAAV PAQKLNNNGI 660
 SVLVVGVGPV LSEGLRLAG PRDSLHVA YADLRYHQDV LIEMLOGEAK QPVNLCRPS 720
 QNNGSCVLQ NGSYRCKCRD GNEGPHCENR FLRRP

Seq ID NO: 88 DNA sequence
 Nucleic Acid Accession #: NM_019894
 Coding sequence: 1..1314

1 11 21 31 41 51
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 15 ATGTTACAGG ATCCTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCTGCGC 60
 AAACCCCGTA TCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCATCAT CATAGCACTA 120
 CTGAGCCTGG CGAGTATCAT CATTGTGGTT GTCTCATCA AGGTGATTCT GGATAAATAC 180
 TACTTCTCTT GCGGCGAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGAGAG 240
 CTGGACTGTC CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300
 CGAGTGGCAG TCGCCTCTC CAAGGACCGA TCCACACTGC AGGTCTGGA CTGGCCACA 360
 20 GGGAACTGGT TCTCTGCTG TTTGGAACA TTACAGAAAG CTCTGCTGA GACAGCCTGT 420
 AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG OCCAGACCAG 480
 GATCTGGATG TTGTTGAAAT CACAGAAAC AGCCAGGAGC TTGCGATGGG GAATCTAAGT 540
 GGGCCCTGTC TCTCAGGCTC CTGCTCTCC CTGCACTGTC TTGCTGTGG GAAGAGCCTG 600
 AAGACCCCCC GTGTGTTGGG TGGGAGGAG GCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
 25 AGCATCCAGT AGCACAACA GCACTCTGT GGAGGAGCA TCCCTGAGCC CCATGGGTC 720
 CTCACGGCAG CCGACTGCTT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA 780
 GGCTCAGACA AACTGGGAG CTTCCTATCC CTGGCTGTGG CCAAGATCAT CATCATTGAA 840
 TTCACCCCA TGTACCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC 900
 ACTTTCTCAG GCAACATGAC GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
 30 GCCACCCCA TCTGGATCAT TGGATGGGGC TTTACGAAGC AGAATGGAGG GAAGATGTCT 1020
 GACATACTGC TGGAGCGCTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT 1080
 GGGTACCAGG GGGAAATGAC CAGAAAGATG ATGTGTGAG GCATCCCGGA AGGGGGTGTG 1140
 GACACCTGCC AGGGTGACAG TGGTGGGCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
 35 GTGGGCATG TTAGCTGGGG CTATGGCTG GGGGCCCGA GCACCCGAG AGTATACACC 1260
 AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA

Seq ID NO: 89 Protein sequence:
 Protein Accession #: NP_063947.1

1 11 21 31 41 51
 | | | | |
 40 MLQDPDSQDP LNSLDVKFLR KPRIPMETFR KVGIPILIAL LSLASIIIV VLIKVILDKY 60
 YFLOGQLHP IPRKQLDGE LDCPLGEDEE HCVRSPPEGP AVAVRLSKDR STLQVLDSAT 120
 GWNFSACFDN PTEALAEATC RQMGYSKPT FRAVEIGPDQ DLDVVEITEN SQELMRNNS 180
 45 GPCLSGSLVS LHCLACGKSL KTRPVVGEE ASVDSWPHQV SIQYDKQHVC GSGILDPHWV 240
 LTAACHPRKH TDVFNWVTRA GSDKLGSFSP LAVAKIIIE PNPMPKXND IALMKLQFPL 300
 TFSGTVRPIC LPPFDEELTP ATPLWIIQWG FTKQNGGKMS DILLQASVQV IDSTRCNADD 360
 AYQGEVTEKM MCAGIPEGGV DTCQGDSSGP LMYQSDQWHV VGIVSWGYGC GGPSTPGVYT 420
 KVSAYLNWY NVWKAEI

Seq ID NO: 90 DNA sequence
 Nucleic Acid Accession #: NM_002776.1
 Coding sequence: 82..912

1 11 21 31 41 51
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 55 ACCAGCGGCA GACCACAGGC AGGGCAGAGG CAGCTCTGGG TCCCTCCCT CCTTCTATC 60
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 GCGCGGCTC TGGCGAAGCT GCTGCGGCTG CTGATGGCGC AACTCTGGGC CGCAGAGGCG 180
 GCGCTGTCTC CCAAAAGCA CACGCGCTTG GACCCGAAAG CCTATGGCGC CCGTGGCGG 240
 60 CGCGGCTCGC AGCCCTGGCA GGTCTCGCTC TTCAACGGCC TCTCGTTCCA CTGCGCGGGT 300
 GTCTGTGGT ACCAGAGTTG GGTGCTGAGC GCGCGCACT GCGGAAACAA GCCACTGTGG 360
 GCTGAGTAG GGGATGATCA CTGTCTGCTT CTTAGGGGG AGCAGCTCCG CCGGACGACT 420
 CGCTCTGTG TCCATCCCAA GTACCAACAG GGCTCAGGCC CCATCCTGCC AAGCGGAAG 480
 GATGAGCAG ATCTCATGTT GCTAAAGCTG GCCAGGCCG TAGTGCCGG GCGCCGCTC 540
 65 CGGGCCCTGC AGCTTCCCTA CCGTGTGCT CAGCCCGGAG ACCAGTGCCA GGTGCTGGC 600
 TGGGGACCA CGGCGGCCG GAGAGTGAAG TACAACAAG GCCTGACCTG CTCCAGCATC 660
 ACTATCTCTA GGCCTAAAGA GTGTGAGGTC TTCTACCTG GCGTGGTCAC CAACAACATG 720
 ATATGTGCTG GACTGGACCG GGGCCAGGAC CCTTGCCAGA GTGACTCTGG AGGCCCTCTG 780
 GTCTGTGAGC AGACCTCCCA AGGCATCTC TGTGGGGTG TTTACCCCTG TGGCTCTGCC 840
 70 CAGCATCCAG CTGTCTACAC CCAGATCTGC AATATACATG CTGGATCA TAAAGTCATA 900
 CGCTCCAAT GATCCAGATG CTACGCTCCA GCTGATCCAG ATGTTATGCT CTGCTGATC 960
 CAGATGCCCA GAGGCTCCAT CGTCCATCT CTCTCTCCC AGTGGGCTGA ACTTCCCT 1020
 TGTCTGCACT GTTCAAACT CTGCGCCCT CCACACCTCT AAACATCTCC CTCTCACT 1080
 CATTCGCCCA CCTATCCCA TTCTCTGCT GTACTGAAGC TGAATGCAG GAAGTGGTGG 1140
 75 CAAAGGTTTA TTCCAGAGAA GCCAGGAAGC CGGTATCAC CCAGCCTCTG AGAGCAGTTA 1200
 CTGGGGTCA CCAACCTGAC TTCTCTGCC ACTCCCGCT GTGTGACTTT GGGCAAGCCA 1260
 AGTGCCCTCT CTGAACCTCA GTTCTCTCAT CTGCAAAATG GGAACAATGA CGTGCTTACC 1320
 TCTTAGACAT GTTGTGAGGA GACTATGATA TAACATGTGT ATGTAATCT TCATGTGATT 1380
 80 GTCATGTAAG GCTTAACACA GTGGGTGGTG AGTCTGACT AAAGTTACC TGTGTCTGT 1440
 AAAAAAAAA AAAA

Seq ID NO: 91 Protein sequence
 Protein Accession #: NP_002767.1

1 11 21 31 41 51
 | | | | |
 85 MRAPHLHLSA ASGARALAKL LPLIQAQLWA AEAALLPQND TRLDPEAYGA PCARGSQPHQ 60

VSLFNLGSLFH CAGVLVDQSW VLTAAHCGNK PLWARVGDH LLLLQGEQLR RTRSVVHPK 120
 YHQGSPIPLP RRTDHDHML LKLARFVVPV PRVRLQLFY RCAQPGDQCC VAGWGTTAAR 180
 RVKYNKGLTC SSITLLSPKE CEVFFYPGVVT NNMICAGLDR GQDPCQSDSG GPLVCDTELQ 240
 GILSWGVYPC GSAQHPAVYT QICKYMSWIN KVIRSN

Seq ID NO: 92 DNA sequence
 Nucleic Acid Accession #: NM_032044.1
 Coding sequence: 182-658

1 11 21 31 41 51
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 AAGATATAAA AGCTCCAGAA ACCTTGACTG GGACCACTGG AGACACTGAA GAAGGCAGGG 60
 GCCTTAGAGT TCTTGGTTGC CAAACAGATT TGCAGATCAA GGAGAACCAC GGAGTTTCAA 120
 AGAAGCGCTA GTAAGGTCTC TGAGATCCTT GCACTAGCTA CATCCTCAGG GTAGGAGGAA 180
 GATGGCTTCC AGAAGCATGC GGCTGCTCCT ATTGCTGAGC TGCTGGGCCA AACACGAGGT 240
 CCTGGGTGAT ATCATCATGA GACCCAGCTG TGCTCCTGGA TGGTTTTACC ACNAGTCCAA 300
 TTGCTATGGT TACTTCAGGA AGCTGAGGAA CTGGTCTGAT GCGAGCTCG AGTGTCAGTC 360
 TTACGGAAC GGAGCCACCT TGCCATCTAT CTTGAGTTTA AAGGAAGCCA GCACCATAGC 420
 AGAGTACATA AGTGGCTATC AGAGAAGCCA GCGGATATGG ATTGGCCTGC ACGACCCACA 480
 GAAGAGGCGC CAGTGGCAGT GGATTGATGG GGCATGTAT CTGTACAGAT CTGTGCTCGG 540
 CAAGTCCATG GGTGGGAACA AGCACTGTGC TGAGATGAGC TCCAATAACA ACTTTTTAAC 600
 TTGGAGCAGC AACGAATGCA ACAAGCGCCA ACACITCTCT TGCAAGTACC GACCATAGAG 660
 CAAGAATCAA GATTCTGCTA ACTCCTGCAC AGCCCGCTCC TCTTCTTTC TGCTAGCCTG 720
 GCTAAATCTG CTCTATTATT CAGAGGGGAA CCTAGCAAA CTAAGAGTGA TAAGGGCCCT 780
 ACTACACTGG CTTTTTAGG CTTAGAGACA GAAACTTTAG CATTGGCCCA GTAGTGGCTT 840
 CTAGCTCTAA ATGTTTGCCC CGCCATCCTT TTCCACAGTA TCCTTCTTCC CTCCTCCOCT 900
 GTCTCTGGCT GTCTCGAGCA GTCTAGAAGA GTGCTCTGCC AGCCTATGAA ACAGCTGGGT 960
 CTTTGGCCAT AAGAAGTAAA GATTTGAAGA CAGAAGGAAG AAACCTCAGGA GTAAGCTTCT 1020
 AGACCCCTTC AGCTTCTACA CCTTCTGCC CTCTCTCCAT TGCTGCAACC CCACCCACAG 1080
 CACTCAACTC CTGCTTGTTC TTCTTTGGC CATAGGAAGG TTTACCACTA GAATCCTTGC 1140
 TAGGTTGATG TGGGCCATAC ATTCTTTTAA TAAACCATTG TGTACATAAG AAAAAAAAAA

Seq ID NO: 93 Protein sequence
 Protein Accession #: NP_114433.1

1 11 21 31 41 51
 | | | | |
 MASRSMRLLL LLSCLAKTGV LGDIIMRPSC APGWFYHKSN CYGYFRKLKN WSDAELEQCS 60
 YGNAGHLASI LSLKEASTIA EYISGYQRQS PIWIGLHDPQ KRQWQWIDG AMYLRSWSG 120
 KSMGGNKICA EMSSNNNFLT WSSNEQNRQ HFLCYKRP

Seq ID NO: 94 DNA sequence
 Nucleic Acid Accession #: XM_051860
 Coding sequence: 1..4086

1 11 21 31 41 51
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 GAGCTAGGCC TCAGCAGAG CCCAGCGCGG TGCTATCGGA CAGAGCCTGG CGAGCGCAAG 60
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 AGCTACCACT CCGCTTGCCC ACGCCCCGGG AGCTCGCGGC GCTTGGCGGT CAGCGACCACT 180
 ACGTCCGGGG CCGCTGCGCT CCTGGCCCGG GAGGCGTGAC ACTGTCTCGG CTACAGACCC 240
 AGAGGGAGCA CACTGCCAGG ATGGGAGCTG CTGGGAGGCA GGAATCTCTC TTCAAGGCCA 300
 TGCTGACCAT CAGCTGGCTC ACTCTGACCT GCTTCCCTGG GGCCACATCC ACAGTGGCTG 360
 CTGGGTGCCC TGACCAGAGC CCTGAGTTGC AACCTTGGAA CCTTGGCCAT GACCAAGACC 420
 ACCATGTGCA TATGGGCCAG GGCAAGACAC TGCTGCTCAC CTCTTCTGCC ACGTCTATT 480
 CCATCCACAT CTCAGAGGGA GGCAAGCTGG TCATTAAAGA CCACGACGAG CCGATTGTTC 540
 TGGGAACCGG GCACATCTGT ATTGACAACG GAGGAGAGCT GCATGCTGGG AGTGGCCCTC 600
 GCCCTTTCCA GGGCAATTTC ACCATCATTT TGTATGGAAG GGCTGATGAA GGTATTTCAGC 660
 CCGATCCTTA CTATGGTCTG AAGTACATTG GGGTTGGTAA AGGAGGCGCT CTGAGTTGC 720
 ATGGACAGAA AAGGCTCTCC TGGACATTTC TGAACAAGAC CCTTCAACCA GGTGGCATGG 780
 CAGAAGGAGG CATTTTTTTT GAAAGGAGCT GGGGCCACCG TGGAGTTATT GTTCATGTCA 840
 TCGACCCCAA ATCAGGCACA GTCATCCATT CTGACCGGTT TGACACCTAT AGATCCAAGA 900
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 TTGCACTGAA TGATGAAGGT TCTCGAAATC TGGATGACAT GGCCAGGAAG GCGATGACCA 1020
 AATTGGGAAG CAAACACTTC CTGCACCTTG GATTTAGACA CCTTGGAGT TTCTAACTG 1080
 TGAAAGGAAA TCCATCATCT TCAGTGAAG ACCATATTGA ATATCATGGA CATCGAGGCT 1140
 CTGCTGCTGC CCGGTATTTC AAATTGTTCC AGACAGAGCA TGGCGAATAT TTCAATGTTT 1200
 CTTTGTCCAG TGAGTGGGTT CAAGACGTGG AGTGGACGGA GTGGTTCGAT CATGATAAAG 1260
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 TATGCAATCG TCCCATTTGAT ATACAGGCCA CTACAAATGA TGGAGTTAAC CTCAGCACCG 1380
 AGGTGTTCTA CAAAAAGGC CAGGATTATA GGTTTGCTTG CTACGACCGG GGCAGAGCCT 1440
 GCGGAGCTA CCGTGTACGG TTCTCTGTG GGAAGCCTGT GAGGCCCAAA CTCACAGTCA 1500
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 AACCTGGAGA TACCTGGTC ATTGCCAGTA CTGATTACTC CATGTACCAG GCAGAAGAGT 1620
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 TGAGCGGAA CATCATATG ATGGGGGAGA TGGAGGACAA ATGCTACCCC TACAGAAACC 1800
 ACATCTGCAA TTTCTTTCAC TTGATACCT TTGGGGCCA CATCAAGTTT GCTCTGGGAT 1860
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 TCAAGGAAGA TGGGCGGAG GAAAGCAACA CTTTTCAGCA CTGTCTGGC CTCTTGTCA 2160
 AGTCTGGAAC CTCTCTCCC TCGGACCGTG ACAGCAAGAT GTGCAAGATG ATCAGAGAGG 2220
 ACTCTACCC GGGGTACATC CCCAAGCCCA GGCAAGACTG CAATGCTGTG TCCACCTTCT 2280
 GGATGGCCAA TCCCAACAC AACCTCATCA ACTGTGCGCG TGCAGGATCT GAGGAAACTG 2340
 GATTTTGGTT TATTTTTCAC CACGTACCAA CCGGCCCTC CGTGGGAATG TACTCCCCAG 2400

5	GTATTTCAGA GCACATTCAC CTGGGAAAAT TCTATAACAA CCGAGCACAT TCCAACTACC 2460
	GGGCTGGCAT GATCATAGAC AACGGAGTCA AAACCCCGA GGCCTCTGCC AAGGACAAGC 2520
	GGCCGTTCTT CTCAATCATC TCTGCCAGAT ACAGCCCTCA CCAGGACGCC GACCCGCTGA 2580
	AGCCCGGGGA GCGGGCCATC ATCAGACACT TCATTGCCTA CAAGAACCAG GACCACGGGG 2640
	CCCTGGCTGG CCGCGGGGAT GTGTGGCTGG ACAGCTGGCG GTTTGCTGAC AATGGCATTG 2700
	GCCTGACCTT GGCACGTGGT GGAACCTTCC CGTATGACGA CGGCTCCAG CAAGAGATAA 2760
	AGAACAGCTT GTTTGTGTGC CAGAGTGGCA ACCTGGGGAC GGAATATGAT GACAATAGGA 2820
	TCTGGGGCCC TGGCGGCTTG GACCATAGCG GAAGGACCTT CCTATAGGC CAGAATTTTC 2880
	CAATTAGAGG AATTACGTTA TATGATGGCC CCATCAACAT CCAAACTGC ACTTTCGAA 2940
10	AGTTTGTGGC CCTGGAGGGC CGGCACACCA GCGCCCTGGC CTTCGGCTGG AATAATGCCT 3000
	GGCAGAGCTG CCCCATTAAC AACGTGACCG GCATTGCTT TGAGGACGTT CCGATTACTT 3060
	CCAGAGTGTT CTTCGAGAGC CTTGGGCCCC GTTCAACCA GCTGGACATG GATGGGGATA 3120
	AGACATCTGT GTTCCATGAC GTGACGGCT CCGTGTCCGA GTACCCCTGC TCCTACCTCA 3180
	CGAAGAAATG CAATCGGCTG GTCCGGCACC CAGATGCTAT CAATGTTCCC GACTGGAGAG 3240
15	GGGCCATTGG CAGTGGGTGC TATGCACAGA TGTACATTCA AGCCTACAAG ACCAGTAACC 3300
	TGCGAATGAA GATCATAGAG AATGACTTCC CCAGCCACCC TCTTTACCTG GAGGGGGCGC 3360
	TCACCAAGAG CACCCATTAC CAGCAATACC AACCGGTTGT CACCCCTGAC AAGGGCTACA 3420
	CCATCCATG GAGCCAGAGC GCGCCGCGCG AACTCGCCAT CTGGCTCATC AACTTCAACA 3480
	AGGCGCACTG GATCCGAGTG GGGCTCTGCT ACCCGCGAGG CACCAATTTC TCCATCTCT 3540
20	CGATGTTCAC CAATCGCTCG CTGAAGCAAA CGTCCAAGAC GGGCGTCTTC GTGAGGACCT 3600
	TGCAGATGGA CAAGATGGAG CAGAGCTACC CTGGCAGGAG CCCTACTTAC TGGGACGAGG 3660
	ACTCAGGGCT GTTGTTCCTG AAGCTGAAAG CTCAGAACGA GAGAGAGAGG TTTGCTTTCT 3720
	GCTCCATGAA AGTCTGTGAG AGGATAAAGA TTAAGCTCT GATTCCAAG AACGCAAGCG 3780
	TCAGTGACTG CACAGCCACA GCTTACCCCA AGTTCACCGA GAGGCTGTG GTAGAGGTGC 3840
25	CGATGCCCAA GAAGCTCTTT GGTCTCTCAG TGAAAACAAA GGAACATTTT TTGAGGTGA 3900
	AGATGAGAGG TTCCCAAGAG CACTTCTTCC ACTCTGGAA CGACTTCGCT TACATTGAAG 3960
	TGGATGGGAA GAAGTACCCC AGTTCGGAGG ATGGCATCCA GGTGGTGGTG ATTGACGGGA 4020
	ACCAAGGGCG CGTGGTGGAG CACACGAGCT TCAGGAACCT CATTCTGCAA GGCATACCAT 4080
	GGCAGCTTTT CAATATGTGT GCGACCATCC CTGACAAATC CATAGTGCTT ATGGCATCAA 4140
30	AGGGAAGATA CGTCTCCAGA GCGCCATGGA CCAGAGTGCT GGAAGAGCTT GGGGACAGA 4200
	GGGGTCTCAA GTTGAAGAG CAATGGGCAT TCGTTGGCTT CAAAGGCAGC TTCGGGCCCA 4260
	TCTGGGTGAC ACTGGACACT GAGGATCACA AAGCCAAAT CTTCGAAGTT GTGCCCATCC 4320
	CTGTGTGAGG GAAGAAGAGG TTGTGAGGAC AGCTGCCGCC CGGTGCCACC TCGTGTGATA 4380
	CTATGACGGT GACTCTTGGC AGCAGACCAG TGGGGGATGG CTGGTCCCC CAGCCCTGTC 4440
35	CAGCAGTGC CTGGGAAGGC CGTGTTCAG CCTGATGGG CCAAGGGAAG GCTATCAGAG 4500
	ACCCTGGTGC TGCCACCTGC CCTACTCAA GTGTCTACCT GGAGCCCCTG GGGCGGTGCT 4560
	GGCCTATGCT GGAACATTTT ACTTCTCTGC AGGCTCTTGG GTGCTTCTCT CCTATCTGTG 4620
	CCTCTCACT GGGGGTTTGG GGACCATATC AGGAGACCTG GGTGTGTGCT ACAGCAAGAA 4680
40	TCCACTTTGG CAGGAGCCCT GACCCAGCTA GGAGGTAGTC TGGAGGGCTG GTCATTACA 4740
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	AGAATGGCT ATCCTTGGGG AAGAGGCAAG CCTTGCCTCT GGCCTGTGCC ACCTTTCAGG 4920
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45	GAGATTCCAG AATCTGTGCT CATTTCACAT GGTACCTGGA ACCCAACAGT TCATGTGAT 5040
	CCACTGATAT CAGTATGCT GGGTGCCCA GCGCACACGG GATGGAGAGG TGAGAACTAA 5100
	TGCTTAGCTT GAGGGGTCTG CAGTCCAGTA GGGCAGGAG TCAGGTCCAT GTGCACTGCA 5160
	ATGCCAGGTG GAGAAATCAT AGAGAGGTAA AATGGAGGCC AGTGCCATT CAGAGGGGAG 5220
	GCTCAGGAAG GCTTCTTGTCT TACAGGAATG AAGGCTGGGG GCATTTTGCT GGGGGAGAT 5280
50	GAGGACGCT CTGGAATGCG TCAGGGATTG AGCCCTCCCT GCGCTGCTCT GCTGAAGCTG 5340
	GTGACTACGG GTTCGCCCTT TGCTCACGTC TCTCTGGCCC ACTCATGATG GAGAAGTGTG 5400
	GTGAGAGGGG AGCAATGGGC TTTGCTGCTT ATGAGCACAG AGGAATTGAG TCCCCAGGCA 5460
	GCCCTGCTCT TGACTCCAAG AGGTGAAGT CCACAGAGT GAGCTCTGCT CTTAGGGCTC 5520
	CATTGCTCT TCATCCAGGG AACTGAGCAC AGGGGGCCTC CAGGAGACCC TAGATGTGCT 5580
55	CGTACTCCCT CGGCTGGGA TTTCAGAGCT GGAATATAG AATATATCTA GCCCAAGGCC 5640
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	GAGGGCTTGG GAGGCCCCAC CCTAGCCCTT GCTGCCACAC CACATTGCTT CAACAACCGG 5760
	CCCAGAGTG CCCAGGCATC CCTGAGGTAG CTCTTGGAAA TGGGGACAAG TCCCTCGAA 5820
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60	GCACACAAAC CCGCCCTCCC CTGTGTGTG GGGGTCCCTC TGGCCTTCA TTTGTTCAT 5940
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	TCCTGTCTCT GCAGCTCTAC AGGTGAGGCC CAGCAGAGG AGTAGGGCTC GCCATGTTTC 6060
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65	GCTCCTGTA GAGGGAGAAC TCTATCTGTG GTTTATAATC TTGACGAGG CACCAGATC 6240
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	CCTTCAAGA GGGCCTGCTT GGCTCCCTCC ACCCACTGC ACCCATGAGA CTGGTCCAA 6360
	GAGTCCATTC CCCAGGTGGG AGCCAACTGT CAGGGAGGTC TTTCCACCA AACATCTTT 6420
	AGCTGCTGGG AGGTGACCAT AGGGCTCTGC TTTTAAAGAT ATGGCTGCTT CAAAGGCCAG 6480
70	AGTCACAGGA AGGACTTCTT CCAGGGAGAT TAGTGGTGAT GGAGAGGAGA GTTAAATGA 6540
	CCTCATGCTC TCTTGTGCA CGGTTTTGTG GAGTTTTCAC TCTTCTAATG CAAGGGTCTC 6600
	ACACTGTGAA CCACTTAGGA TGTGATCACT TTCAGGTGGC CAGGAATGTT GATGTCTTT 6660
	GGCTCAGTTC ATTTAAAAA GATATCTATT TGAAAGTTCT CAGAGTTGTA CATATGTTTC 6720
	ACAGTACAGG ATCTGTACAT AAAAGTTTCT TTCTTAAACC ATTCACCAAG AGCCATATC 6780
75	TAGGCATTTT CTGTGTAGCA CAAATTTTCT TATTGCTTAG AAAATGTGCC TCCTTGTAT 6840
	TTCTGTTTGT AAGACTTAAG TGAGTTAGGT CTTTAAAGAA AGCAAGGCTC CTCTGAAATG 6900
	CTTGTCTTTT TTCTGTGTGC GAAATAGCTG GTCCCTTTTC GGGAGTTAGA TGTATAGAGT 6960
	TTTGTATGAT AAACATTTCT TGTAGGCATC ACCATGAACA AAGATATATT TTCTATTAT 7020
	TATTATATG TGCACTTCAA GAAGTCACTG TCAGAGAAAT AAAGAATTGT CTTAAATGTC

Seq ID NO: 95 Protein sequence

Protein Accession #: XP_051860.2

1	11	21	31	41	51	
MGAAGRQDFL	FKAMLTISWL	TLTCFPGATS	TVAAGCPDQS	PELQPNWPGH	QDHHVHIGQ	60
GKTLTLLTSSA	TVYSIHISEG	GKLVKDHDE	PIVLRTRHIL	IDNGGELHAG	SALCFPGGNF	120

5	TIILYGRADE	GIQPDPPYGL	XYIGVKGKGA	LELEGQKCLS	WFLNKTLEH	GGMAEGGYFF	180
	ERSWGHGVI	VHVIDPKSGT	VIHSDRFDTY	RSKKESERLV	QYLNVPDGR	ILSVAVNDEG	240
	SRNLDDMARK	AMTLGSKHF	LHLGFRHWS	PLTVKGNPS	SVEDHIEYHG	HRGSAARVP	300
	KLFQTEHGBY	FNVLSSSEW	QDVEWTEWFD	HDKVSQTKGG	EKISDLWKAH	PGKICNRPID	360
	IQATTMDGVN	LSTEVVYKGG	QDYRFACYDR	GRACRSYVR	FLCGKPVPRK	LTVTIDTNVN	420
	STILNLEDIV	QSWKPGDTLV	IASDYSMYQ	AEEFQVLPCR	SCAPNQKVA	GKPMYLIHGE	480
	EIDGVDMAE	VGLLSRNITV	MGEMEDKCYF	YRNHCNFFD	FDTFGGHIKF	ALGFKAHLE	540
	GTELKHMGGQ	LVGQYPIHFH	LAGDVDERGG	YDPPTYIRDL	SIHHTPSRCV	TVHGSNGLLI	600
10	KDVVGYNLSG	HCFPTEDGPE	ERNTPDHCLG	LLVKSGLTLP	SDRDSKMKCM	ITEDSYPGYI	660
	PKPRQDCNAV	STFWMANPNN	NLINCAAAGS	ETGTFWFIH	HVPTGFSVGM	YSPGYSEHIP	720
	LGKPYNNRAH	SNYRAGMIID	NGVKTTEASA	KDKRPFLSII	SARYSPHQDA	DPLKPREPAI	780
	IRHFIAIKYKQ	DHGAWLRRGD	VWLDSCRPAD	NGIGLTLASG	GTFPYDDGSK	QEIKNSLFVG	840
	ESGNVGTBM	DNRWGFGLG	DHSGRTLPIG	QNFPIRGIQL	YDGINIQNC	TFRKPVALEG	900
15	RHTSALAPRL	NNAMQSCPHN	NVTGIAFEDV	PITSRVFPGE	PGPWFNQMDM	DGDKTSVFHD	960
	VDGVSVEYPG	SYLTNDNNWL	VRHPCINVP	DWRGAICSGC	YAQMYYIAQY	TSNLRMKIHK	1020
	NDPFSHPLYL	EGALTSTHY	QYQPVVTLQ	KGYTIHWDQ	APAEIAIWL	NFNKGDWIRV	1080
	GLCYPRGTF	SILSDVNRNL	LKQTSKTGVF	VRTLQMDKVE	QSYFGRSHY	WDEDSGLLFL	1140
	KLKAQNEREK	PAPCSMRGCE	RIKIKALIPK	NAGVSDCTAT	AYPKPTEARV	VDVPMPKLKE	1200
20	GSQKTKDHF	LEVMBSSSKQ	HFFHLWMDFA	YIEVDGKYPV	SSEDDIQVWV	IDGNQGRVVS	1260
	HTSFRNSILQ	GIPWQLFNIV	ATIPDNISIVL	MASKGRYVSR	GPWTRVLEKL	GADRGLKLKE	1320
	QMAFVGFKGS	FRPIWTLDT	EDHKAKIPQV	VPFVVKKKK	L		

Seq ID NO: 96 DNA sequence

Nucleic Acid Accession #: NM_020436 and AK001666

Coding sequence: 63-3224

25	1	11	21	31	41	51	
	CAGGAATTG	TGGCGGAGAG	GGCAAATAAC	TGCGGCTCTC	CCGCGCGCCC	GATGCTCGCA	60
30	CCAATGTCAG	GCGCAAGCAG	GCGAAACCCC	AGCACATCAA	CTCGGAGGAG	GACCAAGGCG	120
	AGCAGCAGCC	GCAAGCAGCAG	ACCCCGGAGT	TGCGAGATGC	GGCCCCAGCG	GCGCCCCGCG	180
	CGGGGAGGCT	GGGTGCTCCA	GTGAACCAAC	CAGGGAATGA	CGAGGTGGCG	AGTGAGGATG	240
	AAGCCACAGT	AAAGCGGCTT	CGTCGGGAGG	AGACGCAAGT	CTGTGAGAAA	TGCTGTGCGG	300
	AGTCTTCAG	CATCTCTGAG	TTCTCTGGAAC	ATAAGAAAAA	TTGCACTAAA	AATCCACCTG	360
35	TCCTCATCAT	GAATGACAGC	GAGGGGCGTG	TGCTTCAGAA	AGACTTCTCC	GGAGCTGTAC	420
	TGAGCCACCA	GCCCCACAGT	CCCGGCGAGT	AGGACTGTCA	CAGGAGAAAT	GCGCGCAGCT	480
	CAGAGGACAT	GAGGAGAGAG	CCGGATGCGG	AGTCTGTGGT	GTACCTAAAG	ACAGAGACAG	540
	CCCTGCCACC	CACCCCCCAG	GACATAAGCT	ATTTAGCCAA	AGGCAAGTGG	GCCAACTACT	600
	ATGTGACCTT	GCAGGCACTA	CGGGGACCCA	AGGTGGCGGT	GAATCAGCGG	AGCGCGGATG	660
40	CATCTCCCTG	CCCCGTGCGT	GGTGCCAAAC	GCATCCCGTG	GGTCTCGAG	CAGATCTTGT	720
	GTCTGCAGCA	GCAGCAGTCA	CAGCAGATCC	AGCTCACCGA	GCAGATCCGC	ATCCAGGTGA	780
	ACATGTGGGC	CTCCGAGGCT	CTCCACTCAA	GCGGGGACAG	GGCGGACACT	CTGAAGACCT	840
	TGGGCGACCA	CAGCTCTCAG	CAGGTTTCTG	CAGCTGTGGC	TTTGCTCAGC	CAGAAAGCTG	900
	GAAGCCAAAG	TCTGTCTCTG	GATGCGCTGA	AACAAGCCAA	GCTACCTCAC	GCCAACTATC	960
45	CTTCTGCCAC	CAGCTCCCTG	TCCCAGGGGC	TGGCACCCCT	CACCTGGAAG	CCGGATGGGA	1020
	CCCGGGTGCT	CCCGAAGCTC	ATGTCCCGCC	TCCGAGCGCG	TTTGCTTCTC	CAGGCCCGCG	1080
	GCTCGGTGCT	CTTCCAGAGC	CCCTTCTCCA	CTGTGGCGCT	AGACACATCC	AAGAAAGGGA	1140
	AGGGGAGGCT	ACCGAATATC	TCCCGGCTGG	ATGTCAAACC	CAAGACGAGG	GCGGCCCTCT	1200
50	ACAAGCACAA	GCTTAAGTAC	TGTAGCAAGG	TTTTGGGAC	TGATAGCTCC	TTGCAGATCC	1260
	ACCTCGCTC	CCACACTGGA	GAGAGACCTT	TGCTGTGCTC	TGTCTGTGGT	CATCGCTTCA	1320
	CCACCAAGGG	CAACCTCAG	GTGCACTTTC	ACCGACATCC	CCAGGTGAAG	GCAAAACCCC	1380
	AGCTGTTTGC	CGAGTTCAG	GACAAAGTGG	CGGCCGGCAA	TGGCATCCCC	TATGCACTCT	1440
	CTGTACTGTA	CCCCATAGAT	GAACCGAGTC	TTTCTTTAGA	CAGCAAACTT	GTCTTGTATA	1500
	CCACCTCTGT	AGGCTTACCT	CAGAATCTTT	CTTCGGGGAC	TAATCCCAAG	GACCTCACGG	1560
55	GTGGCTCCTT	GCCCGGTGAC	CTGCAGCCTG	GGCCTTCTCC	AGAAAGTGAG	GGTGGACCCA	1620
	CATCTCCCTG	GGTGGGACCA	AACTATAATT	CCCCAAGGGC	TGGTGGCTTC	CAAGGGAGTG	1680
	GGACCCCTGA	GCCAGGGTCA	GAGACCCCTGA	AATTGCAGCA	GTGTGTGGAG	AACATTGACA	1740
	AGGCCACCA	TGATCCCAAC	GAATGTCTCA	TTTGCCACCG	AGTCTTAAGC	TGTGAGAGCT	1800
	CCCTCAAGAT	GATTATCGC	ACCCACACCG	GGGAGAGACC	GTTCAGATGT	AAGATCTGTG	1860
60	GCGGAGCCTT	TTCTACCAAA	GGTAACCTGA	AGACACACCT	TGGGGTTTCA	GGAACCAACA	1920
	CATCCATTAA	GACGAGCAT	TGCTGCCCCA	TCTGCCAGAA	GAAGTTCACT	AATGCCGTGA	1980
	TGCTGCAGCA	ACATATTCCG	ATGCACATGG	CGCGTCAGAT	TCCCAACACG	CCCCTGCCAG	2040
	AGAATCCCTG	TGACTTTACG	GGTCTTGAGC	CAATGACCGT	GGGTGAGAAC	GGCAGCACCG	2100
	GCGCTATCTG	CCATGATGAT	GTGATCGAAA	GCATOGATGT	AGAGGAAGTC	AGCTCCGAGG	2160
65	AGGCTCCGAG	CAGCTCTCTC	AAGGTCCCCA	CGCCTCTTCC	CAGCATCCAC	TCCGCATCAC	2220
	CCACGCTAGG	GTTTGCCATG	ATGGCTTCTT	TAGATGCCCC	AGGGAAGTGG	GGTCTGCCCC	2280
	CTTTTAACCT	GCAGGCGCAG	GGCAGCAGAG	AAAACGCTTC	CGTGAGAGC	GATGGCTTGA	2340
	CCAACGACTC	ATCCTCGCTG	ATGGGAGACC	AGGAGTATCA	GAGCCGAAGC	CCAGATATCC	2400
70	TGGAACCCAC	ATCCTTCCAG	GCACTCTCCC	CGGCCAATAG	TCAAGCCGAA	AGCATCAAGT	2460
	CAAAAGTCTC	CGATGCTGGG	AGCAAAAGCAG	AGAGCTCCGA	GAACAGCCGC	ACTGAGATGG	2520
	AAGGTGCGAG	CAGTCTCCCT	TCCAGCTTTA	TCCGAGCCCC	GCCGACCTAT	GTCAAGGTTG	2580
	AAGTTCTCTG	CACATTGTGT	GGACCTTCGA	CATTGTCCCC	AGGGATGACC	CCTTTGTATG	2640
	CAGCCGAGCC	ACGCGCAGAG	GCCAAAGCAAC	ATGGCTGCAC	ACGGTGTGGG	AAGAACTTCT	2700
	CGTCTGCTAG	CGCTCTTACG	ATCCAAGAGC	GGACTCACAC	TGGAGAGAAG	CCTTTTGTGT	2760
75	GCAACATTGG	TGGCGAGCT	TTTACCACCA	AAGGCAACTT	AAAGGTTTCA	TACATGACAC	2820
	ACGGGGCGAA	GAACTAATCA	GCCCGCGGTG	GAAGGAAGTT	GGCCATCGAG	AACACCATGG	2880
	CTCTGTAGG	TACGGACGGA	AAAAGAGTCT	CAGAAATCTT	TCCCAAGGAA	ATCTGCGCCC	2940
	CTTCAGTGAA	TGTGGACCTT	GTGTGTGGA	ACCAATACAC	CAGCATGCTC	AATGGCGGTC	3000
	TGGCCGTGAA	GACCAATGAG	ATCTCTGTGA	TCCAGAGTGG	GGGGTTTCTT	ACCTCTCCCG	3060
80	TTTCTTGGG	GGCCACCTCC	GTGTGTGAATA	ACGCCACTGT	CTCCAAGATG	GATGGCTCCC	3120
	AGTCGGGTAT	GAGTCAGAT	GTGGAAGAAC	CAAGTGCTAC	TGAAGCGGTT	CCCAACACCC	3180
	AGTTTCTCTA	CTTCTCGGAA	GAAGAACAGA	TTGCGGTGAG	CTAAGGGAGA	ACTTGGCTGG	3240
	AAGGAGCAAT	GCAGACACAG	TGAATCTCTT	AGAACTCTGT	TTGTTTGTGA	AGAACTCATC	3300
85	TCCTCTGTTT	TTCTTTTCTT	TACTGATATG	CAATGATGTG	TTACTACGTT	GGTGTGTGAC	3360
	ACAACTCTAG	GCAAGTGCTA	CAATCAGGAT	TGTTGCTATG	CTGCTTTGCA	AAAAAGTTG	

Seq ID NO: 97 Protein sequence:
Protein Accession #: NP_065169.1

	1	11	21	31	41	51	
5	MSRRKQAKPQ	HINSEEDQGE	QOPQQQTPEF	ADAAPAAPAA	GELGAPVNH	GNDEVADE	60
	ATVKRLRREE	THVCEKCAE	FFSISEFLEH	KKNCTKNPPV	LIMDSSEGPV	PSDFSGAVL	120
	SHQPTSPGSK	DCHRENGSS	EDMKEKPDAB	SVVYLKTETA	LPPTPDISY	LAKGKIVANTN	180
	VTLQALRGTK	VAVNQRSADA	LPAPVPGANS	IPWVLEQILC	LQQQQLQQIQ	LTBQIRIQVN	240
10	MWASHALHSS	GAGADTLKTL	GSHMSQQVSA	AVALLSQKAG	SQGLSLDALK	QAKLPHANIP	300
	SATSSLSPLG	APPTLKPDGT	RVLNFMVSR	PSALLPQAPG	SVLFQSPFST	VALDTSKGKG	360
	GKPPNISAVD	VKPKDEAALY	KHKCKYCSKV	FGTDSLLQIH	LRSHGTGERPF	VCSVCGHRPT	420
	TKGNLKVHFF	RHPQVKANPQ	LFAEPQDKVA	AGNGIPYALS	VFDPIDEPSL	SLDSKPVIVT	480
	TSVGLPQNL	SGTNPKDLTG	GSLPGDLQPG	PSPSESGGPT	LPGVGPNNYS	PRAGGFQSGG	540
15	TPEPGSETLK	LQQLVENIDK	ATTDPNECLI	CHRVLSQSS	LKMHYRTHGT	ERPFQCKICG	600
	RAFSTKGNLK	THLGVHRTNT	SIXTQHSCPI	QKKFTNAV	LQGHIRMBMG	GQIFNTPLPE	660
	NPCDFTGSEP	MTVGENGSTG	AICHDVIES	IDVEEVSSQE	APSSSKVPT	PLPSIHSASP	720
	TLGFAMMASL	DAPQVGPAP	FNLRQGSRE	NGSVESDGLT	NDSSSLAGDQ	ZYQSRSPDIL	780
	ETTSFQALSP	ANSQAESIKS	KSPDAGSKAE	SENSRSTEME	GRSLPSTFI	RAPPTVVKVE	840
20	VPGTFTVPST	LSPGMTLLA	AQPRRQAKQH	GCTRCGNFS	SASALQIHER	THTGKPFVC	900
	NICGRAPFTK	GNLKVHYMT	GANNNSARRG	RKLAIENTMA	LLGTDGKRVS	EIPFKEILAP	960
	SVNVDPVVWN	QYTMNLNGEL	AVKTNEISVI	QSGGVPTLPV	SLGATSVVNN	ATVKMDGSGQ	1020
	SGISADVEKP	SATDGVPRKHQ	FFHFLKENKI	AVS			

Seq ID NO: 98 DNA sequence
Nucleic Acid Accession #: NM_000612.2
Coding sequence: 553..1095

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30	TTCTCCCGCA	ACCTTCCCTT	CGCTCCCTCC	GGTCCCCCCC	AGCTCCTAGC	CTCCGACTCC	60
	CTCCCCCTCT	CAGCGCCGCG	CTCTCGCCTT	GGCCGAACCA	AAGTGGATTA	ATTACACGCT	120
	TTCTGTTTCT	CTCTGCTGCT	TTCTCTCCCG	CTGTGCGCCT	GCCCGCTCTC	CGCTGCTCTC	180
	TCTCCCCCTC	GCCCTCTCTT	CGGCCCCCCC	CTTTCACGTT	CACCTGTGCT	CTCCCACTAT	240
	CTCTGCCCCC	CTCTATCCTT	GATACACAG	CTGACCTCAT	TTCCCGATAC	CTTTTCCCCC	300
35	CCGAAAAGTA	CAACATCTGG	CCCGCCCCAG	CCCGAAGACA	GCCCGTCTCT	CCTGGACAAT	360
	CAGACGAATT	CTCCCCCTCC	CCCCAAAAAA	AAAAGCCATC	CCCCCGCTCT	GCCCGTCCG	420
	ACATTGCGCC	CCCGCGACTC	GGCCAGAGCG	GCGCTGGCAG	AGGAGTGTCC	GCGAGGAGGG	480
	CCAACGCCCG	CTGTTGGGTT	TGCGACACGC	AGCAGGGAGG	TGGGCGGCAG	GGTCCCGGCG	540
	TTCCAGACAC	CAATGGGAAT	CCCAATGGGG	AAGTCGATGC	TGGTGCTTCT	CACCTTCTTG	600
40	GCCTTGGCCT	CGTCTGCTAT	TGCTGCTTAC	CGCCCCAGTG	AGACCTGTGT	CGGCGGGGAG	660
	CTGGTGAGCA	CCCTCCAGTT	CGTCTGTGGG	GACCGCGGCT	TCTACTTCAG	CAGGCGCGCA	720
	AGCCGTGTGA	GCGGTGCGAG	CCGTGCGATC	GTTGAGGAGT	GCTGTTTCCG	CAGCTGTGAC	780
	CTGGCCCTCC	TGGAGACGTA	CTGTGCTACC	CCGCCCAAGT	CCGAGAGGGA	CGTGTGACCC	840
45	CCTCGACGAC	TGCTTCCGGA	CAACTTCCCC	AGATACCCCG	TGGCCTCAAT	CTTCCAATAT	900
	GACACCTGGA	AGCAGTCCAC	CCAGCGCCTG	CGCAGGGGCC	TGCCTGCCCT	CCTGCGTGCC	960
	CGCCCGGGTG	ACGTGCTCGC	CAAGGAGCTC	GAGGCGTTCA	GGGAGGCGCA	ACGCTACCGT	1020
	CCCTGATTGC	CTCTACCCAC	CCAGACCCCG	GCCCAAGGGG	GCGCCCCCCC	AGAGATGGCG	1080
	AGCAATCGGA	AGTGAGCAAA	ACTGCGCGAA	GCTGTCAGCC	CGGCGCCACC	ATCCTGCAGC	1140
	CTCCTCTGGA	CCACGGAAGT	TTCCATCAGG	TTCCATCCCG	AAATCTCTCT	GGTTCGACGT	1200
50	CCCTCGGGGG	CTTCTCCTGA	CCAGTCCCGC	GTGCCCCGCC	TCCCCGAAAC	AGGCTACTCT	1260
	CCTCGGCCCC	CTCATCGGG	CTGAGGAAGC	ACAGCAGCAT	CTTCAACAT	GTACAAAATC	1320
	GATTGGCTTT	AAACACCTTT	CACATACCTT	CCCCC			

Seq ID NO: 99 Protein sequence
Protein Accession #: NP_000603.1

	1	11	21	31	41	51	
55	MGIPMGKSM	VLLTFLAPAS	CCIAAYRPS	TLGGELVDT	LQFVCGDRGF	YFSRPASRVS	60
	RRSRGIVEBC	RTVCDLALL	ETVCATPAKS	ERDVSTPPTV	LPDNFPRYPV	GKFFQYDTWK	120
60	QSTQRLRRGL	PALLRARRGH	VLAKELEAPR	BAKRHRPLIA	LPTQDPAHGG	APPEMASNRK	

Seq ID NO: 100 DNA sequence
Nucleic Acid Accession #: NM_004217.1
Coding sequence: 58..1092

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65	GGCCGGGAGA	GTAGCAGTGC	CTTGGACCCC	AGCTCTCCTC	CCCCCTTCTC	TCTAAGGATG	60
	GCCCGAAGG	AGAACTCTTA	CCCTGGGCCC	TACGGCCGAC	AGACGGCTCC	ATCTGGCCTG	120
	AGCACCTCTG	CCGACGAGT	CTCCGGGAAA	GAGCCTGTCA	CCCCATCTGC	ACTTGTCTCT	180
70	ATGAGCCGCT	CCAATGTCCA	GCCACAGCT	GCCCTGGGCC	AGAAGGTGAT	GGAGATATGC	240
	AGTGGGACAC	CGACATCTT	AACGCGGCAC	TTCACAATTG	ATGACTTTGA	GATTGGGCGT	300
	CCTCTGGGCA	AAGGCAAGTT	TGGAAACGTG	TACTTGGCTC	GGGAGAAGAA	AAGCCATTTC	360
	ATCGTGGCGC	TCAAGTCTCT	CTTCAAGTCC	CAGATAGAGA	AGGAGGGCGT	GGAGCATCAG	420
	CTGCGCAGAG	AGATCGAAAT	CCAGGCCAC	CTGCACCATC	CCAACATCCT	GCGTCTCTAC	480
75	AACTATTTT	ATGACCGGAG	GAGGATCTAC	TTGATTCTAG	AGTATGCCCC	CGCGGGGAG	540
	CTCTACAAGG	AGCTGCAGAA	GAGCTGCACA	TTTGAAGAGC	AGCGAACAGC	CACGATCATG	600
	GAGGAGTTGG	CAGATGCTCT	AATGTACTGC	CATGGGAAGA	AGGTGATTCA	CAGAGACATA	660
	AAGCCAGAAA	ATCTGCTCTT	AGGGCTCAAG	GGAGAGCTGA	AGATTGCTGA	CTTCGGCTGG	720
	TCTGTGATG	CGCCCTCCCT	GAGGAGGAAG	ACAATGTGTG	GCACCTGGA	CTACCTGCC	780
80	CCAGAGATGA	TGAGGGGGCG	CATGCACAA	GAGAAGGTGG	ATCTGTGGTG	CATTGGAGTG	840
	CTTTGCTATG	AGCTGCTGTG	GGGGAACCCA	CCCTTTGAGA	GTGCATCACA	CAACGAGACC	900
	TATCGCCGCA	TGCTCAAGT	GGACCTAAAG	TTCCCGCTT	CTGTGCCAC	GGGAGCCAG	960
	GACCTCATCT	CCAAATGCTG	CAGGCATAAC	CCCTCGGAAC	GGCTGCCCT	GGCCAGGTC	1020
	TCAGCCCAAC	CTTGGGTCCG	GGCCAACTCT	CGGAGGGTGC	TGCTCCCTC	TGCCCTTCAA	1080
85	TCTGTGCGCT	GATGGTCCCT	GTCATTCACT	CGGGTGGGTG	TGTTTGTATG	TCTGTGTATG	1140
	TATAGGGGAA	AGAAGGATC	CCTAATCTTT	CCCTTATCTG	TTTTCTACCT	CCTCCTTTGT	1200

TTAATAAAGG CTGAAGCTTT TTGT

Seq ID NO: 101 Protein sequence
Protein Accession #: NP_004208

1	11	21	31	41	51	
MAQKENSYPW	PYGRQTAPSG	LSTLPQRVLR	KEPVTPLSALV	LMSRSNVQPT	AAPGQKVMEN	60
SSGTPDILTR	HFTIDDFEIG	RPLGKGFKN	VYLAREKKSH	FIVALKVLFK	SQIEKEGVEH	120
QLRREIEIQA	HLHHPNILLR	YNYFYDRRRI	YLILEYAPRG	ELYKELQKSC	TFDEQRTATI	180
MEELADALMY	CHGKQVIHRD	IKPENLLGL	KGELKIADFG	WSVHAPSLRR	KIMCGTLDYL	240
PPMIBORMH	NEKVDLMCIQ	VLCEYLLVGN	PPFESASHNE	TYRRIVKVDL	KFPASVPTGA	300
QDLISKLLRH	NPSERLPLAQ	VSAHPWVRAN	SRRLVPPSAL	QSWA		

Seq ID NO: 102 DNA sequence
Nucleic Acid Accession #: AK025790
Coding sequence: 56..1642

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AGTATCCCAG	GAGGAGCAAG	TGGCAOGTCT	TCGGACCTAG	GCTGCCCTCG	CCGTCAATGTC	60
GCAAGGGATC	CTTTCTCCGC	CAGCGGGCTT	GCTGTCCGAT	GACGATGTGG	TAGTTTCTCC	120
CATGTTTGAG	TCACACAGCTG	CAGATTGGGG	GTCTGTGGTA	CGCAAGAAC	TGCTATCAGA	180
CTGCTCTGTC	GTCTCTACCT	CCCTAGAGGA	CAAGCAGCAG	GTTCCATCTG	AGGACAGTAT	240
GGAGAAGGTT	AAAGTATACT	TGAGGGTTAG	GCCTCTGTGA	CCTTCAGAGT	TGGAACGACA	300
GGAAAGATCAG	GGTTGTGTCC	GTATTGAGAA	TGTGGAGACC	CTTGTTCTAC	AAGCACCCAA	360
GGACTCTTTT	GCCTGAGAGA	GCAATGAACG	GGGAATTGGC	CAAGCCACAC	ACAGGTTTAC	420
CTTTTCCAG	ATCTTTGGGC	CAGAAGTGGG	ACAGGCATCC	TTCTTCAACC	TAAGTGTGAA	480
GGAGATGGTA	AAGGATGTAC	TCAAAGGGCA	GAAGTGGCTC	ATCTATACAT	ATGGAGTCAC	540
TAAGTCAGGG	AAAGCCCAACA	CGATTCAAGG	TACCATCAAG	GATGGAGGGA	TTCTCCCCCG	600
GTCCCTGGCG	CTGATCTTCA	ATAGCCTCCA	AGGCCAACTT	CATCCAAAC	CTGATCTGAA	660
GCCTCTGTCT	TCCAATGAGG	TAATCTGGCT	AGACGACAG	CAGATCCGAC	AGGAGGAAAT	720
GAAGAAGCTG	TCCTGTCTAA	ATGGAGGCTT	CCAAGAGGAG	GAGCTGTCCA	CTTCTTTGAA	780
GAGGAGTGTC	TACATCGAAA	GTCCGATAGG	TACCAGCAC	AGCTTCGACA	GTGGCATTGC	840
TGGGCTCTCT	TCATCAGTTC	AGTGTACGAG	CAGTAGCCAG	CTGGATGAAA	CAAGTCATCG	900
ATGGGACACG	CCAGACACTG	CCCCACTACC	TGTCCCGGCA	AACATTCTCG	TCTCCATCTG	960
GATCTCATT	TTTGAGATCT	ACAACGAACT	GCTTTATGAC	CTATTAGAAC	CGCTTAGCCA	1020
ACAGGCGAAG	AGGCGAGACT	TGCGGCTATG	CGAGGATCAA	AATGGCAATC	CCTATGTGAA	1080
AGATCTCAAC	TGGATTCTAT	TGCAAGATGC	TGAGGAGGCC	TGGAAGCTCC	TAAAGTGGG	1140
TGTAAGAAC	CAGAGCTTTG	CCAGCACCCA	CCTCAACCA	AATCCAGCC	GCAGTCACAG	1200
CATCTTTCA	ATCAGGATCT	TACACCTTCA	GGGGGAAGGA	GATATAGTCC	CCAAGATCAG	1260
CGAGCTGTCA	CTCTGTGATC	TGGCTGGCTC	AGAGCGCTGC	AAAGATCAGA	AGAGTGGTGA	1320
AOGGTTGAAG	GAAGCAGGAA	ACATTAACAC	CTCTCTACAC	ACCCGCGGCC	GCTGTATTGC	1380
TGCGCTCTGT	CAAAACGAGC	AGAACCGGTC	AAAGCAGAAC	CTGGTCCCTC	TCCGTGACAG	1440
CAAGTTGACT	CGAGTGTTC	AAGGTTTCTT	CACAGGCCGA	GGCCGTTCTC	GCATGATTGT	1500
CAATGTGAAT	CCCTGTGCAT	CTACCTATGA	TGAAACTCTT	CATGTGGCCA	AGTTCTCAGC	1560
CATTGCTAGC	CAGGTGACTT	GTGCGATGCC	CACCTATGCA	ACTGGGATTC	CCATCCCTGC	1620
ACTCGTTTCA	CAAGGAACAT	AGTCTTCAGG	TATCCGCCAG	CTTAGAGAAA	GGGGCTAAGG	1680
CAGACACAGG	CCTTGATGAT	GATATTGAAA	ATGAAGCTGA	CATCTCCATG	TATGGCAAA	1740
AGGAGCTCT	ACAAGTTGTG	GAAGCCATGA	AGACACTGCT	TTTGAGGAAA	CGACAGGAAA	1800
AGCTACAGCT	GGAGATGATC	CTCCGAGATG	AAATTGCAA	TGAGATGGTA	GAACAGATGC	1860
AACAGCGGGA	ACAGTGGTGC	AGTGAACATT	TGGACACCCA	AAAGGAACCTA	TTGGAGGAAA	1920
TGTATGAAGA	AAAACCTAAAT	ATCCTCAAGG	AGTCACTGAC	AAGTTTTTAC	CAAGAAGAGA	1980
TTCAAGGAGG	GGATGAAAG	ATTGAAGAGC	TAGAAGCTCT	CTTGCCAGAA	GCCAGACAAC	2040
AGTCAGTGGC	CCATCAGCAA	TCAGGGTCTG	AATTGGCCCT	ACGGCGGTCA	CAAAGGTGG	2100
CAGCTTCTGC	CTCCACCCAG	CAGCTTCAGG	AGGTTAAAGC	TAAATTACAG	CAGTGCAAG	2160
CAGAGCTAAA	CTCTACCACT	GAAGAGTTGC	ATAAGTATCA	GAAATGTGTA	GAACCAACAC	2220
CCTCAGCCAA	GCCTTTTACC	ATTGATGTGG	ACAAGAAGTT	AGAAGAGGGC	CAGAAGAATA	2280
TAAGGCTGTT	GGGACAGAG	CTTCAGAAAC	TTGGTGAATC	TCTCCAATCA	GCAGAGAGAG	2340
CTTGTTCGCA	CAGCACTGGG	GCAGGAAAC	TTGCTCAAGC	CTTGACCACT	TGTGATGACA	2400
TCTTAATCAA	ACAGGACGAG	ACTCTGGCTG	AACTGCAGAA	CAACATGGTG	CTAGTGAAAC	2460
TGGAGCTTGG	GAAGAAGGCA	GCATGTATTG	CTGAGCAGTA	TCATCTGTG	TTGAACTTCC	2520
AAGGCCAGGT	TTCTGCCAAA	AAGCGCCTTG	GTACCAACCA	GGAAATCAG	CAACCAACCC	2580
AACAACCAAC	AGGGAAGAAA	CCATTCCCTT	GAAATTTACT	TCCCGGAACA	CCAACTGTCC	2640
AAAGCTCAAC	AGACTGCAGC	CCTTATGCCC	GGATCCTACG	CTCAGCGCGT	TCCCTTTTAC	2700
TCAAATCTGG	GCCTTTTGGC	AAAAAGTACT	AAGGCTGTGG	GGAAAGAGAA	GAGCAGTCAT	2760
GGCCCTGAGG	TGGGTGAGCT	ACTCTCCTGA	AGAAATAGGT	CTCTTTTATG	CTTTACCATTA	2820
TATCAGGAAT	TATATCCAGT	ATGCAATACT	CAGACACTAG	CTTTTTTCTC	ACTTTTGTAT	2880
TATAACCAAC	TATGTAACT	CATGTTGTTG	TTTTTTTTTA	TTTACTTATA	TGATTCTTAT	2940
GCACACAAA	ACAGTTATAT	TAAAGATATT	ATTGTTTACA	TTTTTTTATG	AATTCCTAAAT	3000
GTAGCAAAAT	CATTAAACAA	AATTATAAAA	GGGACAGAAA	AA		

Seq ID NO: 103 Protein sequence
Protein Accession #: NP_005724.1

1	11	21	31	41	51	
MSQGLSPPA	GLLSDDVVV	SPMFESTAAD	LGSVVRKNLL	SDCSVSTSL	EDKQQVPS	60
SMEKVYVYLR	VRPLLPSELE	ROEDQGCVR	ENVETLVLA	PKDSFALKSN	ERGIGQATH	120
PTFSQIFGPE	VQASFPNLT	VKEMVDVLK	QGNWLIYTYG	VNSGKTETI	QGTIKDGIL	180
PRSLALIFNS	LQGLHPTPD	LKPLLSNEVI	WLDKQIRQE	EMKLSLLNG	GLQEEELST	240
LKRSVYIESR	IGTSTSPDSG	IAGLSSISQC	TSSSQLDETS	HRMAQPDTP	LPVPANIRPS	300
IWISFFETYN	ELLYDLLEPP	SQQRKRQTLR	LCEDQNGNPF	VKDLNWIHQV	DAEEAWKLLK	360
VGRKNQSFAS	THLNQNSRS	HSIFSIIRILH	LQGEDIVPEK	ISELSLCLDLA	GSEKCKDOKS	420
GERLKEAGNI	NTSLHTLGR	IAALRQNQON	RSKQNLVPPR	DSKLTRVFCQ	FFTGRGRSCH	480
IVNVNPCAAT	YDETLHVAKP	SALASQVICA	CPTYATGPIPI	PALVEQGT		

Seq ID NO: 104 DNA sequence

Nucleic Acid Accession #: NM_006952.1

Coding sequence: 11..793

	1	11	21	31	41	51	
5	AATCCCGACA	ATGGCGAAG	ACAACCTCAAC	TGTTCCGTTGC	TTCCAGGGCC	TGCTGATTTT	60
	TGGAATATGT	ATTATTGGT	GTTGCGGCAT	TGCCCTGACT	GCGGAGTGCA	TCTTCCTTGT	120
	ATCTGACCAA	CACAGCCTCT	ACCCACTGCT	TGAAGCCACC	GACAAACGATG	ACATCTATGG	180
	GGCTGCCTGG	ATCGGCATAT	TTGTGGGCAT	CTGCCTCTTC	TGCCTGTCTG	TTCTAGGCAT	240
10	TGTAGGCATC	ATGAAGTCCA	GCAGGAAAT	TCCTCTGGCG	TATTTTCATT	TGATGTTTAT	300
	AGTATATGCC	TTTGAAGTGG	CATCTTGAT	CACAGCAGCA	ACACAAACGAG	ACTTTTTCAC	360
	ACCCAACTTC	TTCTGAAGC	AGATGCTAGA	GAGGTACCAA	AACAAACGCC	CTCCAACCAA	420
	TGATGACCAG	TGGAATAACA	ATGGAGTCAC	CAAAACCTGG	GACAGGCTCA	TGCTCCAGGA	480
	CAATTGCTGT	GGCTAAATG	GTCCATCAGA	CTGGCAAAAA	TACACATCTG	CCTTCCGGAC	540
	TGAGAAATAT	GATGCTGACT	ATCCCTGGCC	TGCTCAATGC	TGTGTTATGA	ACAATCTTAA	600
15	AGAACCTCTC	AACCTGGAGG	CTTGTAACCT	AGGCGTGCC	GGTTTTTATC	ACAATCAGGG	660
	CTGCTATGAA	CTGATCTCTG	GTCCAATGAA	CCGACACGCC	TGGGGGGTTG	CCTGGTTTGG	720
	ATTTGCCATT	CTCTGCTGGA	CTTTTGGGT	TCTCTGGGT	ACCATGTTCT	ACTGGAGCAG	780
	AATTGAATAT	TAAGAA					

Seq ID NO: 105 Protein sequence

Protein Accession #: NP_008883.1

	1	11	21	31	41	51	
25	MAKDNSTVRC	FQGLLIFGNV	IIGCGIALT	RECIFVSDQ	HSLYPLEAT	DNDDIYGAAW	60
	IGIFVIGICLF	CLSVLIGIVGI	MKSSRKILLA	YFILMPFIVA	FEVASCITAA	TQRDFPTPNL	120
	FLKQMLERIQ	MNSPPNNDQ	WKNNGVTKW	DRMLQDNCC	GVNGPSDWQK	YTSAFRTENN	180
	DADYFWPRQC	CVMNKLKEPL	NLEACKLGVP	GFYHNQCYE	LISGPMNRHA	WGVAVFGPAI	240
	LCWTFWVLLG	TMFYWSRIEY					

Seq ID NO: 106 DNA sequence

Nucleic Acid Accession #: NM_002740.1

Coding sequence: 178..1968

	1	11	21	31	41	51	
35	CCGCGGTTCC	GGCTGCTCCG	GCGAGGCGAC	CCTTGGGTCC	GCGCTGCGGG	CGAGGTGGGC	60
	AGGTAGGTGG	GCGGAGCGCC	GCGGTTCTCC	GGCAAGCGCA	GGCGGCGGAG	TCCCCACCGG	120
	CGCCCGAAGC	GCCCCCGCGA	CCCCCGGCTT	CCAGCGTTGA	GGCGGGGCGG	TGAGGAGATG	180
	CCGACCCAGA	GGGACACGAG	CACCATGTCC	CACACGCTCG	CAGGCGGCGG	CAGCGGGGAC	240
40	CATTCCCACC	AGGTCCCGGT	GAAAGCCTAC	TACCGCGGGG	ATATCATGAT	AACACATTTT	300
	GAACTTCCA	TCTCCTTTGA	GGGCTTTTGC	AATGAGGTTT	GAGACATGTG	TTCTTTTGAC	360
	AACGAACAGC	TCCTTCAACAT	GAAATGGATA	GATGAGGAAG	GAGACCCGTG	TACAGTATCA	420
	TCTCAGTTGG	AGTTAGAAGA	AGCCTTTAGA	CTTTATGAGC	TAAACAAGGA	TTCTGAACCT	480
	TTGATTCACT	TGTTCCCTTG	TGTACCAGAA	CGTCTGGGA	TGCTTGTCTC	AGGAGAGAT	540
45	AAATCCATCT	ACCGTAGAGG	TGCACGCGCG	TGGAGAAAGC	TTTATTGTGC	CAATGGCCAC	600
	ACTTTTCAAG	CCAGCGGTTT	CAACAGGCGT	GCTCACTGTG	CCATCTGCAC	AGACCGAATA	660
	TGGGCACTTG	GACGCCAAGG	ATATAAGTGC	ATCAACTGCA	AACCTCTGGT	TCATAAGAAG	720
	TGCCATAAAC	TGCTCACAAT	TGAATGTGGG	CGGCATTCTT	TGCCACAGGA	ACCAAGTATG	780
	CCCATGGATC	AGTCATCCAT	GCATTCTGAC	CATGCACAGA	CAGTAATTCC	ATATAATCCT	840
50	TCAAGTCATG	AGAGTTTGGG	TCAAGTTGGT	GAAGAAAAAG	AGGCAATGAA	CACCAAGGAA	900
	AGTGGCAAG	CTTCATCCAG	TCTAGGTCTT	CAGGATTTTG	ATTGTCTCGG	GGTAATAGGA	960
	AGAGGAAGTT	ATGCCAAAGT	ACTGTTGGTT	CGATTAAAAA	AAACAGATCG	TATTATAGCA	1020
	ATGAAGATTG	TGAAAAAAGA	GCTTGTTAAT	GATGATGAGG	ATATTGATTG	GGTACAGACA	1080
	GAGAAGCATG	TGTTTGAGCA	GGCATCCAAT	CATCCTTTCC	TTGTTGGGCT	GCATTCTTGC	1140
55	TTTCAGACAG	AAAGCAGATT	GTTCTTTGTT	ATAGAGTATG	TAAATGGAGG	AGACCTAATG	1200
	TTTCATATGC	AGCGACAAGG	AAAACCTCCT	GAAGAACATG	CCAGATTTTA	CTCTGCAGAA	1260
	ATCAGTCTAG	CATTAAATTA	TCCTCATGAG	CGAGGGATAA	TTTATAGAGA	TTTGAAGCTG	1320
	GACAAATGAT	TACTGGACTC	TGAAGGCCAC	ATTAACCTCA	CTGACTACGG	CATGTGTAAG	1380
	GAAGGATTAC	GGCCAGGAGA	TACAACCAGC	ACTTTCTGTG	GTACTCCTAA	TTACATTGCT	1440
60	CCTGAAATTT	TAAGAGGAGA	AGATTATGGT	TTCAGTGTG	ACTGGTGGGC	TCTTGGAGTG	1500
	CTCATGTTTG	AGATGATGGC	AGGAAGGTCT	CCATTGATA	TTGTTGGGAG	CTCGATAAC	1560
	CCTGACCAGA	ACACAGAGGA	TTATCTCTTC	CAAGTTATTT	TGGAAAAACA	AATTGCGATA	1620
	CCAGTCTCTC	TGCTCTGAAA	AGCTGCAAGT	GTTCTGAAGA	GTTTCTTAA	TAAGGACCCCT	1680
	AAGGAACGAT	TGGGTTGTCA	TCCTCAAACA	GGATTGTGCT	ATATTGAGG	ACACCGGTTT	1740
65	TTCCGAAATG	TTGATTGGGA	TATGATGGAG	CAAAAACAGG	TGGTAACCTCC	CTTTAAACCA	1800
	AATATTTCTG	GGGAATTTGG	TTTGGACAAC	TTTGATTCTC	AGTTTACTAA	TGAACCTGTC	1860
	CAGCTCACTC	CAGATGACGA	TGACATTGTG	AGGAAGATTG	ATCAGTCTGA	ATTTGAAGGT	1920
	TTTGAGTATA	TCAATCCTCT	TTTGATGCTC	GCAGAGAAGT	GTGCTGATC	CTCATTTTTC	1980
	AACCATGTAT	TCTACTCATG	TTGCCATTTA	ATGCATGGAT	AACTTGTGCT	CAAGCCTGGA	2040
70	TACAATTAAC	CATTTTATAT	TTGCCACCTA	CAAAAAACA	CCCAATATCT	TCTCTGTAG	2100
	ACTATATGAA	TCAATTATTA	CATCTGTTTT	ACTATGAAAA	AAAAATTAAT	ACTACTAGCT	2160
	TCCAGACAAT	CATGTCAAAA	TTTAGTTGAA	CTGGTTTTTC	AGTTTTTAAA	AGGCCTACAG	2220
	ATGAGTAATG	AAGTTACCTT	TTTTGTTTAA	AAAAAAAAAA	G		

Seq ID NO: 107 Protein sequence

Protein Accession #: NP_002731.1

	1	11	21	31	41	51	
75	MSHTVAGGGS	GDHSQVRVK	AYYRGDIMIT	HFEPSSISFEG	LCNEVRDMCS	FDNRQLFTMK	60
80	WDEEGDPCT	VSSQLELEEA	PRLYELNKDS	ELLIHVFPV	PERPGMPCPQ	EDKSIYRGA	120
	RRWRKLYCAN	GHTPQAKRPN	RRARCAICTD	RIWGLGRQGY	KCINCKLLVH	KKCHKLVTTIE	180
	CGRHSLPQEP	VMPMDQSSMH	SDHAQTVIPY	NPSSHESLDQ	VGEERKAMMT	RESGRASSSL	240
	GLQDFDLRLV	IGRSYAKVL	LVRLKKTDR	YAMRVVKKEL	VNDDDEDWV	QTEKHVFEEQA	300
	SNRPFVLVGL	SCFQTESRLP	FVIEYVNGGD	LMFEMQRQRK	LPEEHARFYS	AEISLALNVL	360
85	HERGIIYRDL	KLDNVLLDSE	GHIKLTIDYGM	CKEGLRPGDT	TSTFCGTFNY	IAPFELRGED	420
	YGPSVDNWAL	GVLMEFMAG	RSPEDIVGSS	DNPDQNTEDY	LFPVILEKQI	RIPRSLSVKA	480

ASVLKSFLLNK DPKERLGGCHP QTGFADIQGH PFFRNVWDWM MEQKQVVPFF KPNISGEFGL 540
DNFDSQFTNE EVQLTDDDD IVRKIDQSEF EGPEYINPLL MSARECV

Seq ID NO: 108 DNA sequence
Nucleic Acid Accession #: NM_000349.1
Coding sequence: 127..984

1 11 21 31 41 51
| | | | |
10 GGGACTCAGA GGGGAAGCTT GAGGGGCTCA GGAAGGACGA AGAACCACCC TTGAGAGAAG 60
AGGCAGCAGC AGCGGGCGCA GCAGCAGCGG CAGCGACCCC ACCACTGCCA CATTTGCCAG 120
GAAACAATGC TGCTAGCGAC ATTCAAGCTG TGCGCTGGGA GCTCCTACAG ACACATGCCG 180
AACATGAAGG GGCTGAGGCA ACAGGCTGTG ATGGCCATCA GCCAGGAGCT GAACCGGAGG 240
GCCCTGGGGG GCCCACCCCC TAGCACGTGG ATTAACCAGG TTCGGCGCGG GAGCTCTCTA 300
15 CTCGGTTCTC GGCTGGAAGA GACTCTCTAC AGTGACCAGG AGCTGGCCTA TCTCCAGCAG 360
GGGGAGGAGG CCATGCAGAA GGCTTGGGTC ATCCTTAGCA ACCAAGAGGG CTGGAAGAAG 420
GAGAGTACAG AGGACAAATGG GGACAAAGTG ATGAGTAAAG TGGTCCCAAG TGTGGGCAAG 480
GTGTTCCGGC TGGAGGTGCT GGTGGACCAAG CCCATGGAGA GGCTCTATGA AGAGCTCGTG 540
GAGCGCATGG AAGCAATGGG GGAGTGGAAAC CCCAATGTCA AGGAGATCAA GGTCTGCGAG 600
20 AAGATCGGAA AAGATACATT CATTACTCAC GAGCTGGCTG CCGAGGCAGC AGGAAACCTG 660
GTGGGGCCCC GTGACTTTGT GAGCGTGGCG TGTGCCAAGC GCCGAGGCTC CACCTGTGTG 720
CTGGCTGGCA TGGACACAGA CTTCGGGAAC ATGCTTGAGC AGAAGGGTGT CATCAGGGCG 780
GAGCAGGGTC CCACTTGCAT GGTGCTTAC CGTGTGGCTG GAAGTCCCTC TAAGACCAAA 840
CTTACGTGGC TACTCAGCAT GACCTCAAG GGGTGGCTGC CCAAGAGCAT CATCAACCAG 900
25 GTCTGTGCCC AGACCCAGGT GGATTTTGGC AACCACTGCG GCAAGCGCCT GGAGTCCAC 960
CCTGCTCTG AAGCCAGGTG TTGAAGACCA GCCTGTCTGT CCCAAGCTGT CCCAGCTGCA 1020
CTGGTACACA CGCTCATCAG GAGAAATCCCT ACTGGAAGCC TGCAAGTCTA AGATCTCCAT 1080
CTGGTACAGG TGGGATGGGT GGGGTTCTGT TTTAGAGTAT GACACTAGGA TTCAGATTGG 1140
30 TGAAGTTTTT AGTACAAGA AAGCAGGAT GAGGCTCTTG GATTAAAGG TAACCTCATT 1200
CACTGATTAG CTATGACATG AGGTTTCAGG CCCCTAAAT AATTGTAAAA CTTTTTTTCT 1260
GGGCCCTTAT GTACCCACCT AAAACCATCT TAAATGTCT AGTGGCTGAT ATGGGTGTGG 1320
GGGATGCTAA CCACAGGGCC TGAGAAGTCT TGCTTTATGG GCTCAAGAAAT GCCATGCGCT 1380
GGCAGTACAT GTGCACAAAG CAGAACTCTA GAGGCTCTCC TGCAGCCCTC TGCTCTCTCC 1440
GGCCGCTGCA CAGCAACAC ACAGAACCAAG CAGCACCCCA CAGTGGGTGC CTTCCAGAAA 1500
35 TATAGTCCAA GCTTTCTCTG TGGAAAAAGA CAAACTCAT TAGTAGACAT GTTCCCTTAT 1560
TGCTTTTATA GGCCACGATC AGAATAAAGA ATCATAATTC ACACC

Seq ID NO: 109 Protein sequence
Protein Accession #: NP_000340.1

1 11 21 31 41 51
| | | | |
40 MLLATPKLCA GSSYRHRNM KGLRQQAUMA ISQELNRRAL GGPTPTSTWV QVRRSSLLG 60
SRLEETLYSD QELAYLQQGE EAMQKALGIL SNQEGWKES QQDNGDKVMS KVPDVGKVF 120
RLEVVVDQPM ERLYEELVER MEAMGEWNPV VKEIKVLQKI GKDTFITHL AAEAAGNLVG 180
45 PRDFVSVRCA RRRGSTCVLA GMDTDFGMP EOKGVIRAEH GFTCHVLHPL AGSPSKTKLT 240
WLLSIDLKGW LPKSIINQVL SQTQVDFANR LRKRLESHA SEARC

Seq ID NO: 110 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 131-682

1 11 21 31 41 51
| | | | |
50 GCTGGGAGCC TGGGCGGGA GCCGGGTGAG GCGCCCGAGA GGCTCGGTGG GCGCGGGCGG 60
CGAGATATGC CACACTCTG CTTGCTGTTG GCAACCTCC TGGACTAGGC TGCTCTTGT 120
55 AATCAGATGG ATGTTATATA AGAGTTCGGA CCGCCAGCA CACAAGTCA GCATGCTGCT 180
CCTCTGTAC GCTCTGCTA TAGCTGTTGT CCAGATCGTT ATCTTCTCAG AAGCTGGGC 240
ATTTCGCAAG AACATCAACT TCTATAATGT GAGGCTCTCT CTGACCCCTA CACCATTTCC 300
AARTAGCTTC AAGTGTCTTA CTGTGAAAA CGCAGGGGAT AATTATACT GCAATCGATG 360
GGCAGAAAGC AATGTTGTG CACAAAATAC ACAGTACTGT TTGACAGTTC ATCACTTAC 420
60 CAGCCACGGA AGAAGCACAT CCATCACCAA AAGTGTGCC TCCAGAAGTG AATGTCATT 480
TGTCGGTGGC CACCACAGCC GAGATTCTGA ACATAAGGAG TGTAGTCTCT GCTGTGAAG 540
AATGATCTGC AATGTAGAAT TACCCACCAA TCACACTAAT GCAGTGTGTT CGTAATGCA 600
CGCTCAGAGA ACATCTGGCA GCAGTGCCCC CACACTCTAC CTACAGTGC TTGCTGGGT 660
CTTTGTGCTT CCATTGCTGT GATGCCACCA TTCCTAGGAG AGGCAGAGAC CAGCCTCTAA 720
65 AGCACAAGCC AAAAAGTGTG TGAACGGTGA ACTTTGGAGT GAAGATCAAT CTTCAGCTG 780
GTGAAGAGTG CACATTGGAC CTCAGGCGA AAGCCAGTGG TTTGCTTGA TAAATGTTT 840
CCGATGAGG CCACAGGACT GAGGATGGGA ATTTGGCAGG GCCTGAGAAG ATGCTGTGAC 900
TTCCAGGCTT CCTGTCAAA GAGAGCTACG TTTGGGCGT TCTGCAGAGA GGATCTGGC 960
AACTAGTCCC ACCTGACTAG GCCTTTAGCT GAAAGGATT CTGACCTCC TTGACTGCT 1020
70 CAGAGGCTGC CAGGTCAAC CCTCTGTTT ATGTGATTAG CTCAGAGCAT CTCTATGAAA 1080
TCTAACCTTT CCCTCATGA GAAAGCAGTT TTCGCCACCA ACAGCATAGT CAATGAGAAA 1140
GGCAACTGTA CGAAGAAAAC TTCCAGTGA ACTAATATGA AATCTATTG CAAATTATGG 1200
GGGGAATATA AGCTTTTAAA TTATACAATG T

Seq ID NO: 111 Protein sequence
Protein Accession #: AAM20908.1

1 11 21 31 41 51
| | | | |
75 MLYKSSDRPA HKVSMILLCH ALAIAVVQIV IPSSEWAPAK NINFYNVRRP LDPTPPFNSF 60
KCPTCENAGD NYNCNRWED KWCPQNTQYC LTVHHFTSHG RSTSIKKKA SRSECHVFC 120
80 HHSRDSSETE CRSCCEGMIC NVELPTNHTN AVFAVMEAR TSGSSAFTLY LPVLAWVFL 180
PLL

Seq ID NO: 112 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 228-884

	1	11	21	31	41	51	
	CGCCGCGCGG	CCCCAGGCGG	GTGCGCTGGG	AGCCTGGGCC	GGGAGCCGGG	TGAGGGCGCC	60
5	GAGAGGCTCG	GTGGGCGCGG	GCGGCGAGGA	CTCTGCTGGA	GCAGGACTTC	AGAGTGTGTTG	120
	TTTTAGCCT	GCTTTTAAAG	TGATTTGAAG	AGAGCGGCTT	TGAAGATATG	CCACACTTCT	180
	GCCTGCTGTT	GGCAACCCCT	CTGGACTAGG	CTGCTCTTGT	TAATCACAATG	GATGTTGCTG	240
	ATTACTCTGA	GTGCAAACTT	TTTCACTGTT	CCAGAGAGGA	GCCTGACAAC	CACATTCTCC	300
	TTCTCAAGGT	GTGGTGCTTA	CTGCGCAGGC	TGACCAAGATA	TAAGAGTTGG	GACCGCCGAG	360
10	CACACAAGGT	CAGCATGCTG	CTCCTCTGTC	ACGCTCTGCG	TATAGCTGTT	GTCCAGATCG	420
	TTATCTTCTC	AGAAAGCTGG	GCATTGCGCA	AGAACATCAA	CTTCTATAAT	GTGAGGCCCTC	480
	CTCTCGACCC	TACACCAATT	CCAAATAGCT	TCAAGTGCTT	TACTTGTGAA	AACGCAAGGG	540
	ATAAATTATA	CTGCAATCGA	TGGGCGAAG	ACAAATGGTG	TCCACAAAT	ACACAGTACT	600
	GTTTGACAGT	TCTTCACTTC	ACCAGCCACG	GAAGAAGCAC	ATCCATCACC	AAAAAGTGTG	660
15	CCTCCAGAG	TGAATGTCAT	TTGTGCGTT	GCCACCACAG	CCGAGATTCT	GAACATACGG	720
	AGTGTAGGTC	TTGCTGTGAA	GGAATGATCT	GCAATGTAGA	ATTACCCACC	AATCACACTA	780
	ATGCACTGTT	TGCCGTAATG	CACGCTCAGA	GAACATCTGG	CAGCAGTGCC	CCCACACTCT	840
	ACCTACCACT	GCTTGCCCTG	GTCTTTGTGC	TTCCATTGCT	GTGATGCCAC	CATTCTTAGG	900
	AGAGGCGAG	ACGAGCCTCT	AAAGCACAAG	CCAAAACTG	TGTGAACGGT	GAACCTTGA	960
20	GTGAAGATCA	ATCTTGCACT	TGGTGAAGAG	TGCACATTGG	ACCTCAAGGC	GAAAGCCAGT	1020
	GGTTTGCTTG	GATAAAATGT	TCCGCGATGA	GGCCACAGGA	CTGAGGATGG	GAATTGCGCA	1080
	GGGCTTGAGA	AGATGCTCTG	ACTTCCAGGC	TTCTTGCTCA	AAGAGAGCTA	CGTTTGGGCA	1140
	GTTCTGCAGA	GAGGATCCTG	GCAACTAGTC	CCACCTGACT	AGGCCTTTAG	CTGAAGAGAT	1200
	TTCTTGACCT	CCTTGACTGC	CTCAGAGGCT	GCCAGGTCAA	ACCTCTTGT	TTATGTGATT	1260
25	AGCTCAGAGC	ATCTCTATGA	AATCTAAGCC	TTCCCTCAT	GAGAAAGCAG	TTTTCCCCAC	1320
	CAACAGCATA	GTCAATGAGA	AAGGCAACTG	TACGAAGAAA	ACTTCCAGTG	GAACATAAT	1380
	GAATCTATT	TGCAAAATT	GGGGGAAAT	AAAGCTTTA	AATTATATA		

Seq ID NO: 113 Protein sequence

Protein Accession #: Eos sequence

	1	11	21	31	41	51	
	MDVADYSECK	PFHCSRREPD	NHILLKVMC	LLRLTRYKS	SDRPAHKVSM	LLCHALAI	60
	VQIVIFSES	WAPAKNINFY	NVRPLDPTP	FNPFKCFPC	ENAGDNYNCR	WAEDKWCPO	120
35	NTQYCLTVHH	FTSHGRSTSI	TKKASRSEC	HFVGCCHSRD	SEHTECRSCC	EGMICNVELP	180
	TNHTNAVFAV	MHAQRTSGSS	APTLYLPVLA	WVFLPL			

Seq ID NO: 114 DNA sequence

Nucleic Acid Accession #: EOS sequence

Coding sequence: 402-1025

	1	11	21	31	41	51	
	ACTTCTGAG	CGGGCTGGC	TGGGTGGGAA	CAGGCTCCTT	GCCGCTCCC	CAGGCTGGC	60
	CACTACCACA	CTGCCGCCCG	CCTGGGCCTC	CTTTCAACCT	CGTGGTGGAG	CCCTGCGGTT	120
45	TCCAGCGGGA	CGCCGGCCCG	GGGCTGCTCC	CTCGCGGGCG	AGGCTCAGCT	GTCCCGGCC	180
	GGCCCTCTCC	CGCGCCCGCG	GTGGTTCAGG	GCAGGGAGGA	GCCGCGCCCG	GCCCGCGCGG	240
	GTAGCAGCCA	AGCGCGCCCG	CAGGCGGGTG	CGCTGGGAGC	CTGGGCGGGG	AGCCCGGTGA	300
	GGGCGCGGAG	AGGCTCGGTT	GGGCGGGGCG	GCGAGATATG	CCACACTTCT	GCCTGCTGTT	360
	GGCAACCTCT	CTGACTAGG	CTGCTCTTGT	TAATCACAATG	GATGTTGCTG	ATTACTCTGA	420
50	GTGCAAACTT	TTTCACTGTT	CCAGAGAGGA	GCCTGACAAC	CACATTCTCC	TTCTCAAGAT	480
	ATAAGAGTTC	GGACCGCCCA	GCACACAAGG	TCAGCATGCT	GCTCCTCTGT	CACGCTCTCG	540
	CTATAGCTGT	TGTCCAGATC	GTTATCTTCT	CAGAAAGCTG	GGCATTGTC	AAGAATATCA	600
	ACTTCTATAA	TGTGAGGCTT	CCTCTGAGCC	CTACACCAAT	TCCAAATAGC	TTCAGTGCT	660
	TTACTTGTGA	AAACGCGAGG	GATAATTATA	ACTGCAATCG	ATGGGCGAGG	GACAAATGGT	720
55	GTCCACAAAA	TACACAGTAC	TGTTTGACAG	TTTCACTTCT	CACAGCCAC	GGAAGAAGCA	780
	CATCCATCAC	CAAAAAGTGT	GCCTCCAGAA	GTGAATGTCA	TTTTGTGCTG	TGCCACCACT	840
	GCGAGATTC	TGAACATACG	GAGTGTAGGT	CTTGTCTGTA	AGGAATGATC	TGCAATGTAG	900
	AATTACCCAC	CAATCAGACT	AATGCAGTGT	TTGCGTAAAT	GCAGCTCAG	AGAATCATCTG	960
	GCAGCAGTGC	CCGCACTCTG	TACCTACCCG	TGCTTGCTGT	GCTCTTTGTT	CTTCCATTGC	1020
60	TGTGATGCCA	CCATTCTCTG	GAGAGGCGAG	GACCAAGCTC	TAAAGCACA	GCCAAAACT	1080
	GTGTGAACGG	TGAACCTTGG	AGTGAAGATC	AATCTTGAC	TTGGTGAAGA	GTGCACTATG	1140
	GACCTCAAGG	CGAAAGCCAG	TGGTTTGCTT	GGATAAAATG	TTCCGCGATG	AGGCCACAGG	1200
	ACTGAGGATG	GGAAATTTGG	AGGGCTGAG	AAGATGGTCT	GACTTCCAGG	CTTCTGCTG	1260
	AAAGAGAGCT	ACGTTTGGGC	AGTTCTGCAG	AGAGGATCCT	GGCACTAGT	CCCACCTGAC	1320
65	TAGGCCTTTA	GCTGAAAGGA	TTTCTTGACC	TCCTTGACTG	CCTCAGAGGC	TGCCAGGTCA	1380
	AACCCCTCTG	TTTATGTGAT	TAGCTCAGAG	CATCTCTATG	AAATCTAACC	CTTCCCTCA	1440
	TGAGAAAGCA	GTTTTCGCCA	CCAACAGCAT	AGTCAATGAG	AAAGGCAACT	GTACGAAGAA	1500
	AACTTCCAGT	GGAATTAATA	TGAAATCTAT	TTGCAAAATTA	TGGGGGGAAT	TAAAGCTTTT	1560
	AAATTATACA	ATGT					

Seq ID NO: 115 Protein sequence

Protein Accession #: EOS sequence

	1	11	21	31	41	51	
	MLLITLSANL	FTVPERSLTT	TPSPSRYSKS	DRPAHKVSM	LLCHALAI	VQIVIFSES	60
75	AFAPKINIFYN	VRPLDPTTP	FNPFKCFPC	NAGDNYNCR	WAEDKWCPO	TQYCLTVHH	120
	TSHGRSTSI	KKKASRSECH	FVGCCHSRDS	ERTECRSCCE	GMIQVELPT	NHTNAVFAVM	180
	HAQRTSGSSA	PTLYLPVLAW	VFLP				

Seq ID NO: 116 DNA sequence

Nucleic Acid Accession #: EOS sequence

Coding sequence: 1-1059

	1	11	21	31	41	51	
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85	TGCCGTGTAT	CTGCAGGGTG	CCCTTGCTTA	AGCCCTTGA	CCTCTTGGT	TATAGTTTCC	120

5
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GGTGCTGATG AAGAAGCTGC AGCAAGTGAT CCAGAAGATC TAGCTAAGAT CATTGATGAA 300
GATGTGAAAG GCATTGTACA GAAGAAGATG AGAATCACAG TAAACCAAAC AAAGGAAATG 360
CAGAGAGATG ATTTTCAGCT GAATATTGGA AATGTAAAT GCCACACGTT GGATGAGATG 420
ATTATCCGAG CTCAGACTTG GGAATAGTC ATGCTTCTGG ACCAAGTGCC AGGTCCCTGGC 480
CCTACACAAC AGGTAGATGG TTGGATATAT TTGGATAATG GAGCTTTCCA AACAGAAGCA 540
AAACACAAC CCACATGATG AAAATATAAA GAAACTGAAC CAGTGTGTCT TTTCAACATA 600
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TATAACTGCA ATCGATGGGC AGAAGACAAA TGGTGTCCAC AAAATACACA GTACTGTGTTG 780
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GACCTCCTTG ACTGCTCAG AGGCTGCCAG GTCAAACCTT CTGTTTATG TGATTAGCTC 1440
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GCATAGTCAA TAGAAAAGC AACTGTACGA AGAAAACCTC CAGTGGAACT AATATGAAAT 1560
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Seq ID NO: 117 Protein sequence

Protein Accession #: Eos sequence

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1 11 21 31 41 51
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FMRMKERSHA HNIKVQGEAG GADEEAAAASD PEDLAKIIDE DVKGIVQKKM RITVNTKEM 120
QKRYFQNLNIG NVKCHTLDLM IIRAQTWEIV MLLDQVPGPG PTQQVDGWYI LDNGAFQTEA 180
KHKPTDVKYK ETEPVCLFTI DIRVRTAQHT RIKQKVSITS MATPPFNSFK CPTCENAGDN 240
YNCNRWAEDK WCPQNTQYCL TVRHFTSHGR STSITKKCAS RSECHFVGCH HSRDSEHTEC 300
RSCCEGMICN VELPTNHTNA VFAVMEHQRT SGSSAPLTLYL FVLANVFVLP LL
  
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Seq ID NO: 118 DNA sequence

Nucleic Acid Accession #: XM_038659.6

Coding sequence: 528-1688

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GATACGCACC CACAGTGGCT GATTGGGGGG TAACCGTGTG ATTTGCTTGC AACACTGGCA 180
CCTCTGCCCT CCACCCCGGG AGTGAGCAGT GAGTGAGGCT CGGCTCTGGG CGCTGGCTCC 240
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GTCTTCTCTG TGATGCAATC GCTAGGTGCG CAGTCTCCG CCGGAGAGAG GCGGCTCTCG 360
AATCCAGCCC GCCAAGTSTA CTGCGCCCGC CCTCGGGCAC TGCCCCAGGT CTGTGCTCAG 420
CCGGGACCCG GCTCTGAGC GCGAGACCCG GTCCACACCG CCAGGGGCTA CGACCTTTGG 480
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GTAACGAGATG CTCCGAGAG TGTAACCGAG AAGGAGGATC AAAAGAGGTG GTGGGGAATT 600
TTAAGGCTAA AGACCTAATA GTCAACACAG CTACCATTTT AAAGGAAAAA CCAGACCCCA 660
ATAATCTGGT TTTTGGAACT GTGTTCAAG ATCATATGCT GACGGTGGAG TGGTCTCTAG 720
AGTTTGGATG GGAGAAACCT CATATCAAGC CTCTTCAGAA CCTGTCAATT CACCCTGGCT 780
CATCAGCTTT GCACATATGA GTGGAAATTAT TTGAAGGATT GAAGGCATTG CGAGGAGTAG 840
ATAATAAAT TCGACTGTTT CAGCCAAACC TCAACATGGA TAGAATGTAT CGCTCTGCTG 900
TGAGGGCAAC TCTGCCGTA TTTGACAAAG AAGAGCTCTT AGAGTGTAT CAACAGCTTG 960
TGAAATTGGA TCAAGATAGG GTCCCATATT CAACATCTGC TAGTCTGTAT ATTCTCTCTA 1020
CATTCAITGG AACTGAGCCT TCTCTTGAG TCAAGAAGCC TACCAAGCC CTGCTCTTTG 1080
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GGGCCAATCC CAAGATGTGA AGAGCCTGGA AAGGTGGAAC TGGGGACTGC AAGATGGGAG 1200
GGAATTACGG CTCATCTCTT TTGCCCCAAT GTGAAGCAGT AGATAATGGG TGTGAGCAGG 1260
TCCTGTGGCT CTATGGAGAG GACCATCAGA TCACTGAAGT GGGAACTATG AATCTTTTTC 1320
TTTACTGGAT AAATGAAGAT GGAGAAGAAG AACTGGCAAC TCCTCCACTA GATGGCATCA 1380
TTCTTCCAGG AGTGACAAGG CGGTGCATTC TGGACCTGGC ACATCAGTGG GGTGAATTTA 1440
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TGAGAGAGAT GTTTGGCTCT GTTACAGCCT GTGTGTGTTG OCCAGTTTCT GATATACTGT 1560
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TCTTGAGCAA ATTAACGTAT ATCCAGTATG GAAGAGAAGA GAGCGACTGG ACAAATTGTG 1680
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GGGACAGACT GTTGCAATTG AATTGTGATA GATTTCCTTG GCTACCTGTG CATAATGTAG 1800
TTTGTAGTAT CAATGTGTTA CAAGAGTGAT TGTTCCTTCA TGCCAGAGAA AATGAATTGC 1860
AATCATCAAA TGGTGTTCCT TAACCTGGTA GTAGTAACCT ACCTTACCTT ACCTAGAAAA 1920
ACATTAAATG AAGCCATATA ACATGGGATT TTCTCAATG ATTTTAGTGC CTCCTTTTGT 1980
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 ACTCCTTTGA CCTATTCTT CATATAGTAG TCTAGGAAA AGTTGCAGGT AATTAAACT 3780
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 CCATCAACAC ATTTTATACT TTGCTATCTC AATTTATTG TGGCGAGACT TGTCATTGT 3900
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 AGCCCTTTTC ATCAGACCCA GTGAAACTA AGGATAGATG TTTAAAACT GGAGGTCTCC 4020
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 GAAAAATGT AAGAC

Seq ID NO: 119 Protein sequence
Protein Accession #: XP_038659.2

1 11 21 31 41 51
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 EWSSEPGWEK PHIKPLQNL LHPGSSALHY AVELFEGLKA FRGVNDKIRL POPNLNMDRM 120
 EYSAVRATLP VPKKEELLE IQLVLKLDQE WVPYSTASL YIRPTFITE PSLGVKKPTK 180
 ALLFVLLSPV GPYPSSGTFN PVSLWANPKY VRANKGGTGD CKMGNGYSS LFAQCEAVDN 240
 GCQQVWLNYG EDHQITEVGT MNLFLYWIN DGEELATPP LDGIILPGVT RRCILDLAHQ 300
 WGEFKVSEYR LTMDDLTALE EGNRVREMP SGTACVVCVF SDILYKGETI HIPTMENGPK 360
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Seq ID NO: 120 DNA sequence
Nucleic Acid Accession #: NM_005377
Coding sequence: 121..1194

1 11 21 31 41 51
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 CGCTCCACGA CGCCACGGA GGACATCTGG AAGAAATTCG AGTTGGTGCC GCCGCCCTGG 240
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 GGGTGGCGTG GGGACGAGAC GGAATCCGAG GACTACTGGA AAGCTTGGGA CGCGAACTAC 360
 GCCTCCCTCA TCCGCGTGA CTGCAATGAG AGCGGCTTCT CCACCCAGGA GCGCTGGAG 420
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 GGCACCCCGG ACTACATCTC CGAGCTCGAA GCGGCAACC TAGCGCCCAT CTTCCTCTGT 540
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 AGATTTTGCC CCAGCTGGAC TCTGCAGCTC CACGTGGAAT CCAGTGCCT GCCTCCAGTC 2880
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Seq ID NO: 121 Protein sequence

Protein Accession #: NP_005368

1 11 21 31 41 51
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 GCAGDETBSQ DYWKANDANY ASLIRDCMH SGFSTQEPLE RAVSDLLAVG APSGYSPEKF 120
 ATFDYTFELE AGNLAPFPFC LLGEPKIQAC SRSESPDSE GEEIDVTVKK RQSLSTRKPV 180
 IIAVRADLLD PFMNLPHISL HQQQHNYAAP FPPESCQFEG APKMPPEKEA LEREAPGGKD 240
 DKEDEEIVSL PFVESEAQS QPKPIHYDT ENWTKKKYHS YLERKRENDQ RSRFLALRDE 300
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Seq ID NO: 122 DNA sequence

Nucleic Acid Accession #: AB006625.2

Coding sequence: 356..4750

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5 CAATGAGACC TCTGTAATTC ACTCTCTGCC TTTTGGTGAA CAAACATTTC GCCCTCGAGG 2880
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Seq ID NO: 123 Protein sequence

Protein Accession #: BAA22956.2

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Seq ID NO: 124 DNA sequence
Nucleic Acid Accession #: NM_007196
Coding sequence: 180..1962

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Seq ID NO: 125 Protein sequence
Protein Accession #: NP_009127

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30 LNLQLLRDQA SLGSKVKPIS LADHCTQPGQ KCTVSGWGTV TSPRENFPTD LNCAEVKIFP 180
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Seq ID NO: 126 DNA sequence
Nucleic Acid Accession #: NM_014791.1
Coding sequence: 171..2126

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Seq ID NO: 127 Protein sequence
Protein Accession #: NP_055606.1

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Seq ID NO: 128 DNA sequence
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 Coding sequence: 169-1323

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Seq ID NO: 129 Protein sequence

Protein Accession #: NP_001287.2

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Seq ID NO: 130 DNA sequence

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 CAGCTGCCCA CTGCAAAAAA CCGAATCTTC AGGTCTTCCT GGGGAAGCAT AACCTTCGGC 480
 AAAGGGAGAG TTCCCAAGGAG CAGAGTCTCT TGTTCGGGCG TGTGATCCAC CCTGACTATG 540
 ATGCCGCCAG CCATGACCCG GACATCATGC TGTTCGCCCT GGCAAGCCCA GCCAAACTCT 600
 CTGAATCAT CCAGCCCTCT CCCCTGGAGA GGAAGTCTCT AGCCAAACAC ACCAGCTGCC 660
 ACATCTCTGG CTGGGGCAAG ACAGCAGATG GTGATTTCCT TGACACCATC CAGTGTGCAT 720
 ACATTCACCT GGTGTCCCTG GAGGAGTGTG AGCATGCCTA CCTTGGCCAG ATCAACCCAGA 780
 ACATGTGTGT TGTCTGGGAT GAGAAGTACG GGAAGGATTC CTGCCAGGCT GATTCTGGGG 840
 GTCCGCTGCT ATGTGGAGAG CACCTCCGAG GCCTTGTGTC ATGGGGTAAC ATCCCTGTGT 900
 GATCAAGAGA GAAGCCAGGA GTCTACACCA ACGTCTGCAG ATACACGAAC TGGATCCAAA 960
 AAACCATTCG GGCCAAAGTA CCCTGACATG TGACATCTAC CTCCCGACCT ACCACCCAC 1020
 TGGCTGGTTC CAGAACGTCT CTCACTAGA CCTTGCTTCC CTTCTCTTCC TGCCAGCTC 1080
 TGACCTGAT GCTTAATAAA CGCAGCGAGC TGAGGGTCTT GATTCTCCCT GGTTTTATCC 1140
 CAGCTCCATC CTGTCATCAC TGGGAGGAGC GTGATGAGTG AGGACTTGGG TCCTCGTCT 1200
 TACCCCAACC ACTAAGAGAA TACAGGAAA TCCCTTCTAG GCATCTCTCT TCCCAACACC 1260
 TTCCACAGT TTGATTCTCT CCTGCAGAGG CCCAGCCAGC TGTCTGGAAT CCCAGCTCG 1320
 CTGCTTACTG TCGGTGTCCC CTTGGGATGT ACCTTTCTTC ACTGCAGATT TCTCACTGT 1380
 AAGATGAAGA TAAGGATGAT ACAGTCTCCA TCAGGCAAGT GCTGTTGGAA AGATTTAAGA 1440
 TTTACACCT ATGACATACA TGGGATAGCA CTTGGGCCGC CATGCATCA ATAAAGAATG 1500
 TATTTT

Seq ID NO: 131 Protein sequence

Protein Accession #: NP_002765

1 11 21 31 41 51
 MKKLMVVLISL IAAAWAEQN KLHVGPCDK TSHFYQAALY TSGHLLCGGV LIHPLNVLTA 60
 AHCKKPNLQV FLGKHNLRQR ESSQEQSSVV RAVIHPDYDA ASHDQDMLL RLARPAKLSE 120
 LIQPLPLERD CSANTTSCBI LGWKTADGD PPDTIQAYI HLVSREECH AYPGQITQNM 180
 LCAGDEKYKG DSCQGDSSGP LVCGDHLRGL VSWGNIPCGS KEKPGVYTNV CRYTNWIKRT 240
 IQAK

Seq ID NO: 132 DNA sequence

Nucleic Acid Accession #: AY038071.1

Coding sequence: 1..1685

1 11 21 31 41 51
 ATGAGCAATC AGTACCAGGA GGAGGGCTGC TCCGAGAGGC CCGAGTGCAA AAGTAAATCT 60
 CCAACTTTGC TCTCTCTCTA CTGCATCGAC AGCATCTCTG GCCGGAGGAG CCCGTGCAAA 120
 ATGCGGTTCG TGGGAGCCCG GCAGAGCTTG CCTGCTCCCG TGACCAAGCG CGCCGACCCG 180
 GAAAGGCCCG TGCAAGGCTC CCCTAAGAGC AGCAGCGCCC CGTTCGAGGC CGAGCTGCAC 240
 CTGCGGCCCA AGCTGCGGGC CCTGTACGGC CCGGGCGGGG CCGGCTCTCT TCAGGGTGGC 300
 GCAGCGCGCG CGCGCGCGCG GCGCGCGCGG CCGGCGAGCG CCGCCACGGC CACGGCGGGT 360
 CCAGCGGGGG AGGCCCTCTC GCGGCCACCG CCAACCGCGC GGCCCGGGGA ACGGCGGGAC 420
 GGCGCAGGGG CGCGCGCGCG AGCGCGCGCG GCGCGCGCGG CGGCGTGGGA CAGCTCAAG 480
 ATCAGCCAGG CGCGCAGGCT GAGCATCAGC CGCAGCAAGT CGTACCGCA GAACGGGGCG 540
 CCTTCTGTGC CGCGCGCGCG CGCGCTGGAC GAGCTGGCGG GCCCGGGGGG CGTACCGCAC 600
 CCGGAGGAGC GCTTGGCGCT GCGCGCGCGC CCGGGCAGCG CCCCGGCTGC GGGTGGTGGC 660
 ACCGGCACCG AGGACGACGA GGAGGAGCTG CTGGAGGAGC AAGAAGATGA GGACAGGAG 720
 GAGGAATCTG TGGAGACGGA CGAGGAGGAG CTGCTGGAGG ACGACGCGCG CGCGCTGCTC 780
 AAGGAGCCCC GCGGCTGTCT TGTGGCGCGC ACTGGCGCGG TGGCGCGAG AGCTGCGGCT 840
 CAGGTGGCCA CAGAGGGCGG GGAGCTGTCA CCCAAGGAG AGCTGTGCTG GCAACCCGAA 900
 GACGCTGAGG GCAAGGACCG CGAGGACAGC GTGTGCTCT CTGCGGGCAG CGACTCGAG 960
 GAGGGGCTGC TGAAACGCAA ACAGAGGCGC TACGCGACCA CGTTACCTAG CTACAGCTG 1020

GAGGAAC TGG AGCGGGCCCTT CCAGAAGACG CACTACCCGG ACGTCTTCAC CAGGGAGGAA 1080
 CTGGCCATGA GGCCTGGACTT GACCGAGGCC CGAGTCCAGG TCTGGTTCCA GAAACGTCGG 1140
 GCCAAGTGGC GCAAGCGGGA GAAGGCAGGC GCGCAGACCC ACTCCCCCTGG GCTGCCCCCTC 1200
 CCGGGGCCGC TCTCCGCCAC CCACCGCTC AGCCCCCTACC TGGACGCCAG CCCCCTCCCT 1260
 CGGCACCAAC CGCGCTCGA CTCCGCTTGG ACTGCGCTGG CCGCGCGCGC CGCGCGCGCC 1320
 TTCCCGAGCC TACCTCCGCC TCCGGGCTCG GCCAGCCTGC CGCCAGCGG GCGCGCGCTG 1380
 GGCTGAGCA CTTCCTCGG AGCGGCAGTG TTCCGACACC CAGCTTTCAT CAGCCCCGCA 1440
 TTCCGCAGGC TCTTTTCCAC AATGSCCCCC CTGACCAGCG CGTGGACCGC GGCCCGCGCTC 1500
 CTGAGACAGC CCACACCGC CGTGGAGGCG GCAGTGCGAT CGGGCGCCCT GGCCGACCCG 1560
 GCCACGGCGG CCGCAGACAG ACGCGCTCT AGCATAGCGG CGCTGAGGCT CAAGGCCAAG 1620
 GAGCACGGCG CGCAGCTCAC GCAGCTCAAC ATCTTCCCGG GCACACGAC CAGGCAAGGAG 1680
 GTGTGC

Seq ID NO: 133 Protein sequence
 Protein Accession #: AAK93901.1

1 11 21 31 41 51
 MSNQVEEGC SERPECKSKS PTLSSVYCID SILGRSPCK MRLGAAQSL PAPLTSRADP 60
 EKAVGSPKS SSAPPEAELH LPPKLRRLYG PGGRLQLQA AAAAAAAAAA AAAATATAG 120
 PRGEAPPPPP PTARCGERPD GAGAAAAAAA AAAAAMDTLK ISQAPQVSIS RSKSYRENGA 180
 PFVPPFPALD ELGGPGGVTH PEERLGVAGG PGSAPAAGGG TGTEDEEEL LEDEDEDEE 240
 BELLEDDEEE LLEDARALL KEPRRCVAA TGAFAAAAA AVATEGGELS PKEELLHPE 300
 DAEGKDGEDS VCLSGSDSE EGLLKRKQR YRTTPTSYQL EELERAPQKT HYPDVFTREE 360
 LAMRLDLTEA RVQVWFQNR AKWRKREKAG AQTHFPGLPF PGPLSATHPL SPYLDASFPF 420
 FHRPALDSAM TAAAAA AAAA PPSLPPPPG ASLPPSGAPL GLSTFLGAAV FRHPAPISPA 480
 FGELPSTMAP LTSASTAAL LRQPTPAVEG AVASGALADP ATAAADRRAS SIAALRLKAK 540
 EHAAQLTQLN ILPGTSTGKE VC

Seq ID NO: 134 DNA sequence
 Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
 TTTTTTTTT TTTTTTAAA GCAGATCATC TCTCCAAATC ATCACTTCTA TCAAGCCTAT 60
 TGCTTGAGCA GTGTTATAGC ACTCAGCCCT CAGGGCAAGG ATAAGTCTTC ACCATTGTCA 120
 CAGTAGCAC ACACATATTC AGCCATATCA TGCTGAATGG GAATACAGGA CTTGTAGAA 180
 ACAGAACTGA TTCTGCGAGA ATATCCTGAG ATACTTATCA AGCTGTAAA GGAGACATCA 240
 GTCTTTTGTG TGATTGCCC TTGACACCTC CTCAGGAAA GTATCTAGAA ATTCTTGTCT 300
 TTCTGAAGAA CCTCAGACC TCTTAGGTC AATGTAGGT AAGTGCCCTG CAGATCTCCC 360
 TAGAATAGAA AAGCACCTTG AAAACTGTAG TCTGACTTAA TAGACACAAA TATAATGAAA 420
 GCACTAATTC ATAGATCTCT GTTATTGAA GGAAGAAAGCA GCAAGGCA CAAGCTTCAG 480
 ATATTGGTCT TGCACAGAA AAAGCTGGAA TTCTACC

Seq ID NO: 135 DNA sequence
 Nucleic Acid Accession #: NM_006799
 Coding sequence: 19..963

1 11 21 31 41 51
 GCGCGGGAG AGGAGGCCAT GGGCGCGCGC GGGCGGCTGC TGCTGGGCT GCTGCTGGCT 60
 CGGGCTGAC TCAGGAAGCC GGAGTCGCGG GAGGCGGCGC CGTTATCAGG ACCATGCGGC 120
 CGACGGGTCA TCACGTCCGC CATCGTGGGT GGAGAGGACG CGAATCTCGG GCGTTGGCGG 180
 TGGCAGGGGA GCGTCGCGCT GTGGGATTCC CACGTATGCG GAGTGAGCCT GCTCAGCCAC 240
 CGCTGGGCAC TCACGGCGGC CAGCTGCTTT GAAACCTATA GTGACCTTAG TGATCCCTCC 300
 GGGTGGATGG TCCAGTTTGG CCAGCTGACT TCATGCCAT CCTCTGGAG CCGCAGGCC 360
 TACTACACCC GTTACTTGT ATCGAATATC TATCTGAGCC CTGCTACCT GGGGAATTCA 420
 CCCTATGACA TTGCTTGGT GAAGCTGTCT GCACCTGTCA CCTACACTAA ACACATCCAG 480
 CCACTCTGTC TCAGGCGCTC CACATTGAG TTTGAGAACC GGACAGACTG CTGGGTGACT 540
 GGCTGGGGGT ACATCAAGAA GGATGAGGCA CTGCCATCTC CCCACACCTC CCAGGAAGTT 600
 CAGGTGCGCA TCATAACAA CTCTATGTGC AACCACTCT TCCTCAAGTA CAGTTTCCGC 660
 AAGGACATCT TTGAGACAT GTTTGTGCT GGCAATGCC AAGGCGGGAA GGATGCTGC 720
 TTGCTGACT CAGGTGGACC CTGCGCTGT AACAGAATG GACTGTGTA TCAGATTGGA 780
 GTGCTGAGCT GGGAGTGGG CTGCTGCTGC CCAATCGGC CGGTGTCTA CACCAATATC 840
 AGCCACCACT TTGAGTGGAT CCAGAGCTG ATGCGCCAGA GTGGCATGTC CCAGCCAGAC 900
 CCTCTCTGSC CGTACTCTT TTTCCCTCTT CTCTGGGCTC TCCACTCTCT GGGCGCGTCT 960
 TGAGCTTACC TGAGCCATG CAGCCTGGG CCACTGCCAA GTACGGCCTT GGTCTCTTCT 1020
 TGCTTGTGTT GGAATAAAC ACATTCCAGT TGATGCCCTG CAGGGCATTC TTCAAAA

Seq ID NO: 136 Protein sequence
 Protein Accession #: NP_006790

1 11 21 31 41 51
 MGARGALLLA LLLARAGLRK PESQEAAPLS GPGRRRVITS RIVGGEDAEL GRWPWQGLSR 60
 LWDSHVCGVS LLSHRWALTA AHCFETYSDL SDPSGMMVQF GQLTSMPSPF SLQAYYTRYF 120
 VSNILSPRY LQNSPYDIAL VKLSAPVYTT KHIQPICLQA STFEPENRTD CNVTGWYIK 180
 EDEALPSPHL LQEVQVAIIN NSMCNHLFLK YSFRKIDFGD MVCAGNAQGG KDACFGDSGG 240
 PLACNKNGLW YQIGVVSVGW GCGRPNRPV YTNISHPEW IQKLMAQSGM SQPDPSWPLL 300
 FFPILLWALPL LGPV

Seq ID NO: 137 DNA sequence
 Nucleic Acid Accession #: Bos sequence
 Coding sequence: 1..939

1 11 21 31 41 51
 ATGGGCGCGC GCGGGCGCGT GCTGCTGGCG CTGCTGCTGG CTGCGGCTGG ACTCAGGAAG 60
 CCGGAGTCGC AGGAGGCGGC GGCCTTATCA GGACCATGCG GCGGACGGGT CATCACGTGG 120
 CGCATCGTGG GTGGAGAGGA CGCGAATCT GGGCGTTGGC CGTGGCAGGG GAGCCTGCGC 180

CTGTGGGATT CCCACGTATG CGGAGTGAGC CTGCTCAGCC ACCGCTGGGC ACTCAGGGCG 240
 GCGCACTGCT TTGAACTGA CCTTAGTGAT COCTCCGGGT GGATGGTCCA GTTGGCCAG 300
 CTGACTTCCA TGCCATCTCT CTGGAGCCTG CAGGCCTACT ACACCGGTIA CTTCGTATCG 360
 AATATCTATC TGAGCCCTCG CTACCTGGGG AATTCACTCT ATGACATTGC CTGGTGAAG 420
 CTGTCTGCAC CTGTCACTCA CACTAAACAC ATCCAGCCCA TCTGTCTCCA GGCTCTCCAC 480
 TTTAGATTGG AGAACCAGGAC AGACTGCTGG GTGACTGGCT GGGGTACAT CAAAGAGGAT 540
 GAGGCACTGC CATCTCCCA CACCTCCAG GAAGTTCAGG TCGCATCAT AAACAACCTCT 600
 ATGTGCAACC ACTCTTCTCT CAGTACAGT TTCCGCAAGG ACATCTTTGG AGACATGGTT 660
 TGTGCTGGCA ATGCCAAGG CGGGAAGGAT GCCTGCTTCG GTGACTCAGG TGGACCCITG 720
 GCCTGTAACA AGAATGGACT GTGGTATCAG ATTGGAGTCG TGAGCTGGGG AGTGGGCTGT 780
 GGTGCGCCCA ATCGGCCCGG TGTCTACAC AATATCAGCC ACCACTTTGA GTGGATCCAG 840
 AAGCTGATGG CCCAGAGTGG CATGTCCAG CCAGACCCCT CCTGGCCACT ACTCTTTTTC 900
 CCTCTTCTCT GGGCTCTCCC ACTCTGGGG COGCTCTGA

Seq ID NO: 138 Protein sequence

Protein Accession #: Bos sequence

1 11 21 31 41 51
 MGARGALLLA LLARAGLRK PESQEAAPLS GPCGRRVITS RIVGGEDAEL GRWPWQGLSR 60
 LMDSHVCGVS LLSHRNALTA AHCFTDLSD PSQWVQFQO LTMSPFWSL QAYTRYFVS 120
 NYLSPRYLQ NSPYDIALVK LSAFVTYTKH IQPICLOAST FEFENRTDCH VTGWYIKED 180
 EALPSPHTLQ EVQVAIINNS MCNHLFLKYS FRKDIFQDMV CAGNAQGGKD ACFDGSGLPL 240
 ACNKNGLNYQ IGVVSWGVGC GRPNRPGVYT NISHRFEWIQ KLMAQSGMSQ PDPSPWLLFF 300
 PLLNALPLLQ PV

Seq ID NO: 139 DNA sequence

Nucleic Acid Accession #: NM_014344

Coding sequence: 131..1444

1 11 21 31 41 51
 GCGGCCGCGA TGGGGCCGAA GCGCCCGAAG CCGCGAGGCC CACAACTGC GGGGCCCGCC 60
 TCGCCGCGCG GACCCGGGTG CCTGGGCTCG GCTTGAAGCG CGCGCGCGCC ACCCGGCACAG 120
 CCGCGGAGC ATGGGCAAGG GGATGCGGGG CGCGCGCGCC ACCCGGGGC TCTGGCTGCT 180
 GCGCTGGGCG CGCGCGCGAG ACAGCTCTCC AGGGCTCTCG CGCGCGCGCA CGAGCTGCTC 240
 CGCTCTCCCG CGCGCGCGAG ACAGCTCTCC ACAGCTCTCG CGCGCGCGCA CGAGCTGCTC 300
 GCGCGCGCTC CGCTCTCCCG TCGCCCGCGC CCGCGCGCGC GCGCGCGCGC GCGCGCGCGC 360
 GAAAACTTTC CGGGCGCTCG TCACCTCTGC GCGCGCGCGC GCGCGCGCGC GCGCGCGCGC 420
 CCGGAGCGAG CCGGAGCGAG ACCTGCTCAG CAGGAGCGCC CGCGCGCGAG AGAGCGCGCG 480
 GGTGACCGGG GCGCTCTTCT GGAGCGCGCG CCGGAGCGAG CAGGAGCGCC CGCGCGCGCG 540
 GGAGCGCGAG GCGCGCGCGT GGCTGAGGCG GGCTGCGCGC GCGCGGATGG TGGCCCTGGA 600
 GCGCGGGGGT TGGGGCGCGA GCTCCAAACG ACTGGCGCGT TTTGCGGAG GCACCGCGCG 660
 CTGCGTGGCG TACGGGATCA ACCCGGAGCA GATTGAGGCG GAGGCGCTGT CTTACTATCT 720
 GCGCGCGCTG CTGGGCTTCC AGCGCCACGT GCGCGCGCTG GCGCGCGCTG GCGCGCGCTG 780
 TCGGGGCGCG CAGTGGGCGC AGGTGCGAGG GAGCTGCGC GCTGCGCACT GGACCGAGGG 840
 CAGCGTGGTG AGCTGACAC GCTGGCTGCC CAACCTCACG GAGCTGGTGG TCGCGCGCGC 900
 CTGGCGCTCG GAGGAGCGCG GCTGCGCGCG CCGCGCGCGT GCGCGGGGTG AGCTGGCCAA 960
 CCTCAGCCAG GCGGAGCTGG TGAACCTAGT ACAATGGACC GACTTAATCC TTTTCGACTA 1020
 CCGGAGCGCG AACTTCGACC GCTCGTAAG CAACCTCTTC AGCTGCGATC GCGGAGCGCG 1080
 GGTGATGAG CGGGGCTTGG TGCAAGGCTA CCGGAGTAC GGCATGTGGG ACAAGTATAA 1140
 CGAGCGCGTG TTGCTGCTAG TGTGCTGTTT CCGGAGCGCG ACCCGCGCGC GCGTCTGGA 1200
 GCTGACCGCG GGACAGGAGC CCGCGCGCGC GCTGCTGCGC CTCTACCGCG GCCACGAGCC 1260
 TCGCTTCCCG GAGCTGGCGC CCGTTCGAGA CCGCGCGCGT CAGCTGCTAC AGCGCGCGCT 1320
 CGACTTCTTC GCGGAGCACA TTTTGCCTAG TAAGGCGAAG TACGGCGCGC GGTCTGGGAC 1380
 TTAGTGTGAC CGGGAGGAAA AGAGAGAGAT CTGGGCTTGG GGTATGGATG ATGGGGGAAA 1440
 GGGCGGTGCG CTCTGCCACT GTCAGGAGCC AGCGCGCCAA CGCCACCGC CAAAGGTGTC 1500
 TAAAAATTC AGCTTTTCA CCACTTGCC CTCTCTTCA ATCCACGCT GTTCTCTTTC 1560
 AAGTTCTGG GAGGAGGAA TCAACGAGGC GAGAAGTGA ACATTTCTTC CACCCAGCTT 1620
 ATAAAAGGAT TCTTTACTGT GCCAGCAGCG GGATTGGATC CGAAGAACT GGCTACTGGG 1680
 GTTTGGCCCC CGAGTGGCGG TCCCTGTGGG AGATGCAACC CATTCTTGGG CCCCCCTCAT 1740
 TCCCTTTCCG AAAAAGGAAA ACTTGCCTTT GAGCGCTTGA GCTAATTCTG CAATTTTCTA 1800
 CCAACAGAG CGCTGGTGGC CCGGAGCAG GCGTGTGACA TTGGCTGGTG GAGCCCTTTC 1860
 CTGTGTTCTC CCTTGTTC AGCGCGCGCA TGGTGAATC ACTGTTCCAA GCAGGGGAGC 1920
 GGCTCGGAT AGGACAAAGA GAGCAGGACC TCCAGACTCT GGGGAGCCCT GCAGACCTTG 1980
 ACAATTTGCC TGACTCATTC CTGACCTCTT GTCATTTTGG CCGTAAGGCT ACAAAATCAG 2040
 GGTGAGCTGT ATGCACTAAG TCAATAATG AATTCTTCC TCCCTCTCGC AACCGACCAA 2100
 AATTTTGACA ACATGATGT TCAACAGAG GAAAAAATA TCAGTTTAT GCACCTTATT 2160
 TTGTTTGTAT TTTCAATTTT TATTAAGAAA AAATTTTATT TTACAGAAAT TACCTTCTCT 2220
 GTATATATGT GCATAAAGT TGGTGTAAAT ATACTAAACA AACTTATATT TCAATAAAG 2280
 GGAGTTTAAA ATTTAAAAA AAAAAA

Seq ID NO: 140 Protein sequence

Protein Accession #: NP_055159

1 11 21 31 41 51
 MGRMRGAAA TAGLNLALG SLLALWGLL PPRTELPASR PPEDRLPRRP ARSGGPAPAP 60
 RPFLPPPLAW DARGGSLRTF RALLTLAAGA DGPPRQSRSE PRMHVSARQP RPEESAIVHG 120
 GVFWSRGLEB QVPPGFSEAQ AAAMLEAARG ARMVALERCG CGRSNRLAR FADGTRACVR 180
 YGINPEQIQG EALSYYLARI LGLQRHVPLP ALARVEARGA QWAQVQBELR AAHWTEGSVV 240
 SLTRWLPNLT DUVVPAPWRS EDGRRLPLRD AGSELANLSQ AELVDLVQWT DLILFDYLT 300
 NFDRLVSNLP SLQWDPVVMQ RATSNLHRGP GGALVPLDNE AGLVHGYRVA GMDKYNELP 360
 LQSVCVFRER TARRVLELHR GQDAARLLR LYRRHEPRFP ELAALADPHA QLLQRRDLPL 420
 AKHILHCKAK YGRRSGT

Seq ID NO: 141 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 11..574

1	11	21	31	41	51	
5	GTCCGCCAAG	ATGCTGCTCC	CAGTCCCTCT	GCTGTCTGCA	GOCCAGCCTT	CACCCCTCTG 60
	CATGGGGAAA	TGCTCTACAG	ACTTCTGCCC	ATGGCTGTAT	GTACGCACGG	ACAGAGCTAG 120
	CAATGACCTT	GCTGGCAGGT	ATGATAGGAA	GCCTCTTCTG	TCACAGGATT	CATTCCCAGA 180
	CAATGACCCC	AAATGCTCTG	CCCTGCTCCC	CCCCCCCC	AACATCAAAA	TAGCCGAGAA 240
10	AAATGCTCTT	CTCGGAGCCA	AATGTGTGGT	GATGCTTTAC	AATCAGAAAT	TCCTACAGTG 300
	GCCTGAGGCT	TCCACCACTA	AAACGCAAGC	TGTAGATACC	TATTGCTTGG	ATTATAAGCC 360
	TTCCAAGGGA	AGAAGGTGGG	CTGCAAGAGC	ACCAAGCACC	AGATACACAT	ATGGGACTAT 420
	CACCAAGAG	AGAGACTACT	GCGCGGAAGA	CCAGACTATC	GAGAGCTGGA	GAGAAGAAGG 480
	TTCCCAAGTG	GGCTTGAAGC	TTGCTGTGCT	TGGTATTTC	ATCATTTGTTG	TGTTTGTCTA 540
15	CTCGACTGTG	GAAATAAAGT	CGCTGTTTGG	TTAAGTAAAT	TAGG	

Seq ID NO: 142 Protein sequence

Protein Accession #: Eos sequence

1	11	21	31	41	51	
20	MPAFVPLLSA	AQPSFSCMGK	SSTDFCPWLY	VRTDRASNDP	AGRYDRKPLL	SQDSFPDNDP 60
	KCLSLLEPPP	NKIAEIKNAL	LGAKCVVMPY	NQKFLQWPEA	STTKRKAVD	YCLDYKPSKG 120
	RRNAARAPST	RITYGTITKE	RDYCAEDQTI	ESWREEGFPV	GLKLAVLGIF	IIVVFVYLTV 180
	ENKSLFG					

Seq ID NO: 143 DNA sequence

Nucleic Acid Accession #: XM_050183.6

Coding sequence: 39..365

1	11	21	31	41	51		
30	GATTCTACCA	TCAGAAAAGA	GGCCAAACTT	CTATCATCAT	GGTGGATGTG	AAGTGTCTGA 60	
	GTGACTGTAA	ATTGCAGAAC	CAACTTGAGA	AGCTTGGATT	TTACCTTGGC	CCAATACTAC 120	
	CTTCACACAG	AAAGTTGTAT	GAAAAAAGT	TAGTACAGTT	GTGTGCTCTA	CCTCCCTGTG 180	
	CACCACTGT	GATGAATGGA	CCCAGAGAGC	TGGATGGAGC	GCAGGACAGT	GATGACAGCG 240	
35	AAGTGGGCT	GCAAGAGCAC	CAAGCACCG	AATCACATAT	GGGACTATCA	CCAAAGAGAG 300	
	AGACTACTGC	GCGGAGAGCC	AGACTATCGA	GAGCTGGAGA	GAAGAAGGTT	TCCCAAGTGG 360	
	CTTGAAGCTT	GCTGTGCTTG	GTAATTTTCT	CATTGTGGTG	TTTGTCTACT	TGACTGTGGA 420	
	AAATAAGTGG	CTGTTTGGTT	AAGTAATTTA	GGAGCAAGCC	AATGCTCCAA	GCGAGGCCTC 480	
	CTGCTTCAG	AAAGAACCAA	AACACTACCC	TGAAGGGCCA	GCCTAGCCTG	CAGCCCTCCC 540	
40	TTGCAGGGAG	CCTTCCCTTG	CACGTGTGCT	CTCTCACAGA	TGGGTGTCTG	GGCTCAGCCA 600	
	GGTGGAAAGG	ACCTGCCTAA	CCAGGCACCT	GTGTTAAGAG	CATGATGGTT	AGGAAATCCC 660	
	CCAAGTCATG	TCAACTCTCA	TAAAGGTGTC	TTCATATTTT	GAGCAGGCGT	CAAAC	

Seq ID NO: 144 Protein sequence

Protein Accession #: XP_050184.1

1	11	21	31	41	51	
45	MVDVKCLSDC	KLQNLQLEKL	FSPPGPIFST	RKLYEKQLVQ	LLVSPPPCAPP	VMNGPRELDG 60
	AQSDSDSEGG	LQHQAPESH	MGSLPKRETT	ARKTRLSRAG	EKKVSQNA	

Seq ID NO: 145 DNA sequence

Nucleic Acid Accession #: NM_002204.1

Coding sequence: 74..3229

1	11	21	31	41	51	
55	AGGTGAACAG	GTCCTCAGCG	CCAGCTCCGC	CCCTCAGCG	GCTCTGCGCG	GGACCCCGCT 60
	TCCGCTGGGA	GCCATGGGCC	CCGATGGGCC	CCGCGCGGCC	CGCGCCCGAC	GCCTGATGCT 120
	CTGTGCGCTC	GCCTTGAATG	TGGCGGCGCG	CGGCTGCGTC	GTCTCGCGCT	TCAACCTGGA 180
	TACCGGATTC	CTGGTAGTGA	AGGAGGCGCG	GAACCCGGCG	AGCCTCTTCC	GCTACTCGGT 240
60	CGCCCTCCAT	CGGCAGACAG	AGCGGCAGCA	CGCTACCTG	CTCCTGGCTG	GTGCCCCCGG 300
	GGAGCTCGCT	GTGCGCGATG	GCTACACCAA	CCGGAAGTGT	GCTGTGTACC	TGTGCCCACT 360
	CACGTGCCAC	AAGGATGACT	GTGAGCGGAT	GAACATCACA	GTGAAAATGT	ACCCTGGCCA 420
	TCACATTATT	GAGGACATGT	GGCTTGGAGT	GACTGTGGCC	AGCCAGGGCC	CTGCAGGCAG 480
	AGTTCTGGTC	TGTGCCCAAC	GCTACACCCA	GSTGCTGTGG	TCAGGGTCAG	AAGACCAGCG 540
65	GCGCATGGTG	GGCAAGTGCT	ACGTGCGAGG	CAATGACCTA	GAGCTGGACT	CCAGTGATGA 600
	CTGGCAGACC	TACCACAACG	AGATGTGCAA	TAGCAACACA	GACTACCTGG	AGAAGGGCAT 660
	GTGCCAGCTG	GGCACCAGCG	GTGGCTTCAC	CCAGAACACT	GTGTACTTCC	GCGCCCCCGG 720
	TGCCATACAC	TGGAAAGGAA	ACAGCTACAT	GATTACAGCG	AAGGAGTGGG	ACTTATCTGA 780
	GTATAGTTAC	AAGGACCCAG	AGGACCAAGG	AAACCTCTAT	ATTGGGTACA	CGATGCAGGT 840
70	AGGCAGCTTC	ATCTGCACCC	CCAAAACAT	CACCATTTGT	ACAGGTGCCC	CACGGCACCG 900
	ACATATGGGC	CGCGTGTCTT	TGCTGAGCCA	GGAGGCAGGC	GGAGACCTGC	GGAGGAGGCA 960
	GGTGCTGGAG	GGCTCGCAGG	TGGGCGCTTA	TTTGGCAGC	GCAATTGCC	TGGCAGACTT 1020
	GAACAATGAT	GGGTGGCAGG	ACCTCCTGGT	GGGCGCCCC	TACTACTTCC	AGAGGAAAGA 1080
	GGAAAGTAGG	GGTGCCATCT	ATGTCTTCAT	GAACCAAGCG	GGAACTCTCT	TCCCTGCTCA 1140
75	CCCTCACTC	CTTCTCATG	GCCCCAGTGG	CTCTGCCCTT	GGTTTATCTG	TGGCCAGCAT 1200
	TGGTGACATC	AACCAAGATG	GATTTGAGGA	TATTGCTGTG	GGAGCTCGGT	TGTAAGGCTT 1260
	GGGCAAGAGT	TACATCTATC	ACAGTAGCTC	TAAGGGGCTC	TATGACAGCG	CCGACGAGGT 1320
	AATCCATGGA	GAGAACTGCG	GACTGCCGTG	GTGGGCCACC	TTCCGCTATT	CCCTCAGTGG 1380
	GCAGATGGAT	TGGGATGAGT	ACTTCTACCC	AGACCTTCTA	GTGGGAAGCG	TGTGAGACCA 1440
80	CATTGTGCTG	CTGCGGGCCC	GGCCAGTCAT	CAACATGCTC	CACAGACCTT	TGTTGCCACG 1500
	GCCAGCTGTG	CTGAGCCCTG	CACCTTGCAC	GGCCACCTCT	TGTGTGCAAG	TGGAGCTGTG 1560
	CTTTGCTTAC	AACCAAGATG	COGGGAACCC	CAACTACAGG	CGAAACATCA	CCCTGCGCTA 1620
	CACCTCTGAG	GCTGACAGGG	AOCGCGGGCC	GCCCCGGCTC	CGCTTTGCGG	GCAATGAGTC 1680
	CGCTGTCTTC	CACGGCTTCT	TCTCCATGCC	CGAGATGCGC	TGCCAGAACG	TGGAGCTGCT 1740
85	CCTGATGGAC	AACCTCCGTG	ACAAACTCCG	CCCCATCATC	ATCTCCATGA	ACTACTCTTT 1800
	ACCTTTGCGG	ATGCCCGATC	GCCCCCGGCT	GGGGCTGCGG	TCCCTGGACG	CCTACCCGAT 1860

CCTCAACCAG GCACAGGCTC TGGAGAACCA CACTGAGGTC CAGTTCCAGA AGGAGTGGCG 1920
 GCCTGACAAC AAGTGTGAGA GCAACTTGCA GATGCGGGCA GCCTTCGTGT CAGAGCAGCA 1980
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 5 CGTGACGAAC ACCCGAACCT CGGAGGCGTC CGGCCAGGAG GCCCAGGAG CGCTGCTCAC 2100
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Seq ID NO: 146 Protein Sequence
 Protein Accession #: NP_002195.1

1 11 21 31 41 51
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 55 QTERQRYLL LAGAPRELAV PDGYINRTGA VYLCPHTAHK DDCERMNITV KNDPGHHIIE 120
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 HNEMCNSTND YLETCMCQLG TSGGPTQNTV YFGAPGAYNW KGNYSYIQRK EWDLSSEYSYK 240
 DPEDQGNLYI GVTMGVGSFI LHPKNTITVT GAPRHRHMGV VFLLSQEAGG DLRRRQVLEG 300
 60 SQVQAYFGSA IALADLNDNG WQDLLVGAPY YFERKEEVGG AIYVFMNQAG TSFPAHPSLL 360
 LHGPGSGAFG LSVASIGDIN QDGFQDIAGV APFEGILKQV IYHSSSKOLL RQPQVVIHGE 420
 XLGLPLGATF GYLSGGQMDV DENFYDILLV GSLSDHIVLL RARFVINIVH KTLVPRPAVL 480
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 GFFSMPEMRC QKLELLMDN LRDKLRPIII SMNYSPLPRM FDRPRLGLRS LDAYPILNQA 600
 65 QALENHTEVQ FQKECGPDNK CESNLQMRRA FVSEQQOKLS RLQYSRDVRK LLLSINVNTN 660
 RTSERSGEDA HEALLTLVVP PALLLSSVRP PGACQANETI FCELGMPFKR NQRMELLAP 720
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 GESQMKTVED VGSPLKYEFO VGPMGEGLVG LGTLVLGLEW PYEVSNRKLW LYPTEITVHG 840
 NGSWPCRPFG DLINPLNLTL SDPGDRPSSP QRRRRQLDPG GGQGGPPVTL AAARKAKSET 900
 70 VLTCAATGRAH CVMLECPID APVVTNVTVK ARVWNSTFIE DYRDPDRVRV NGWATLFLRT 960
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 RARTRALYEA KRQKAEMKSO PSETERLTDD Y

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 Coding sequence: 74...3274

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 GGAGCTCGCT GTGCCGAGT GCTACACAA CGGACTGGT GCTGTGTACC TGTGCCACT 360
 CACTGCCAC AAGGATGAT GTGAGCGGAT GAACATACA GTGAAAATG ACCCTGGCCA 420
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	GTGCCAGCTG	GGCACCAGCG	GTGGCTTCAC	CCAGAACACT	GTGTACTTCG	GCGCCCCGGG	720
	TGCTCAACAC	TGGAAGAGAA	ACAGCTACAT	GATTGAGCGC	AAGGAGTGGG	ACITATCTGA	780
5	GTATAGTTAC	AAGGACCCAG	AGGACCAAGG	AAACCTCTAT	ATTGGGTACA	CGATGCAGGT	840
	AGGCAGCTTC	ATCTCTGCACC	CCAAAAACAT	CACCATTGTG	ACAGGTGCCC	CACGGCACCG	900
	ACATATGGGC	GCGGTGTCTT	TGCTGAGCCA	GGAGGCAGGC	GGAGACCTGC	GGAGGAGGCA	960
	GGTGCTGGAG	GGCTCGCAGG	TGGGCGCCTA	TTTTGGCAGC	GCAATTGCC	TGGCAGACCT	1020
	GAACAATGAT	GGGTGGCAGG	ACCTCCTGGT	GGGCGCCCC	TACTACTTCG	AGAGGAAAGA	1080
10	GGAAAGTAGG	GGTGCCATCT	ATGTCTTCAT	GAACCAAGCG	GGAACTCTCT	TCCCTGCTCA	1140
	CCCCCTACTC	CTTCTTCATG	GCCCCAGTGG	CTCTGCTTTT	GGTTTATCTG	TGGCCAGCAT	1200
	TGGTGACATC	AACCAGGATG	GATTTCAGGA	TATTGCTGTG	GGAGCTCGT	TTGAAGGCTT	1260
	GGGCAAGATG	TACATCTATC	ACAGTAGCTC	TAAAGGGGCTC	CTTAGACAGC	CCCAGCAGGT	1320
15	AATCCATGGA	GAGAAGCTGG	GACTGCCTGG	GTTGGCCACC	TTCGGCTATT	CCCTCAGTGG	1380
	GCAGATGGAT	GTGGATGAGA	ACTTCTACCC	AGACCTTCTA	GTGGGAAGCC	TGTGAGACCA	1440
	CATTGTGCTG	CTCGGGGCCC	GGCCAGTCA	CAACATCGTC	CACAAGACCT	TGGTGCCAG	1500
	GCCAGCTGTG	CTGACCCCTG	CACCTTGAC	GGCCACCTCT	TGTGTGCAAG	TGGAGCTGTG	1560
	CTTTGCTTAC	AACCAGAGTG	CGGGGAACCC	CAACTACAGG	GGAAACATCA	CCCTGGCCTA	1620
20	CACCTCTGGG	GCTGACAGG	ACCGCGGCC	GCCCCGGCTC	CGCTTTGCGG	GCAGTGAGTG	1680
	CGCTGTCTTC	CACGGCTTCT	TCTCCATGCC	CGAGATGCGC	TGCCAGAAGC	TGGAGCTGCT	1740
	CCTGATGGAC	AACTCCGGTG	ACAACTCCG	CCCCATCATC	ATCTCCATGA	ACTACTCTTT	1800
	ACCTTTGGGG	ATGCCGATG	GCCCCGGCT	GGGGCTGGGG	TCCCTGGAGC	CCTACCCGAT	1860
	CCTCAACAGG	GCACAGGCTC	TGGAGAACCA	CACCTGAGTC	CAGTCCAGGA	AGGAGTGGGG	1920
25	GCCTGACAA	AAGTGTGAG	GCAACTTGCA	GATGCGGGCA	GCCTTCGTGT	CAGAGCAGCA	1980
	GCAGAGCTG	AGCAGGCTCC	AGTACAGCAG	AGACGTCGGG	AAATTGCTCC	TGAGCATCAA	2040
	CGTGACGAAC	ACCCGAGCTC	CGGAGGCTCT	CGGGAGGAGC	GCCACAGAGG	CGCTGCTCAC	2100
	CCTGGTGGTG	CTCCCGGCTC	TGCTGTGTGC	CTCAGTGCGC	CCCCCGGGGG	CCTGCCAAGC	2160
	TAATGAGAAC	ATCTTTTGGG	AGCTGGGGAA	CCCCCTCAAA	CGGAACAGGA	GGATGAGAGT	2220
30	GCTCATCGCC	TTTGAAGTCA	TGGGGGTGAC	CCTGCACACA	AGGGACCTTC	AGGTGCAGCT	2280
	GCAGCTCTCC	ACGTGAGTTC	ACCAGGACAA	CCGTGGGCCC	ATGATCTCTA	CTCTGCTGTT	2340
	GGACTATACA	CTCCAGACCT	CGCTTAGCAT	GGTAATCAAC	CGGCTACAAA	GCCTCTTTGG	2400
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35	AGGTCTGGAG	TGGCCCTAGC	AAGTCAGCAA	TGGCAAGTGG	CTGCTGTATC	CCACGGAGAT	2580
	CACCGTCCAT	GGCAATGGGT	CCTGGCCCTG	CGAACCACTC	GGAGACCTTA	TCAACCTCTC	2640
	CAACCTCACT	CTTCTGAC	CTGGGACAG	GCCATCATCC	CCACAGCGCA	GGGCGCGACA	2700
	GCTGGATCCA	GGGGGAGGCG	AGGGCCCCC	ACCTGTCACT	CTGGCTGCTG	CCAAAAAAGC	2760
	CAAGTCTGAG	ACTGTCTGAG	CCTGTGCCAC	AGGGCGTGCC	CACCTGTGTT	GGCTAGAGTG	2820
40	CCCCATCCCT	GATGCCCCCG	TTGTACCCAA	CGTGACTGTG	AAGGCACGAG	TGTGGAAACG	2880
	CACCTTCATC	GAGGATTACA	GAGACTTTGA	CGAGTCCGGG	GTAAATGGCT	GGGCTACCTC	2940
	ATTCTCTCCA	ACCAGCATCC	CCACCATCAA	CATGGAGAAC	AAGACCACGT	GGTCTCTGTT	3000
	GGACATTGAC	TGGAGCTGG	TGGAGGAGCT	GCCGGCCGAA	ATCGAGCTGT	GGCTGGTGCT	3060
	GGTGGCCGTG	GGTGACAGGC	TGCTGTGCT	GGGGCTGATC	ATCCTCTCTG	TGTGGAAGTG	3120
45	TGACTCTCTT	AAGCGGACCC	GCTATTATCA	GATCATGCCC	AAGTACCACG	CAGTGGGGAT	3180
	CCGGGAGGAG	GAGCGCTACC	CACCTCCAGG	GAGCACCCCTG	CCCAACAGGA	AGCACTGGGT	3240
	GACCAGCTGG	CAGACTCGGG	ACCAATACTA	CTGACGTCTC	CCTGATCC	ACCCCTCTCT	3300
	CCCCCAGTGT	CCCCCTTCTT	CCTATTATAT	ATAAGTTATG	CCTCTGACAG	TCCACAGGGG	3360
	CCACCACCTT	TGGCTGGTAG	CAGCAGGCTC	AGGCACATAC	ACCTCGTCAA	GAGCATGCAC	3420
50	ATGCTGTCTG	GCCCTGGGGA	TCTTCCACCA	GGAGGGCCAG	CGCTGTGGAG	CTTACAAACG	3480
	CGAGTGCAC	GCATTCCTGT	GCCCTAGATG	CAGTGGGGG	CCACTGCTCG	TGGAGCTGTC	3540
	TGGTGATCA	CGGATGGTGC	ATGGGCTGCG	CGTGTCTCAG	CCTCTGCCAG	CGCCAGCGCC	3600
	AAAACAAGCC	AAAGAGCCTC	CCACCAGAGC	CGGAGGAAA	AGGCCCCCTG	AATGTGTGTA	3660
	CACCTCCCTT	TTACACCTGT	GATCCATCTT	GAGAGGCACA	GTCACTGGAT	TGACTTTGCT	3720
55	GTCAAAACTA	CTGACAGGGA	GCAGCCCCCG	GGCCGCTGGC	TGGTGGGCCC	CCAATTGACA	3780
	CCCATGCCAG	AGAGGTGGGG	ATCCTGCCTA	AGGTTGTCTA	CGGGGGCACT	TGGAGGACCT	3840
	GGGTGTCTCA	GACCCAAACG	CAAGGAAGCT	AGAAAGAGG	ACCCAGAAGG	CTTGTCTTTT	3900
	TGCATCTCTG	TGAAGCCTCT	CTCCTTGCC	ACAGACTGAA	CTCGCAGGGA	GTGCAGCAGG	3960
	AAGGAACAAA	GACAGGCAAA	CGGCAACGTA	GCCCTGGGCTC	ACTGTGCTGG	GGCATGGCGG	4020
60	GATCCTCCAC	AGAGAGGAGG	GGACCAATTC	TGGACAGACA	GATGTTGGGA	GGATACAGAG	4080
	GAGATGCCAC	TTCTCACTCA	CCACTACCAG	CCAGCCTCCA	GAAGGCCCCA	GAGAGACCTC	4140
	GCAAGACCAC	GGAGGGAGCC	GACACTTGAA	TGTAGTAATA	GGCAGGGGGC	CCTGCCACCC	4200
	CATCCAGCCA	GACCCAGCT	GAACCATGCG	TCAGGGGCT	AGAGGTGGAG	TTCTTAGCTA	4260
	TCCTTGGCTT	TCTGTGCCAG	CCTGGCTCTG	CCCCCCCC	ATGGGCTGTG	TCCTAAGGCC	4320
65	CATTGTAGAA	GCTGAGGCTA	GTTCCAAAAA	OCTCTCTGA	CCCCTGCTGG	TTGGCAGCCC	4380
	ACTCCCCAGC	CCGAGCCCTT	TCCATGGTAC	TGTAGCAGGG	GAATTCCCTC	CCCTCCTCTG	4440
	TGCCCTCTTT	GTATATAGGC	TTCTCACCCG	GACCAATAAA	CAGCTCCAG	TTTGT	

Seq ID NO: 148 Protein sequence

Protein Accession #: NP_005492.1

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	QTERQQRLL	LAPAPRELAV	PDGYTNRTGA	VYLCPLTAHK	DDCERMNITV	KNDPGHIIIE	120
75	DMWLGTVAS	GGPAGRVLC	ABRYTQVLMS	GSEDQRRMVG	KCYVRGNLIE	LDSSDDWQTY	180
	HNEMCNSTND	YLETGMCQGL	TSGGFTQNTV	YFAGPAGYNN	KGNYSYMIQRK	EWDLSEYSYK	240
	DFEDQGLYI	GYTHQVGSFI	LHPKNITIVT	GAPRHRHMG	VFLLSQEAGG	DLRRQVLEGG	300
	SGVGAIFGSA	LALADLNNDG	WQDLLVGAPY	YFERKEEVGG	AIYVFMNQAG	TSFPAHPSLL	360
	LEGPSSGAPG	LSVASIGDIN	QDGPQDIAGV	APFEGGLKVY	IYHSSSKGLL	RQPPQVHIGE	420
80	KLGLPGLATF	GYSLSGQMDV	DENFYPDLLV	GSLSDRHIVL	RARPVINIVH	KTLPVPRPAVL	480
	DPALCTATSC	QVVELCFAYN	QSAGNPNYRR	NITLAYTLEA	DRDRRPPRLR	PAGESAVFVH	540
	GFFSNPMEIRC	QKLELLLMON	LRDKLRPIII	SMNYSPLFRM	PDRPRLGLRS	LDAYPIINQA	600
	QALENHTVEQ	PKRECGPDNK	CESNLQMRRA	FVSEQQQKLS	RLQYSRDRVK	LLLSINVTNT	660
	RTSERSGEDA	HEALLTLVVP	PALLLSVSRP	PGACQANETI	PCELGNPFFKR	NQRMELLIAP	720
	EVIGVTILHTR	DLQVQLQLST	SSHQDNLWPM	ILTLVDVYTL	QTSLSMVNHR	LQSPFGGTVM	780
85	GESGMKTVED	VGSPLKYERQ	VGPMGEGLVG	LGTLVLGLEW	PYEVSNGRWL	LYPTEITVHG	840

NGSWPCRPPG DLINPLNLT SDPDRPSSP QRRRQLDPG GGQPPPVTL AAARKAKSET 900
VLTCATGRAH CUVLBCPIPD APVVTNVTVK ARVWNSTFIE DYRDFDRVRV NGWATLFLRT 960
SIFTINMENK TWFSDVIDS ELVEELPAEI ELWLVLVAVG AGLLLGLII LLLWKDFPK 1020
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Seq ID NO: 149 DNA sequence
Nucleic Acid Accession #: NM_006424.1
Coding sequence:

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AACACTGAGG	CACCTGTAA	CAAGATTGAA	CTTCTGCCGT	CCTACTCCAC	GGCTACACTG	240
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AGGCGCTTCC	AGCTGGTGG	AGGAAAAATG	GCAGGACAGT	TCTTCAGCAA	CAGCTCTATT	480
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TCACGACCTT	CAAGTCCAT	CGTTGTGAGC	ATGGTGTCTT	CTTCATTGCT	CAGTGTTCGG	600
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AATGTGACCT	ACAGGAGGAA	CATCGCCAAA	TGCCAGCATA	TCTTTGTGAA	TTTCCACCTC	1140
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GCCTGGACT	CAAGACCGGA	ATGCACGGCC	TTGTAGGGGA	CGCCCCAGAT	TGTCAGGGAT	2160
GGGGGATGG	TCCTTGAGTT	TTGCATGCTC	TCCTCCCTCC	CACCTCTGCA	CCCTTTCACC	2220
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Protein Accession #: NP_006415.1

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DEPTEVDPPW	NLPTLQDSGI	KHSERDTKXK	ILCFPGIGR	LILLGLFLYF	PVCSLDILSS	120
AFQLVGGKMA	GGFFNSNISM	SNPLGLLVIG	VLVTVLVQSS	STSTSIIVSM	VSSLLTVRA	180
AIPIINGANI	GTSTNTIVA	LMQVDRSEF	RRAPAGATVH	DFPNWLSVLV	LLPEVATHY	240
LEIITQLIVE	SPHFNGSDA	PDLLKVITKP	FTKLIVQLDK	KVISQIAMND	ERAKNKSIVK	300
IMCKTPTNKT	QINVTVPSTA	NCTSPSLCWT	DGIQNTWTKN	VTYKENIAKC	QHPVNFHPL	360
DLAVGTILLI	LSLLVLOGCL	IMIVKILGSV	LKGQVATVIR	KTINTDFPPP	PAWLTVGLAI	420
LVGAGMTPIV	QSSSVFTSAL	TPLIGIGVIT	IERAYPLTLG	SNIGTTTTAI	LAALASPGNA	480
LRSLQIALC	HPFFNISGIL	LMYPIPFTRL	PIRMAKGLGN	ISAKYRWFAV	FYLIIFPFLI	540
PLTVFGLSLA	GWRVLVGVGV	PVFPILILVL	CLRLLQSRCP	RVLPRKLQNW	NFLPLWMSRL	600
KPWDVAVSKP	TGCPQMRCCY	CCRVCCRAC	LLOCGPKCCR	CSKCCEDLEE	AQEGQDVFPK	660
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Nucleic Acid Accession #: 1..1119
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GGCTATGCAG	ACATCCATGG	AGACTTACTA	CCTATAAATA	ATGATGATAA	TTATCACAAA	240
GCTGTTCCAA	CGGCCAATCC	ACTGCTTAGG	ATATTATATC	AAAAGAAGGA	AGAAGCAGAC	300
TACAGTGCTT	TGGTACAGGA	CACGCTAATA	AAGAAGAAGA	ATGTTTAAAC	CAACGTATTG	360
COTCTGACA	ACCATAGAAA	AAAGCCACAT	ATAGTCATTA	GTATGCCCCA	AGACTTTAGA	420
CTGTGTCTT	CTATTATAGA	CGTGATATT	CTCCAGAAA	CGCATCGTAG	GGTACGCTCT	480
TACAAATAG	GCACGAGAGA	ACCCCTAGGA	TTCTACATCC	GGGATGGCTC	CAGTGTGAGG	540
GTAACACAC	ATGGCTTAGA	AAAGGTTCCA	GGGATCTTTA	TATCCAGGCT	TGTCCAGGGA	600
GGTCTGGCTC	AAAGTACAGG	ACTATTAGCT	GTTAATGATG	AAGTTTGAAG	AGTTAATGGC	660
ATAGAAGTTT	CAGGGAAGAG	CCTTGATCAA	GTAACAGACA	TGATGATTGC	AAATAGCCGT	720
AACCTCATCA	TACAGTGAG	ACCGGCAAAC	CAGAGGAATA	ATGTTGTGAG	GAACAGTCGG	780
ACTTCTGGCA	GTTCCGGTCA	GTCTACTGAT	AACAGCCTTC	TTGGCTACCC	ACACAGATT	840

GAACCAAGCT TTGAGCCAGA GGATGAAGAC AGCGAAGAAG ATGACATTAT CATTGAAGAC 900
 AATGGAGTGC CACAGCAGAT TCCAAAAGCT GTTCCTAATA CTGAGAGCCT GGAGTCATTA 960
 ACACAGATAG AGCTAAGCTT TGAGTCTGGA CAGAATGGCT TTATTCCTTC TAATGAAGTG 1020
 AGCTTAGCAG CCATAGCAAG CAGCTCAAAC ACGGAATTG AAACACATGC TCCAGATCAA 1080
 AACTCTTAG AAGAAGATGG AACAAATCATA ACATTATGA

Seq ID NO: 152 Protein sequence
 Protein Accession #: XP_030559

1 11 21 31 41 51
 | | | | |
 MNRSHRHGAG SGCLGTMEVK SKFGAEFRFP SLERSKPGKP EEFYGLLOHV HKIFNVDLV 60
 GYADIHGDL PINNDNYHK AVSTANPLLR IFIQKKEAD YSAFGDTLI KKNVLTNVL 120
 RPDNHRKPH IVISMPODFR PVSSIIDVDI LPETHRRVRL YKYGTETPLG FYIRDGSSVR 180
 VTPHGLEKVP GIFISRLVPG GLAQSTGLLA VNDELEVNG IEVSGKSLDQ VTDMMIANSR 240
 NLIITVRPAN QRNNVVRNSR TSGSSGQSTD NSLLGYFQQI EPSFEPEDSD SEEDIIIED 300
 NGVEQQIPKA VPNTESLESL TQIELSFESG QNGFIPSNEV SLAAIASSN TEFETHAPDQ 360
 KLLSEDTII TL

Seq ID NO: 153 DNA sequence
 Nucleic Acid Accession #: NM_003064.2
 Coding sequence: 23..421

1 11 21 31 41 51
 | | | | |
 CAGAGTCACT CCTGCCCTCA CCATGAAGTC CAGCGGCCTC TTCCTCTCC TGGTGCTGCT 60
 TGCCCTGGGA ACTCTGCCAC CTCTGGCTGT GGAAGGCTCT GGAAGTCTCT TCAAAGCTGG 120
 AGTCTGTCTC CCTAAGAAAT CTGCCAGATG CTTAGATATC AAGAAACCTG AGTGCCAGAG 180
 TGACTGGCAG TGTCCAGGGA AGAAGAGATG TTGTCTGAC ACTTGTCGCA TCAAATGCCT 240
 GGATCTCTGT GACACCCCAA ACCCAACAAG GAGGAAGCCT GGAAGTGCC CAGTGACTTA 300
 TGGCCAATGT TTGATGCTTA ACCCCCCCAA TTTCTGTGAG ATGGATGACC AGTGCAAGCG 360
 TGACTTGAAG TGTTCATGCG GCATGTGTGG GAAATCTCTG GTTTCCTCTG TGAAGCTTGG 420
 ATTCTTGCCA TGTCAGGAGG GCTCTGGAGT CCTGCTCTGT GTGGTCCAGG TCCTTTCCAC 480
 CCTGAGACTT GGCTCCACCA CTGATATCCT CCTTTGGGGA AAGGCTTGGC ACACAGCAGG 540
 CTTTCAAGAA GTGCCAGTTG ATCAATGAAT AAATAAACGA GCCTATTCTT CTTTGCCAC

Seq ID NO: 154 Protein sequence
 Protein Accession #: NP_003055.1

1 11 21 31 41 51
 | | | | |
 MKSSGLFPPL VLLALGTLAP WAVEGSGKSF KAGVCPPKKS AQCLRYKKPE QSDWQCPGK 60
 KRCCPDTCGI KCLDPVDTFN PTRRRPGKCP VTYGQCLMLN PPNFCMDGQ CKRDLKCCMG 120
 MCGKSCVSPV KA

Seq ID NO: 155 DNA sequence
 Nucleic Acid Accession #: NM_001306.1
 Coding sequence: 199..861

1 11 21 31 41 51
 | | | | |
 AATTCGCAC GAGGGCAGGT GCAGGCACAC GCGGCGAGAG GGTATGGAGC GAGCCGTTA 60
 GCGGCGGCGG TCGGTGAGTC AGTCCGTCG GCGTCCGTC GGTGCGGGG CCGCAGCTCC 120
 GCGCAGGCCC AGCGGCCCCG GCCCTCTGTC TCCCGGCACC GCGAGCCACC CGGTGGAGCG 180
 GGCTTGGCG CGGCAGCCAT GTCCATGGGC CTGGAGATCA GGGGACCCG GCTGGCGGTG 240
 CTGGGCTGGC TGGGCACCAT CGTGTGCTGC GCGTTGCCA TGTGGCGCGT GTCGGCTTC 300
 ATCGGCAGCA ACATATCAC GTGCGAGAAC ATCTGGGAGG GCCTGTGGAT GAACTGGGTG 360
 GTGCAGAGCA CGGCCAGAT GCAGTGCAAG GTGTAGGACT CGTGTGTCG ACTGCCACAG 420
 GACCTTCAGG CGGCGCGCGC CCTCATGCTG GTGGCCATCC TGTGGCGCG CTTGCGGCTG 480
 CTAGTGGCGC TGGTGGCGCG CCAATGACAC AACTGCGTGC AGGACGACAC GGCCAAGGCC 540
 AAGATCACCA TCGTGGCAGG CGTGTGCTTC CTCTGCGCG CCCTGCTCAC CCTCGTGGCG 600
 GTGTCTGTGT CGGCCAACAC CATTATCCCG GACTTCTACA ACCCGTGGT GCCCGAGGCG 660
 CAGAGCGCGG AGATGGGCGC GGGCCTGTAC GTGGGCTGGG GCGCGCGCGC GCTGCAGCTG 720
 CTGGGGGCGG CGTGTCTCTG CTGCTCGTGT CCCCAAGCGG AGAAGAAGTA CACGGCCACC 780
 AAGGTCTGCT ACTCCGCGCC GCGCTCCACC GCGCCGGGAG CCAGCCTGGG CACAGGCTAC 840
 GACCGCAAGG ACTACGTCTA AGGGACAGAC GCAGGAGAGC CCCACCAACA CCACCACTAC 900
 CAACACCACC ACCACCAAGG CGAGCTGGAG CGGCAACAGG GGCATCCAGC GTGCAGCTTT 960
 GCCTCGGAGG CCAGCCCAAC CCCAGAAGCC AGGAAGCCCC CGCGCTGAGC TGGGGCAGCT 1020
 TCCCCAGCAG CCACGGCTTT GCGGGCGCGG CAGTCGACTT GCGGGCCAGG GGACCAACCT 1080
 GCATGGACTG TGAACCTCA CCCTTCTGGA GCAAGGGGCC TGGGTGACCG CCAATACTTG 1140
 ACCACCCCGT CGAGCCCATG CGGGCGCGTG CCCCCATGTC GCGCTGGGCA GGGACCGGCA 1200
 GCCCTGGAAG GGGCACTTGA TATTTTTCAT TAAAGCCTC TCGTTTATAG

Seq ID NO: 156 Protein sequence
 Protein Accession #: NP_001297.1

1 11 21 31 41 51
 | | | | |
 MSMGLEITGT ALAVLGLWLT IVCCALPMWR VSAFIGSNII TSQNIWEGLW MNCVQSTGQ 60
 MQCKVYDSL ALPQDLQAAR ALIVVAILLA AFGLLVALVG AQCTNCVQDD TAKAKITIVA 120
 GVLFLLAALL TLVPSWSAN TIIRDYPNPV VPEAQKREMG AGLYVGWAAA ALQLLGALL 180
 CCSPPREKK YTATKVVSVA PRSTGPGASL GTGYDRKDVV

Seq ID NO: 157 DNA sequence
 Nucleic Acid Accession #: NM_005564
 Coding sequence: 1..597

1 11 21 31 41 51
 | | | | |
 ATGCCCTAG GTCTCCTGTG GCTGGGCCTA GCGCTGTGTG GGGCTCTGCA TGCCCAAGGCC 60
 CAGGACTCCA CCTCAGACCT GATCCAGACC CCACCTCTGA GCAAGGTCCC TCTGCAGCAG 120

AACTTCCAGG ACAACCAATT CCAGGGGAAG TGGTATGTGG TAGGCCTGGC AGGGGAATGCA 180
 ATTCTCAGAG AAGACAAAGA CCGGCAAAAG ATGTATGCCA CCATCTATGA GCTGAAAGAA 240
 GACAAGAGCT ACAATGTCAC CTCGGTCCTG TTTAGGAAAA AGAAGTGTGA CTACTGGATC 300
 AGGACTTTTG TTCCAGGTTG CCAGCCCGGC GAGTTCACGC TGGGCAACAT TAAGAGTTAC 360
 CCTGGATTAA CGAGTTACCT CGTCCGAGTG GTGAGCACCA ACTACAACCA GCATGCTATG 420
 GTGTCTTTCA AGAAAGTTTC TCAAAACAGG GAGTACTTCA AGATCACCTT CTACGGGAGA 480
 ACCAAGGAGC TGACTTCGGA ACTAAAGGAG AACTTCATCC GCTTCTCCAA ATATCTGGGC 540
 CTCCTGAAA ACCACATCGT CTTCCCTGTC CCAATCGACC AGTGTATCGA CGGCTGA

Seq ID NO: 158 Protein sequence
 Protein Accession #: NP_005555

1 11 21 31 41 51
 | | | | |
 MPLGLMLLGL ALLGALHAQA QDSTSDLIPA PPLSKVPLQQ NFQDNQFQGR WYVVGLAGNA 60
 ILREDKDPQK MYATTIYELKE DKSYNVTSVL FRKKKCDYWI RTPVPGQCPG EFTLGNIKSY 120
 PGLTSYLVVRV VSTNYNQHAM VFFKKVSNR EYFKITLYGR TKELTSELKE NFIRPSKYLK 180
 LPENHIVFPV PIDQCIDG

Seq ID NO: 159 DNA sequence
 Nucleic Acid Accession #: NM_006853.1
 Coding sequence: 26..874

1 11 21 31 41 51
 | | | | |
 AGGAATCTGC GCTCGGGTTC CGCAGATGCA GAGGTTGAGG TGGCTGCGGG ACTGGAAGTC 60
 ATCGGGCAGA GGTCTCACAG CAGCCAAGGA ACCTGGGGCC CGCTCCTCCC CCTCCAGGC 120
 CATGAGGATT CTGCAGTTAA TCCTGCTTGC TCTGGCAACA GGGCTTGTAG GGGGAGAGAC 180
 CAGGATCATC AAGGGGTTCC AGTGCAAGCC TCATCTCCAG CCTGGCAGG CAGCCCTGTT 240
 CGAGAAGACG CGGCTACTCT GTGGGGCGAC GCTCATCGCC CCCAGATGGC TCCTGACAGC 300
 AGCCCACTGC CTCAGCCCC GCTACATAGT TCACCTGGGG CAGCACAACC TCCAGAAGGA 360
 GGAGGGCTGT GAGCAGACCC GGACAGCCAC TGAGTCTTTC CCCACCCCG GCTTCAACAA 420
 CAGCCTCCCC AACAAAGACC ACCGCAATGA CATCATGCTG GTGAAGATGG CATCGCCAGT 480
 CTCATCACC TGGGCTGTGC GACCCCTCAC CCTCTCTCA CGCTGTGTCA CTGCTGGCAC 540
 CAGCTGCTTC ATTTCCGGCT GGGGCGACAC GTCCAGCCCC CAGTTACGCC TGCTCTACAC 600
 CTTGGATGC GCCAATCA CAATCATTGA GCACCAAGAG TGTGAGAAGC CCTACCCCGG 660
 CAACATCACA GACCCATTGG TGTGTGCCAG CGTGACAGAA GGGGGCAAG ACTCCTGCCA 720
 GGGTGACTCC GGGGGCCCTC TGGTCTGTAA CCAGTCTCTT CAAGGCAITTA TCTCCTGGGG 780
 CCAGGATCCG TGTGCGATCA CCCGAAAGCC TGGTGTCTAC ACGAAAGTCT GCAATATATG 840
 GGACTGGATC CAGGAGACGA TGAAGAACAA TTAGACTGGA CCCACCCACC ACAGCCCATC 900
 ACCCTCCATT TCCACTTGGT GTTTGGTTCG TGTTCACCTG GTTAATAAGA AACCTTAAGC 960
 CAAGACCCTC TAAGAACATT CTTTGGGCCCT CCTGGACTAC AGGAGATGCT GTCACTTAAT 1020
 AATCAACCTG GGGTTCGAAA TCAGTGAGAC CTGGATTCAA ATTCTGCCTT GAAATATTGT 1080
 GACTCTGGGA ATGACACAC CTGGTTTGT CTCTGTGTGA TCCCCAGCCC CAAAGACAGC 1140
 TCCTGGCCAT ATATCAAGGT TTCAATAAAT ATTTGCTAAA TGAGTG

Seq ID NO: 160 Protein sequence
 Protein Accession #: NP_006844.1

1 11 21 31 41 51
 | | | | |
 MRILQLILLA LATGLVGSET RIINGFECKP HSQPMQALF EKTRLLCGAT LIAPRWLLTA 60
 AHCLKPRYIV HLGQHNLQKE EGCEQTRTAT ESPFHPGFNN SLPNKDHEND IMLVKMASPV 120
 SITWAVRPLT LSSRCVTAGT SCLISGWGST SSPQLRLPHT LRCANITIIIE HQKCNAYPG 180
 NITDTMVCAS VQEGGKDSQC GDSGGPLVCN QSLQGIISWG QDPCAITRKP GVYTRVKRYV 240
 DWIQTMMKN

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

- 1 1. A method of detecting an ovarian cancer-associated transcript in a cell
2 from a patient, the method comprising contacting a biological sample from the patient with a
3 polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence
4 as shown in Tables 1-26.
- 1 2. The method of claim 1, wherein the biological sample comprises
2 isolated nucleic acids.
- 1 3. The method of claim 2, wherein the nucleic acids are mRNA.
- 1 4. The method of claim 2, further comprising the step of amplifying
2 nucleic acids before the step of contacting the biological sample with the polynucleotide.
- 1 5. The method of claim 1, wherein the polynucleotide comprises a
2 sequence as shown in Tables 1-26.
- 1 6. The method of claim 1, wherein the polynucleotide is immobilized on
2 a solid surface.
- 1 7. The method of claim 1, wherein the patient is undergoing a therapeutic
2 regimen to treat ovarian cancer.
- 1 8. The method of claim 1, wherein the patient is suspected of having
2 ovarian cancer.
- 1 9. An isolated nucleic acid molecule consisting of a polynucleotide
2 sequence as shown in Tables 1-26.
- 1 10. The nucleic acid molecule of claim 9, which is labeled.
- 1 11. An expression vector comprising the nucleic acid of claim 9.
- 1 12. A host cell comprising the expression vector of claim 11.
- 1 13. An isolated polypeptide which is encoded by a nucleic acid molecule
2 having polynucleotide sequence as shown in Tables 1-26.

- 1 14. An antibody that specifically binds a polypeptide of claim 13.
- 1 15. The antibody of claim 14, further conjugated to an effector component.
- 1 16. The antibody of claim 15, wherein the effector component is a
2 fluorescent label.
- 1 17. The antibody of claim 15, wherein the effector component is a
2 radioisotope or a cytotoxic chemical.
- 1 18. The antibody of claim 15, which is an antibody fragment.
- 1 19. The antibody of claim 15, which is a humanized antibody
- 1 20. A method of detecting an ovarian cancer cell in a biological sample
2 from a patient, the method comprising contacting the biological sample with an antibody of
3 claim 14.
- 1 21. The method of claim 20, wherein the antibody is further conjugated to
2 an effector component.
- 1 22. The method of claim 21, wherein the effector component is a
2 fluorescent label.
- 1 23. A method for identifying a compound that modulates an ovarian
2 cancer-associated polypeptide, the method comprising the steps of:
3 (i) contacting the compound with an ovarian cancer-associated polypeptide,
4 the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least
5 80% identical to a sequence as shown in Tables 1-26; and
6 (ii) determining the functional effect of the compound upon the polypeptide.
- 1 24. A drug screening assay comprising the steps of
2 (i) administering a test compound to a mammal having ovarian cancer or a cell
3 isolated therefrom;
4 (ii) comparing the level of gene expression of a polynucleotide that selectively
5 hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26 in a

- 6 treated cell or mammal with the level of gene expression of the polynucleotide in a control
7 cell or mammal, wherein a test compound that modulates the level of expression of the
8 polynucleotide is a candidate for the treatment of ovarian cancer.